

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: DOUGLAS SMITH
- (ii) TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
- (iii) NUMBER OF SEQUENCES: 880
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LAHIVE & COCKFIELD
 - (B) STREET: 60 State Street, Suite 510
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109-1875
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/487,032
 - (B) FILING DATE: 07-JUNE-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Mandragouras, Amy E.
 - (B) REGISTRATION NUMBER: 36,207
 - (C) REFERENCE/DOCKET NUMBER: GTN-001
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617)227-7400
 - (B) TELEFAX: (617)227-5941

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1527 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGTGTTCTC AGGAAATTTT ATCAAGCTTG CAAACCATTA TTGCCGAACA ATTTTCTATA	60
AATATCATCA CTCAGCTTGC TAATAAACTC ACACAAGTTA AAAATCTAAA TTTTTTTGAG	120
AATAAAGACC ATACTATCAA GCTTAACACT ATCCATAACG GACTGCACAT CCGCCCCCTA	180
AATTATGTCA GTAATCTTTT TTTCAATCTA CAACGCATTA TAGGGCTTAT CAGTCTGTTT	240
GGGATATTAT TTTCCATTAG TATTTATCTA CCCTTTATAA TGATTTTTGC AACAGTGCCT	300
TGTATTCTCA TTTCCAACCA TATAGCAAAA AAACATAGTG CTTCCATAGA TAAACTTCAA	360
GACCAAAAAG AAAGCATGCA AAATTACTTA TACTCTGGAC TAGATAACCA AAAGAACAAG	420
GACAACCTAT TATTTAACTT CATGCTAAAT TTTCACCATA AATTTATTGA AACAAAAGAA	480
TTGTATCTCA ATAATTTTGT GAAAGTAGCC CAAAAAACT TAATATTTAC CATATATGCT	540
GATGTTTTAA TCACCACTCT AAGTATTGCA CTATTTTTTC TAATGGTTTT TATTATCCTT	600
TCAAAATTAA TTGGTGTGGG AGCAATTGCT GGGTATATCC AAGCATTTAG CTCTACCCAA	660
CAACAACTAC AAGATTTATC ATTTTATGGA AAGTGGTTTT TTGCTATCAA TAAATACTTT	720
GAAAATTATT TCTGTATTTT AGATTACAAA ATACCGAAAC CAGAAACACA AATCAAATTA	780
GAAGAAAAAA TCCATAGCAT TACATTTGAA AATATTAGTT TCTCTTATCC TAATTCAAAA	840
CTTATTTTTG AAAACTTTAA TCTCTCTTTA CACTCTAATA AAATTTATGC ATTAGTCGGC	900
AAGAATGCTA GCGGAAAAAG CACGCTGATT AATTTATTAT TAGGTTTTTA TACCCCAAAT	960
TCAGGTCAAA TTATCATTA TAACAAATAC CCATTACAAG ACTTGGAAC AAATAGCTAC	1020
CATCAACAAA TGAGTGCCAT ATTTCAAGAT TTTTCTCTTT ATGCTGGGTA TAGCATTGAT	1080
GATAATCTTT TTATGCAAAA CAATATCACT AAAGAGCAAT TGAAGCAAAA AAGAGAAATA	1140
CTAAAATCTT TTGATGAGAA TTTTCAAAAT TGTCTTAATG ATTGCAACAA CACACTATTT	1200
GGAGCGCAAT ATAATGGGGT AGATTTTTCT TTAGGTCAAA AGCAACGCAT AGCTACCATG	1260
AGAGCCTTTT TAAAACCAAG TAATTGCATT GTTTTAGATG AGCCAAGCAG CGCCATCGAT	1320
CCCATTATGG AAAAAGAGTT TTTAGATTTT ATTTTAAAA AATCGCAATC TAAGATGGCT	1380
TTAATTATTA CACACCGCAT GAATAGTGTC AAGCAAGCTA ATGAAATTAT CGTGTTAGAT	1440
CAAGGCAAAC TAATAGAACA GGGCAACTTT GAAACCCTTA TGAAAAACA GGGATTATTT	1500
TGCGAATTGT TTTTGAAACA ACAATAC	1527

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGAGCGCA AGACGCTCCA GAGCATTTTA TGTTTAATAA AAAAAGAAAT GATGAGACCA	60
AAAGGTATTC TAATGAATTG TTGCAGGSCT TGGAAACACC AGGTTCTTAA GCAAAGCACG	120
ACAGGTTTAG TGGTGTGAG CATTATCTCT TCTACAGCCC CCTTTATTGG TTTGTTTGGG	180
ACGGTAGTTG AAATTTTAGA AGCGTTTAAC AATTTGGGCG CGTTAGGTCA AGCTTCTTTT	240
GGAGTGATCG CACCCATTAT TTCTAAGGCG CTTATCGCCA CCGCTGCAGG GATTTTAGCA	300
GCCATTCCAG CCTATTCTTT TTAATTGATC TTAAAGCGCA AGGTGTATGA TTTATCGGTT	360
TATGTGCAGA TGCAAGTGGA TATTTTGTCT TCTAAAAA	399

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGCATGAAC GCATTGAAAG AGGTATTRGA AATAATGAAT GTAAAGAAAT TTTTGGCAAT	60
GAACTCAAAC AAAGAAAGAC AAAATTGATT GAAGACATAG AACGGCGGTT CAAAGAATGC	120
GAGGAACAAT TCCGTGGAAG TGTAGGAAAA AATATTGAAC AACTTGAAGA AAGAGTTAAA	180
GATTCTCTAG CGATTATAAA ACGCATCAAT AACCTTGGTC TTAATCCTAA TTCTAATTTT	240
AATATGGATA GCGGCATTGA TACAATAGGC TTATTTAGTT CAATAGGAGG TTTGGTGTG	300

CTTCTATTGA CGCCTGTAGT AGGTGAGTTT GCGTTAATTG CAGGAGTGGG TTTAGCATT	360
GTGGGGGTAG GTAAATCAAT ATGGAGTTTT TTTGATTCAG ATTATAAAAA ATCCCAACAA	420
AGAAAAGAAG TGGATAAGAA TTTACATCAA ATTTGCGAAA AATTGTGCAG GATG	474

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGCCTGGCG TGTATCAAAT GAGTATAGAG CCTCTTTTAA AAGAATGCGA AGAATTAGTG	60
GGTTTAGGCA TAAAAGCCGT TTTATTGTTT GGCATTCTTA AACATAAGGA CGCTACAGGA	120
AGCCATGCGT TAAATAAGGA TCACATTGTC GCAAAAGCTA CGAGAGAAAT TAAAAACGA	180
TTTAAGGATT TGATCGTTAT AGCGGATTG TGTTTTTGCG AATACACCGA CCATGGGCAT	240
TGCGGGATTT TAGAAAACGC TTCTGTGTCT AACGATAAAA CGCTAAAGAT TTAAATCTT	300
CAAGGGCTTA TTTTGCTGAA AGCGGTGTGG ATATTC	336

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION: 1...195
 (D) OTHER INFORMATION: /note= "FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 HAP1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTGGAAAACA ACAAGAGTTT AAAGCATGCG AATGAGTTAA GGGATAAGCG AGATGAATTA	60
GAGTTTCATT TCGGAGAGCT TTTCGGGGGG AATGTTTTTA AAAGCAGCAT TAAAACCCAT	120
TCGCTCACAG ATAAAGACTC AGCGGACTTT GATGAGAGCT ATAACCTTAA TATCGGGCAT	180
GGGYTCAATA TSATA	195

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1857 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGTTTGTGG CAAGCAAACA AGCTGACGAA CAAAAAAGC TAGTTATAGA GCAAGAGGTT	60
CAAAAGCGGC AGTTTCAAAA AATAGAAGAA CTTAAAGCAG ACATGCAAAA GGGTGTCAAT	120
CCCTTTTTTA AAGTCTTGTT TGATGGGGGG AATAGGTTGT TTGGTTTCCC TGAAACTTTT	180
ATTTATTCTT CTATATTTAT ATTGTTTGTA ACAATTGTAT TATCTGTTAT TCTTTTTCAA	240
GCCTATGAAC CTGTTTTGAT TGTAGCGATT GTTATTGTGC TTGTAGCTCT TGGATTCAAG	300
AAAGATTACA GGCTTTATCA AAGAATGGAG CGAGCGATGA AATTAAAAA ACCTTTTTTG	360
TTTAAGGGCG TGAAAAACAA AGCGTTCATG AGCATTTTTT CcATGAAGCC TAGTAAAGAA	420
ATGGCTAATG ACATCCACTT AAATCCAAAC AGAGAAGACA GGCTTGTGAG CGCTGCAAAC	480
TCCTATCTAG CGAATAACTA TGAATGTTTT TTAGATGATG GGGTGATCCT TACTAACAAC	540
TATTCTCTTT TAGGCACAAT CAAATTGGGG GGCATTGATT TTTTAACCAC TTCCAAAAAA	600
GATCTCATAG AGTTACACGC TTCTATTTAT AGCGTTTTTA GGAATTTTGT TACCCCTGAA	660
TTCAAATTTT ATTTTCACAC TGTTAAAAAG AAAATCGTTA TTGATGAAAC CAATAGGGAT	720

TATGGTCTTA	TTTTTTCTAA	TGATTTTCATG	CGAGCCTATA	ATGAGAAGCA	AAAGAGAGAA	780
AGTTTTTATG	ATATTAGTTT	TTATCTCACC	ATAGAGCAAG	ATTTATTAGA	CACTCTCAAT	840
GAACCCGTTA	TGAATAAAAA	GCATTTTGCA	GACAATAATT	TTGAAGAGTT	TCAAAGGATT	900
ATTAGAGCCA	AGCTTGAAAA	CTTCAAAGAT	AGGATAGAGC	TCATAGAAGA	GCTACTGAGT	960
AAATACCACC	CCACTAGATT	AAAAGAATAC	ACTAAAGATG	GCATTATTTA	CTCCAAACAA	1020
TGCGAATTTT	ACAATTTTCT	TGTGGGAATG	AATGAAGCCC	CTTTTATTTG	CAACAGAAAA	1080
GACTTGATC	TCAAGGAAAA	AATGCATGGT	GGGGTGAAAG	AAGTTTATTT	TGCCAATAAG	1140
CATGGAAAAA	TCTTAAATGA	CGATTTGAGT	GAAAAATATT	TTAGCGCTAT	TGAGATCAGT	1200
GAATACGCC	CTAAATCACA	GAGCGATTTG	TTTGATAAAA	TCAACGCTCT	AGACAGCGAA	1260
TTTATCTTTA	TGCATGCTTA	TTCGCCTAAA	AACTCACAAG	TTTTAAAGGA	CAAAC TAGCT	1320
TTCACCTCTA	GAAGGATTAT	TATTAGTGGA	GGCTCCAAAG	AGCAAGGCAT	GACTTTGGGT	1380
TGCTTGAGCG	AATTAGTGGG	TAATGGTGAT	ATTACGCTAG	GCAGTTATGG	TAATTCTTTA	1440
GTGCTGTTTG	CTGATAGCTT	TGAAAAAATG	AAACAAAGCG	TTAAGGAATG	CGTCTCTAGT	1500
CTTAACGCTA	AAGGTTTTTT	AGCCAACGCA	GCGACTTTCT	CTATGGAAAA	TTACTTTTTT	1560
GCCAAACATT	GCTCTTTTAT	CACGCTTCCT	TTTATTTTTG	ATGTAACTTC	TAACAATTTT	1620
GCTGATTTCA	TAGCGATGAG	AGCGATGAGT	TTTGATGGCA	AAGAAGACAA	TAACGCTTGG	1680
GGCAATAGCG	TGATGACGTT	AAAAAGCGAG	ATCAATTCGC	CTTTTTATTT	GAACTTCCAC	1740
ATGCCCACTg	ATTTTG GTTC	AGCTTCAGCA	gGaCACACTT	TGATACTTGG	CTCAACCGGT	1800
TCAGGTAAGa	ACAGTGTTTA	TGTCCATGAC	TCTAAACGCT	ATGGGGCAAT	TTGCCTA	1857

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTGAAACAT CGTGTGTTGGT TACAATAGGG AGGATCCGGG GCGTTTTTAT CATTAAGGCG	60
CAGTTGTTGC TTCGTGAGGG AGGTTTTATG AATTTTACCG CTTATAACAC GAAGACGCCA	120
GGGCATTTGC ATTTGTATGT GCATAAGGGG CATACGGAAT TAGGCGAGGG TGAAAGGCTG	180
ATTAAACTT TATCCATGAA ATTAGCGCAA GGGTTGCCTA AAGAATGGAG GTTTTCCCT	240
AGCAATGAAT GGCCTAAGGA ATTTAATATT TTAGCTTTAC CTTATGAAGT GTTTGCAAAA	300
GAGCGCGGA GCTCTTGGGC GAAGCATTTA	330

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...204
 - (D) OTHER INFORMATION: /note= "H⁺-transporting ATP synthase alpha chain homolog"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGGCTAAAG ACATCATCAG CGAGTCTCAA AACCTTTGCG CAAGAAAATT CCGCCGTTTG	60
TATGCGTTAT TGAAAGAAAA TGAAATGCTC ATTCGCATCG GATCTTATCA AATGGGGAAC	120
GATAAAGAGC TTGATGAAGC GATTAAGAAA AAGGCTCTAA TGGAGCAATT TTTAGTGCAA	180
GATGAAAACG CTTTACYAGC CTTT	204

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAAATCAC GCCCAATCCT CGCACAGCT TACGCGCTCC AAATGATGGT CAAACAGATC	60
GCTTTTTTTAG AAACCATTTT AGTGGAAAAC GAGCAAGACG CTTTGATTTT GGAAAATTCT	120
TTGATCAAGC AGCTCAAGCC TAAATACAAC ATTCTTTTAA GAGACGATAA AACTTACCCT	180
TATATTTACA TGGATTTTTT TATTGATTTC CCTATCCCTT TAATCACACG AAAAATCTTA	240
AAACAGCCTG GCGTTAAATA TTTTGGCCCT TTTACGAGCG GGGCTAAGGA TATTTTGGAC	300
AGCTTGTATG AATTGCTCCC TTTGGTTCAA AAGAAAAATT GCATCAAGGA TAAAAAGGCA	360
TGCATGTTTT ATCAAATAGA GCGTTGTAAA GCCCCATGCG AGGATAAAAT CACTAAAGAA	420
GAATATTTAA AAATCGCTAA AGAATGTTTA GAAATGATTG AAAATAAAGA CAGGCTCATC	480
AAAGAGCTTG AATTGAAAAT GGAGCGCCTT TCTAGTAACT TCGGTTTTGA AGAAGCCTTA	540
ATTTATAGGG ATAGGATTGC AAAAATCCAA AAAATCGCCC CTTTCACTTG CATGGATTTA	600
GCCAAACTCT ACGATTTGGA TATTTTTGCT TTTTATGGTG GGAACAACAA GGCGGTGTTA	660
GTGAAAATGT TCATGCGTGG GGGTAAAATC ATTTCTTCAG CGTTTGAAAA AATCCACTCT	720
CTCAACGGGT TTGACACTGA TGAAGCGATG AAACAAGCCA TTATCAATCA TTACCAATCG	780
CATTTGCCTT TGATGCCTGA ACAAATCTTA TTGAGCGCTT GTTCTAATGA AACGCTTAAA	840
GAATTGCAAG AGTTTATCTC TCACCAATAT TCTAAAAAAA TCGCTCTTAG CATTCCTAAA	900
AAGGGTGATA AGCTCGCTTT AATAGAAATC GCTATGAAAA ACGCTCAAGA GATTTTTAGC	960
CAAGAAAAAA CCTCTAATGA AGATCGGATC TTAGAAGAAG CGCGATCGCT CTTCAATTTA	1020
GAGTGCGTGC CTTATAGGGT AGAAATCTTT GACACAAGCC ACCATTCAAA CAGCCAATGC	1080
GTGGGGGGAA TGGTCGTGTA TGAAAACAAT GCATTTCAAA AAGACTCTTA TCGGCGCTAC	1140
CATCTAAAAG GCTCTAACGA ATATGATCAA ATGAGCGAAT TGCTCACCAG AAGGGCTTTA	1200
GACTTTGCTA AAGAGCCACC GCCTAATTTG TGGGTGATAG ATGGAGGGAG GGCGBAATTA	1260
AACATCGCTT TAGAAATTTT AAAAAGCAGC GGGAGTTTTG TAGAAGTGAT CGCTATTTCT	1320
AAAGAAAAAA GGGGATTC	1338

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTGAGTTTGG GGGCGTTTCA GGGGTATTAT GGAGGGCTAG TGGATTTAGT GGGGCAAAGG	60
TTGAGCGAAA TTTGGAGCGC GATCCCCATG CTTTTTTTAC TCATTGTGAT TTCTAGCGCG	120
TTCAATTCTA ATTTTTGGAT CATCTTGTTT TTAGTCTTGC TCTTTAGCTG GATGGGGCTT	180
TCTCAAGTCG TGCGCACGGA GTTTTTAAAA GCAAGGAATA TGGACTACAC CAAAGCCGCT	240
AGAGCGTTGG GG	252

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...120
- (D) OTHER INFORMATION: /note= "hypothetical abc transporter in bcr 5'region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAGTGAAG CCTATTTTTT ACACCATAAA AACGCTTCTC AAGTGTCTCT TAATGAACAA	60
GTTTTAAACG TTATGAAACA AGTTCAATTG GATGAAAATT TTTGGAATGT TTCTCTTATG	120

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTGATCCTGA TATTTATCAT CGTGGTGGAA GATCAGAAAG GCATTTTCCC TATCGCAGCG	60
TCAAAAAGAA AAAGCCAAAG CTCTGTGATC ATTGAAGACG TGTGCTTCAG CAAAGAGGAT	120
TTTGTAGAAG GGGCAAAAGC GATTGAGGGG CTTTTAAAAA AACATGGCTT TAAGGATAAT	180
GGCATTATTT TTGGGCATGC GTTAAGCGGG AATTTGCACT TTGTCGTTAC GCCGATTCTA	240
GAAAATGAAG CTGAAAGAAA AGCGTTTGAA AATTTAGTTT CTGAGATGTT TTTAATGGTG	300
AGCAAAAGCT CTGGCTCTAT TAAAGCCGAA CATGGCACAG GCAGGATGGT AGCCCCTTTT	360
GTGGAAATGG AGTGGGGAGA AAAAGCTTAT AAGATCCACA AACAAATCAA GGAATTGTTT	420
GATCCTAATG GCCTTTTAAA CCCTGATGTG ATCATCACAA ACGATAAAGA AATCCACACT	480
AAAAATTTAA AGAGCATTTA CCCTATTGAA GAGCATTTGG ACATGTGCAT GGAATGTGGG	540
TTTTGTGAAA GGATCTGCCC CAGTAAAGAT TTATCCTTAA CGCCACGACA ACGCATCGTC	600
ATCCACAGAG AGGTAGAGCG TTTGAAAGAA AGGGTAAGTC ATGGTCATGA TGAAGATCAG	660
GTTTTACTAG ATGAGCTTTT AAAAGAGTCT GAATACTTAG CGCATGCCAC TTGCGCGGTG	720
TGCCATAATG GTTCCACTTT ATGCCCTTTA GGGATTGATA CCGGGAGYAT CGCTTTAAAT	780
CATTATCAAA AAAACCCTAA AGGCGAAAAG ATCGCTTCAA AGATTCTTAA ATCACATGCA	840
AACGACCACA AGCGTGGCTC GTTTTCTTT AAAARGCGCT TTCGTGGTTT CAAAAACTCA	900

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGAAAGAAA AAAACTTTTG GCCTTTAGGA ATCATGAGCG TGCTTATTTT TGGGCTTGGG	60
ATCGTGGTGT TTTTAGTGGT GTTTGCCCTA AAAAATTCGC CTAAAAATGA TTTAGTGTAT	120
TTCAAGGGTC ATAACGAAGT GGATTTAAAC TTTAACGCCA TGCTTAAAAAC TTATGAAAAC	180
TTTAAATCCA ATTATCGTTT TTCAGTGGGT TTAAAGCCTC TTACCGAAAAG CCCTAAAACC	240
CCCATTTTGC CCTATTTTTC TAAAGGCACG CATGGGGATA AAAAAATCCA AGAAAACCTT	300
TTAAACAACG CTTTGATTTT AGAAAAGTCC AACACGCTTT ATGCACAATT GCAACCGCTC	360
AAACCCGCTT TAGATTCGCC AAATATTCAA GTGTATTTAG CGTTCCTATCC CAGCCAATCC	420
CAGCCCAGAT TATTAGGAAC GCTTGATTGT AAAAACGCAT GCGAACCTTT AAAATTTGAT	480
TTGTTAGAGG GCGATAAAGT GGGGCGCTAT AAGATCCTTT TTAAATTTGT TTTTAAAAAT	540
AAAGAAGAAT TGATTTTGGG GCAACTGCTT TTTTAAAGTA GCATGGCTTG TATGGGTATA	600
TCAATTTTAA AAAACGCTAA AGCATTTTTT AAATACAAAA TA	642

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGCCCATTA AAGGCTCTTT TTTAGCCAGA AACCGCCTGG TGATCGCTTT AACCGATGCG	60
GTGATTATCC CCAAGCGGA TTAAAAAGC GGCTCTATGA GCAGTGCGAG ATTAGCCAG	120

AAATACCAAA AACCCCTTGTT TGTTTTACCC CAACGCCTGA ATGAGAGCGA CGGCACTAAT	180
GAGCTTTTAG AAAAAGGGCA GGCTCAAGGG ATATTTAATA TTCAAAATTT TATAAACACC	240
CTTTTAAAAG ATTACCATTT AAAAGAAATG CCTGAAATGA AAGATGAATT TTTAGAATAT	300
TGCGCGAAAA ACCCTAGCTA TGAAGAAGCG TATCTCAAAT TTGGGGATAA GCTTTTAGAA	360
TACGAGCTGT TGGGTAAGAT TAAGCGCATC AATCATCTCG TGGTGTTAGC A	411

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 816 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...816
 - (D) OTHER INFORMATION: /note= "ATP-BINDING PROTEIN ABC"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGGTAGTAG AATTAAAAAA CATTGAAAAG ATTTATGAAA ACGGGTTTCA TGCTCTAAAA	60
GGCGTGAATT TGGAATTGAA AAAAGGCGAT ATTTTGGGCG TGATAGGCTA TTCAGGGGCG	120
GGGAAATCCA CGCTCATTCG CTTGATCAAT TGTTTAGAGC GCCCCAGTTC TGGCGAAGTT	180
TTAGTCAATG GGGTCAATCT GTTAAACTTA AAGCCTAAAG AATTGCAAAA AGCGCGCCAA	240
AAAATAGGCA TGATTTTCCA GCATTTCAAT TTATTGAGCG CTAAAAACGT GTTTGAAAAC	300
GTGCTTTTCG CTCTAGAAAT CGCCCGATGG GAAAAACTA AGATTAAATC AAGGGTGCAT	360
GAATTGTTGG AATTAGTGGG GTTAGAAGAT AAAGTGCATT TTTATCCTAA ACAGCTCAGC	420
GGCGGGCAAA AACAACGAGT GGCATCGCT AGGAGTTTAG CGAATTGCCC TAATTTGTTG	480
CTTTGCGATG AAGCCACATC CGCTTTGGAT TCTAAAACCA CGCATTCTAT TTTAACGCTT	540
CTAAGCGGCA TTCAAAAAAA GTTTGATTTG AGCATCGTTT TCATCACACA CCAGATTGAA	600
GTGGTTAAAG AATTGTGCAA TCAAATGTGT GTGATCAGCA GCGGCGAAAT CGTAGAAAGA	660
GGCTCGGTGG AAGAAATTTT TGCTAACCCCT AAACATGCTG TTAATAAAGA ATTGCTTGGC	720

ATCAAAAACG AACATGCGGA TCAAAAATCG CAAGACATTT ATCGCATCGT GTTTTTAGGG	780
GAGCATTTAG ACGAGCCGAT CATTTCTAAW TTTTGW	816

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGGGGGCTT TGATAGCCAT GTTTTTTTTA ATGCTCATT AAAAGACTAT CGCTTATAAA	60
GAAGATAAAA AGAGCGCGGC TTAAAGGTC GTGCCTTATT TGGTGGCGTT GATGAGCTTA	120
GCCTTTAGCT GGTATTTGAT CGTGAAGGTT TAAAACGCC TCTATGCGGT GAGTTTGTAA	180
ATCCAGCTCG CTTGCGGTTG TGTCCTTGCG CTTTGTATT TTATCCTTTT TAAAAGATTT	240
GTGTTAAAAA AAGCCCCGCA ATTAGAAAAT AGCCACGAAA GCGTCAATGA GCTTTTAAAT	300
GTCCCTTTGA TTTTGTCC	318

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGATTAAAA GAATTGCTTG TATTTTAAGC TTGAGCGCGA GTTTAGCGTT AGCTGGCGAA	60
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GTGAATGGGT TTTTCATGGG TGCGGGTTAT CAACAAGGTC GTTATGGCCC TTATAACAGC	120
AATTACTCTG ATTGGCGTCA TGGCAATGAC CTTTATGGTT TGAATTTCAA ATTAGGTTTT	180
GTAGGCTTTG CCAATAAATG GTTTGGGGCT AGGGTGTATG GCTTTTTAGA TTGGTTTAAC	240
ACTTCAGGGA CTGAACACAC CAAAACCAAT TTGCTCACCT ATGGCGGCGG TGGCGATTTG	300
ATTGTCAATC TCATTCCTTT GGATAAATTC GCTCTAGGTC TCATTGGTGG CGTTCAATTA	360
GCCGGAACA CTTGGATGTT CCCTTATGAT GTCAATCAAA CCAGATTCCA GTTCTTATGG	420
AATTTAGGCG GAAGAATGCG TGTGGGGAT RCAGTGCCTT TGAAGCGGGC G	471

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGTATCGCC ATGTGTTGAA AGATTTCTCC CTAGATTTTA GCAAAGAAAG CGTTC AAGAG	60
CTGTTTAACC AGCTGGCTAA AGACACTTTT TTATTGCTTT TGCCTGTTTT AATCATTTTA	120
ATGGTGGTGG CGTTTTTGTC TAATGTCTTG CAATTGGCT GGCTCTTTC CCCTAAAGTC	180
ATTGAGCCTA AATTTTCTAA AATCAACCCT ATCAATGGCG TCAAAAACCT TTTTCTTTA	240
AAAAAGATCC TTGATGGGAG TTTGATCACT TTAAAAGTTT TTTTAGCTTT TTTTCTGGG	300
TTTTTCATCT TTTCTTATT TTTAGGGGAA TTAAACCATG CGGCTCTTTT GAATTGCAA	360
GGCCAGTTGT TGTGGTTTAA AAGCAAGGCG TTATGGCTCA TTTCTTCGCT TTTATTTTA	420
TTTTTTGTCT TGGCTTTTGT GGATTTAATC ATCAAACGCC GCCAATACAC TAACTCTTTA	480
AAAATGACTA AACAAGAAGT TAAGGACGAA TACAAACAGC AAGAAGGAAA CCCAGAAATC	540
AAAGCCAAAA TCCGCCAGAT GATGGTAAAA AACGCCACGA ATAAAATGAT GCAAGAAATC	600
CCCAAATCCA ATGTCGTGGT GACTAACCCT ACCCATTATG CCGTCGCTCT CAAATTTGAT	660
GAAGAACACC CTGTGCCTGT GGTAGTGGCT AAAGGCACGG ATTATTTAGC CATTAGGATT	720

AAGGGTATCG CCAGAGAGCA TGACATAGAA ATTATAGAAA ATAAAACGCT CGCTAGAGAG	780
CTTTATAGAG ACGTGAAATT GAACGCCACC ATACCAGAAG AATTGTTTGA GCGG	834

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATGAATACAA GSCCCTTAAT CGCTACGCTT TTGCAAGCGC CTTTGCATGT TTTAGGGATT	60
AGAGAGCCAG TTTCTTTTCA GCCTTTTAC CCCAAACAG AAAAGCCTAA TCGCCCTCAA	120
AAGTTCGCGC ATGTTTCTAG CATGCCAGT TTGGAATTTT TAGAAAAATT GGTGATCCGC	180
TACCTTTTAG AAGACAGAAG CCTATTGGAT TTAGCGGTGG GTTATATCCA TAGTGGGGTA	240
TTCTTGCATA AAAACAAGA ATTTGACGCT TTATGTCAAG AAAAATTGGA CGACCCTAAA	300
TTAGTTGCGT TATTATTAGA TCGGAATTTA CCCCTAAAAA AAGGGGGTTT TGAAAAGGAA	360

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 678 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATGGGGCAGG CATTTTTTAA AAAAATTGTT GGCTGTTTCT GTCTTGGTTA TTTATTTTAA	60
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TCTAGCGCAA TAGAAGCAGT AGCACTTGAC ATTAAGAATT TTAATCGTGG TAGGGTGAAA	120
GTGGTGAATA AGAAGATTGC TTATTTGGGA GATGAAAAAC CTATTACGAT TTGGACTTCA	180
TTAGACAATG TTACCGTGAT CCAACTTGAA AAAGATGAAA CTATTTCTTA CATCACAACA	240
GGTTTCAATA AAGGTTGGAG TATTGTGCCT AATTCTAATC ATATATTCAT TCAACCTAAA	300
TCGGTAAAAA GTAATCTCAT GTTTGAAAAA GAAGCAGTGA ATTTTGCCCT AATGACAAGA	360
GATTACCAAG AATTTTAAAA GACAAAAAAA CTTATCGTAG ATGCGCCTGA CCCTAAAGAA	420
TTAGAAGAAC AAAAAAAGC TCTAGAAAAA GAAAAAGAAG CTAAAGAACA GGCGCAAAAG	480
GCACAAAAAG ATAAAGAGA AAAAAGAAAG GAGGAGCGTG CAAAAATAG AGCCAATTTA	540
GAAAATCTCA CTAACGCTAT GAGTAACCCA CAAATTTGA GCAATAACAA AAATCTTAGC	600
GAATTGATCA AGCAACAGAG AGAAAATGAA TTAGACCAAA TGAACGAAC TAGAGGACAT	660
GCAAGAGCAG GCTCAAGC	678

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 150 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGAATACAG AAATTTTAAC CATCATGTTA GTTGTCTCCG TGCTTATGGG ATTGGTAGGC	60
TTAATAGCGT TTTTATGGGG GGTAAAAGC GGTCAGTTTG ACGATGAAAA ACGCATGCTT	120
GAAAGCGTGT TGTATGACGC GCGAGCGACT	150

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGTTTGTAG CGGCCGGGCT TGGGGCTTAT GCGATCGCGC TTTTCCACCT CTTTACGCAT	60
GCGTTCTTCA AATCCCTCCT TTTCTTAGGC TCAGGCAATG TCATGCATGC GATGGAAGAC	120
AATCTGGATA TTAATAAAAT GGGCGCTTTA TACAAGCCTA TGAGGATCAC AGCTGTCTTT	180
ATGATTATAG GGTCAAGTGGC TTTGTGTGGG ATCTACCCCT TTGCGGGCTA TTTCTCCAAA	240
GACAAGATTT TAGAGGTCGC CTTTGGGATG CACCACCACA TTTTATGGTT TGTCTCTTTG	300
ATTGGGGCGA TCTTTACCGC TTTTATAGC TTCAGACTCA TCATGCTGGT GTTTTTTGCA	360
CCCAAACAAC ATGAAATCAA CCACCCCCCA	390

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 549 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATGTTTATAT CTTCTTCTTA CACGCTGAGT TTTGTATGGC TTTTTTTAAT TTTCTTTTTT	60
TTCAAAAATA AGCCATTGGG TTTGAGGTTT TCGCTCTCTT TGATAAGCGT GATTTTAAGC	120
AATATCGCTT TGAAAGACTC CCTATCGCTC AATGAATTTT TAAGCAGTTT TACAGCCCCC	180
TTAAGCCCCCT TTAGCTGTCT TTTGATCCTT GCTTATGCAA GCTTTTCTTG CCATATACTC	240
AAAAAGCCCC CTTTAGAAAC CTTGCAATCT TATAGCGTCA TGCTGTTTTT CAATCTGTTG	300
CTTTTGACAG ATATTTTAGG GTTTTGCCT TTTCAATCT ACCATCATTT CATGGCTTCT	360
CTGATTTTTA GCGCGCTTTT TTGCAGCAGT TTGTTTTTGA GTAGCCCCTT ATTAGGCGTG	420

ATCGCTTTAG TGGCTTTATC CAGTTCGCTT TTGATGCGTT CTAATTTTCA AATCTTAGAT	480
TCTTTATTGG ATTTCCCAT TTTCTTTTT GTCTTTTTTA AGACTTTATA TCTTGCTAAA	540
AAAAGGTTA	549

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 705 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATGCGCCTAG ATTACGCCCT ATTCAACCAG CATTTAGCAA ATAGCAGAGA AAAAGCTAAA	60
GCGTTGGTTT TAAAAAACA GGTTTTAGTC AATAAAATGG TGGTTTCTAA ACCCTCTTTT	120
ATCGTTAAAG AGGGCGATCA AATTGAACTC ATCGCTCCCA ATCTATTCGT TAGCAGGGCT	180
GGGGAAAAAT TAGGGGCTTT TTTAGAAGAT CATTTTATAG ATTTTAAAGA AAAGGTTGTT	240
TTAGATGTGG GAGCGAGTAA GGGAGGCTTT AGTCAAGTGG CTCTTTTAAA AGGGGCTAAA	300
AAGGTGCTTT GCGTGGATGT GGGGAAAATG CAATTAGATG AAAGTTTGAA AAACGACCAA	360
CGCATAGAAT GTTACGAAGA ATGCGATATT AGAGGGTTTA AAACGCCAGA AAAAATTGAT	420
TTAGCACTTT GTGATGTGAG CTTTATTTCT TTATATTGTA TTTTAGAAGC GATTTTGCCT	480
TTAAGCGGTG AATTTTAAAC GCTTTTCAAA CCGCAATTTG AAGTGGGCAG AACAATAAAA	540
CGCAATAAAA AGGGGGTGGT GATGGATAAA GAAGCCATTT TGAACGCTTT AGAAAACTTT	600
AAAAACCATT TAAAAACAAA GGATTTTCAA ATCTTAACGA TCCAAGAAAG CTTAGTGAAA	660
GGGAAAACG GGAATGTTGA ATTTTTTATC CATTTCAAGC GAGCC	705

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGAGCCTAC CACCGGTTTG CATTTTGAAA GATGTGAATC ACCTTTTACA AGTCTTRCAT	60
TCTTTGGTGG CGTTAGGCAA TTCCATGCTA GTGATTGAGC ATAATTTAGA CATCATCAAA	120
AACGCTGACT ACATTATAGA CATGGGGCCT GATGGGGGGG ATAAGGGCGG GAAAGTCATT	180
GCGAGCGGCA CGCCTTTAGA AGTGGCGCAA AATTGCGAAA AAACCCAAAG CTATACGGGA	240
AAATTTT TAG CTTTGAATT GAAA	264

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 444 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGCAAAATC GATCGCATGA AATACAAGGC GTATCACACA TTAAGAATAA TTATAAATTT	60
TTCACCAAAG AGCTTGACAA TTATATCAGC AAAGGGTATC GCATTGAAGA GATTTATGGC	120
GCGTTTTTGT GGCTCAAAAT CGTAGCCATA GGTTTAGAGT TGGGCGAAGA CGATCCGCAA	180
GTGGTGTTTG AGAGCATCAA CGCTACAGGC GTGCAATTAA AAGGGCTGGA TCTCATCCGC	240
AACTATTTGA TGATGGGGGA AAATYCTGAC AACCAGAATC GTCTTTATAA TACTTATTGG	300
GTGCCTTTAG AAAATTGGCT TGGTGAAAAG GATTTGAATG ATTTTCATCAA AACCTATTTG	360
AGAATCTATT TTGAGGATAG AGTTACAAGA GGGAGAGCGC GAAGTGTATT ACGCGCTAAA	420
AGCCCACCAC AGAGACAATT TCCC	444

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGGATACCA TAAAAAGCAT TCCCATAAGA ACTTTTATTT TACTCTATAA AAGCTCACCA	60
AAATGTGTTG TGTGGCATC AATTACAGTG CTATTTGTCG GCATTCTTYC ATCTCTGAAT	120
ATTCTTGTTA TGATAAAATT GATTGATATT GTGGTGAATC TATTACAAAA GCATACGCAT	180
TTTGAATACA GCTTGCTGTT ACCAACTTTA CTACTATGGG GAGCCTTGCT GTTTTAAACG	240
CATGTGTTCT CAGGAAATTT TATCAAGCTT GCAAACCATT ATTGCCGAAC AATTTTCTAT	300
AAATATCATC ACTCAGCTTG C	321

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATGATCTTTT ACACCACCAT TAAAGAGCCT TTAAAAAACC TCCAATACCG CTATGCGCAA	60
TTTTTTGGCA AGATCAAGCC TTGTTGTTT TTAGAGTCTC TAAAATCATG CTTTTTTCAT	120
ACCTATTCTT TTTCTTTAAC GCGAAAACAA GATTTCAAAT CGCATTGCG CCATTTCATT	180

GACAGCGCCC ATTCCAACGC CTTAGTGGGT AATTTGTATC GAGCGTTATT CATAGGGGAT	240
AGCTTGAATA AAGACTTAAG AGACAGGGCT AACGCGCTAG GGATCAACCA CTTACTGGCC	300
ATTAGCGGGT TTCATTTAGG GATTTTGAGC GCGAGCGTGT ATTTTCTTTT CTCTCTTTTT	360
TATACCCCCT TACAAAAACG CTATTTCCCT TACAGGAACG CTTTTTWA	408

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGAATAAAC CATTTTAAAT CTTACTCATA GCCCTAATTG CCTTTAGCGG CTGTAACATG	60
AGAAAATACT TCAAACCCGC TAAACACCAA ATTAAAGCGA AGCGTATTTT CCTAACCATT	120
TGCAAGAAAG CATCGTTTCG TCTAATCGTT ATGGAGCCAT TT	162

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATGGCGGCTT GGAACACTTT AGTAGAAAAA ATCATCGCTC CTAAACACAA GGTCAAATT	60
GGTTTTGTGG GCAAGTATTT AAGCTTAAAA GAATCTTATA AATCCTTGAT TGAAGCCCTA	120

ATCCATGCGG GGGCGCATCT GGATACGCAA GTCAATATTG AATGGCTGGA TAGCGAGAAT	180
TTTAATGAAA AGACTGATTT AGAGGGCGTT GATGCGATTT TAGTGCCGGG GGGCTTTGGA	240
GAAAGGGGGA TTGAGGGCAA AATTTGCGCC ATTCAAAGGG CTAGGTTAGA AAAACTCCCC	300
TTTTTAGGGA TTTGTTTGGG CATGCAATTA GCGATCGTTG AATTTTGTCTG CAAATGTTTT	360
AGGCTTGAAA GGGGC	375

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGACTAAAG CGTTTGTGCC TTAAAGTTTG TTAGTGAGCG CGATTTTATT AGCGTTTTCG	60
CTCATCTTAA TCCCCACTTC TAAGAGCGCT TATTACGGGT TTTTGCGTCA AAAAAAGAC	120
AAGATTGACA TTAACATCAG AGCGGGTGAA TTCGGGCAA AATTAGGCGA TTGGCTCGTG	180
TATGTGGATA AGACTGAAAA CAATTCCTAT GATAATTTGG TGCTTTTTTC TAATAAAGT	240
CTCTCTCAAG AAAGCTTTAT TTTGGCTCAA AAAGGCAATA TCAACAATCA AAACGGCGTG	300
TTTGAATTGA ATTTGTATAA CGGGCATGCG TATTTCACTC AAGGCGATAA AATGCGTAAG	360
GTTGATTTTG AAGAATTGCA TTTGCGCAAC AAGCTCAAGT CTTTCAATTC TAATGATGCG	420
GCTTATTTGC AAGGCACGGA TTATTTGGGT TATTGGAAAA AAGCCTTTGG TAAAAACGCT	480
AATAAAAATC AAAAACGCCG TTTTCTCAA GCGATCTTAG TTTCCTTGTT CCCTTTAGCG	540
AGCGTGTTTT TAATCCCCTT ATTTGGCATC GCCAACCCGC GATTCAAAAC GAATTGGAGT	600
TATTTCYAWG TCCTTGAGC GGTGGGGTW TATTTTTTAA TGGTGCATGT GATTTCTACG	660
GATTTGTTTT TGATGACCTT TTTCTTCCCC TTTATTTGGG CGTTTATTTT TTATTTATTG	720
TTTAGAAAAT TCATTTTAAA GCGTTAT	747

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATGAGTAAGA GCGCGATTTT TGTTCTTTCT GGCTTTTTAG CGTTCTTGCT CTATGCTTTG	60
TTATTATATG GTTTGTTGTT AGAAAGGCAT AATAAAGAAG CAGAGAAAAT CCTTTTAGAT	120
TTAAATAAAA AGGACGAACA AGCCATTGAC TTGAATTTAG AAGATCTGCC AAGCGAGAAA	180
AAGAATGAAA AAATTRA AAA AGTAACGGAA AACAGGACG ATTTTTTAGA GCCTAAAAGA	240
AGAACCCAAA GAGGAGCC	258

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTGATGGCTC AATCCTTGCT TGTYCATGCC TTTTTGCCG CTTGCTCGC CCTAGCCTTT	60
ATGATCAATC TTTACACCCT TTTTAAAGAA AAGAATTTCA TCCAATTGAA CCGGAAAATC	120
TATCTTGTC A TGCCAGCGAT TTATATTCTT TTAAGCATCG CTCTTTTGAG TGGGGTTTTT	180
ATTTGGGCGA TGCAACAATT TGAATTTTCT TTTAGCGCTG TTGTCATGCT TTTGGGGTTG	240
TTGTTGATGC TCATTGCAGA AATCAAACGC CATAAAAGCG TGAAATTCGC TATCACTAAA	300

AAAGAAAGGA TGAAAGCCTA TATCAAAAAA GCTAAAATCC TGTATTTTTT AGAAACGATT	360
CTTATCATCG TGTTAATGGG CATT	384

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTGCGTAATG TGGTTTTATT CATTTTAACA GCGATCTTTT TAGCGTTCAT GCTTTTAGTG	60
AGTTATTGCA TGCCCCATTA TAGCGTGGCT GTCATTAGCG GGGTGGAAGT CAAAAGAATG	120
AATGAAAATG AAAACACGCC CAATAATAAG GAAGTAAAAA CCCTTGCTAG AGATGTCTAT	180
TTTGTGCAAA CTTACGACCC TAAGGATCAA AAAAGCGTGA CCGTCTATCG TAACGAAGAC	240
ACGCGCTTTG GCTTCCCTTT TTATTTTAAG TTTAATTCGG CTGATATTTC AGCTCTCGCC	300
AAAGTT	306

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATGTTTAAAA AAATCATTTT TTTGTGCGTT TTTTGTAGTAG GGGGATTTGT CATTCCACCC	60
--	----

CTTGAAGCCA TGCCTATTTT GCGCAATAAA ACCCCCAAAA AAAATTACCA AGAAGCCCAT	120
GAAAAGCTCT ATAGAAGCAT CATTAACCGC CAAAASSTCA CGCGTAAAAA AAGCGGGTGG	180
TATTTTTTTAG GGGGGGTTGG CGCTGTAGAA GCCATTAAGG ACTATCAAGG CAAGGAAATG	240
AAAGATTGGA TGCCACGCTC AATT	264

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTGCATTTTA CGTGATCTT TCTAACCTA TTAAATGGA TTTTGCCAGC CAAAACAAG	60
CAGGCGTGCA AAAAGGCCAC CAACCAGATC CATTCAAGGY YTGCAAAACA TCCAGCAAAA	120
TATCCCCCT CAAGTATTAA CCCCTCAATC CAAGCGGGTA TACAAGGGGT GATGCAAGGT	180
TTTGGGGCTT TGAGCAGCAY YTTAGAAGYC CCCYTATTTG TTTTYAAGC AAAATGTGGG	240
TGGATTGGGG GCTTTGAGCA TTATTTATCC CCTTTATATG GGTGGGGCAA GATTCACGAT	300
GGTGCGCATT GCGATTTGAT GCAAAAAGAC GCCAATGGAA GGGGTATCGG CTTGAAAAA	360
GGTCTTCCAC CTTTCAAGGG GCTG	384

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATGCAGAAGT TTTTCTCTCG TTTTAGAAGG TGGGCGTTGC CCTTTTATTT TGTGAGCGCT	60
TTAGCAGCGA TTGATATTGA TGAAGTAACA GAAGCTCAAG CTAATAGCAT TAAATTAAGC	120
GATCAGTTAG TGAGCCTGAG CGATAAGCTT TTAGAAAAAG CGGTGGATAG GGGGCGCAAT	180
ACCGATCACT TAAAAGATCT TAACGATTTG CATGAAAAAA TCAAACATTT GCGCTTGATT	240
TTAGAGCCTA AGCCTAAGGG CAAAGAAGAT AGTCCTAACT TGGGAGGTAA TAAGGATATG	300
AAAACGGTTG AAATCGGAAG CGGT	324

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GTGATTTTAG CGTTCGCCTT TGGCATGAGT CTTCTTGGAT TAGCGGGCAT GTTCATTGAT	60
ATTCCTTTTT TATCCACAGG CGTTCATATC CCTAGAAAAG AGGATATTTT ATGGATTTCT	120
TTAATAGGGA TTAGCGGGAC TTTAGGGCAG TATTTCTTAA CCTATGCTTA CATGAACGCT	180
CCTGCTGGGA TCATCGCCCC CATTGAATAC ACCCGCATTG TTTGGGGGCT ATTGTTTGGG	240
CTGTATTTAG GCGATACATT TTTGGATCTT AAAAGCTCTT TAGGGGTGGC TTTGATCTTA	300
TGTTCAGGCT TGCTCATTGC CTTGCCCCTT CTTTAAAAAG AATTAAAAAA AATT	354

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATGATCTATT TAGGGAAGAA AAATTTTAAC GCCCTTTTGA AAGGGGCGTA TTTAATGGAT	60
GAGCATTTTA GAAACGCCCC TTTTGAAAGC AATTTACCCG TTTTAATGGG ATTAATCTGG	120
CGTGTGGTAT ATCTAACTTT TTTTCCAATC CAAAAGCCA CT	162

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 864 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGGCCGCCA AATCCAAAGC GYAAACGCTT AAAGTCTTTT CAAAATTTTT CAGCAATTTT	60
AAAATCACTA AACTCAAAGA CAACCACGAA GAAGCCCACA AACTTTTTTG AGAAAAATAGC	120
CGTAAAGCCC ATGACA CTGA GATCATTTAC TCCACTTTGC AAGTGGTCCC CAGGTATTCA	180
ATAGAAACCG TGGGCTTTAG TTTGTTGATT TTAGCGGTCG CTTACATCTT ATTCAAATAC	240
GGCGAAGCTA GAATGGTACT CCCTACCATT TCTATGTATG CCCTAGCGCT TTATCGCATA	300
CTCCCTTCTG TAACTGGAGT GATCAGCTAT TATAATGAAA TCGCTTACAA CCAGCTTGCA	360
ACCAATGTTG TTTTAAAG CTTTCTAAG ACCATCGTTG AAGAGGATTT AGTCCCTTTA	420
GACTTTAATG AAAAAATCAC TCTCCAAAAC ATTTCAATCG CTTATAAGTC AAAACACCCG	480
GTTTTAAAAA ATTTCAACCT CACCATTCAA AAAGGTCAAA AAATCGCTCT CATAGGCCAT	540
AGCGGGTGCG GAAAATCCAC GCTGGCGGAT ATTATTATGG GGCTTACCTA CCCTAAAAGT	600
GGGGAAATTT TTATTGATAA CACCCTTTTA ACCAGCGAAA ACAGGCGCTC ATGGCGTAAA	660

AAAATAGGCT ATATCCCCCA AAATATTTAC CTTTTTGATG GCACTGTGGG GGATAATATC	720
GCTTTTGGGA GTGCTATAGA TGAAAAACGC TTGATTAAGG TGTGCAAAAT GGCTCATATC	780
TATGATTTTT TATGCGAGCA TGAGGGCCTT AAAACCCAAG TGGGCGAAGG GCGCTAAGC	840
TTAGCGGCGG TCAAAAACAG CGCA	864

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGCTTGATA TATGGATAGA TATGATAATC TGTATTTTTT ATTTGCTCTT TTTTACGACT	60
CCTTACATTG TAGGCGATAT TTTGCAATTG AAATTTATCC GTCAAAAAC CTGCGAGAAG	120
CCTGTTTTAC TCCCACAAAA GGATTATGAA GAAGCGGGAA ATTATGCTAT TAGGAAAATG	180
CAATTATCCA TTATTTCTCA AATTTTAGAT GGGGTGATCT TTGCTGTTG GGTCTTTTTT	240
GGTTTGACGC ATTTAGAAGA TCTCACGCAT TATTTAAACC TTCCTGAAAC GCTAGGTTAC	300
TTGGTGTTTG CCTTGTTGTT TTTAGCGATT CAAAGCGTTT TAGCTTTACC CATTAGCTAC	360
TATACTACCA TGCATTTGGA TAAGGAATTT GGCTTTTCTA AGGTGAGTTT ATCGTTGTTT	420
TTTAAGGATT TTTTCAAAGG ATTATTGCTC ACTTTAGGCG TGGGGTTGTT GTTGATTAC	480
ACTCTCATAA TGATCATTGA ACATGTGGAG CATTGGGAGA TCAGCTCGTT TTTTGTCTGT	540
TTTGTTTTCA TGATTTTGGC TAATCTTTTT TTACCC	576

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATGCTAAAAA AAATATTTTT AACCAACAGC TTAGGGATTT TATGCTCTAG GATTTTTTGGC	60
TTTTTACGGG ATTTAATGAT GGCCAATATC CTAGGGGCTG GGGTGTATAG CGATATTTTC	120
TTTGTGGCTT TCAAATTGCC TAATCTATTC AGGCGTATTT TTGCGGAGGG CTCTTTTTCT	180
CAAAGCTTTT TACCGAGCTT CATACGGAGT TCCATTAAGG GGGGTTTTGC GAGTTTGGTG	240
GGGCTTATTT TTTGTGGCGT TTTATTCATG TGGTGCTTAT TAGTAGCGCT CAATCCCTTA	300
TGGCTAACCA AACTCCTAGC TTACGGCTTT GATGAAGAAA CGCTCAAACCT ATGCACCCCT	360
ATTGTAGCGA TCAATTTTTG GTATCTTTTA TTGGTGTTTA TCACCACTTT TTTAGGCGCG	420
CTTTTACAAT ACAAACACAG CTTTTTTGCC GCGCTTATGC GCAAGCTTAC TCAATTTATG	480
CATGATTTTA GCCCTTTTGA TTTC	504

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATGAATTTAG AAGTGGCTCT AAAGGCGTTT GAAACGCTAT TGCCATGCAA TAAACAAGAA	60
GTTTTAAAAA ACCTAAAGCC CCTAGATTTA ATCGGCCGTT GCGAGCTTTT AAGCCCTAAC	120
ATTTTAATAG ATGTGGGGCA TAACCCCCAT AGCGCTAAAG CCTTAAAAGA AGAAATCAAA	180
CGCATCTTTA ACGCTCCAAT CGTTTTGATT TATAATTGCT ATCAAGATAA AGACGCTTTT	240
TTGGTGCTAG AAATTTTAAA GTCTGTGGTT AAAAAGGTTT TGATTTTAGA ATTGCATAAT	300

GAAAGAATTA TCCAATTAGA AAAACTTAAA GGGATTTTAG AAACTTTAGG GTTAGAACAC	360
GCCTTGTTTG AAGAACTGAA AGAAAATGAA AATTATTTGG TGTATGGCTC ATTTCTGGTA	420
GCCAACGCTT TTTATGAACG CTATCCAAAG AAGAGGGAT	459

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATGGCTATCG GGTTTCCGTT AGTGTGTTGGG ATTTTACTCA CCCTTTT TAG CCGTTCTTAT	60
TGGCGTGAGT TTGGGGGCGT TTCAGGGGTA TTATGGAGGG CTAGTGGATT TAGTGGGGCA	120
AAGGTTGAGC GAAATTTGGA GCGCGATCCC CATGCTTTTT TTACTCATTG TGATTTC	177

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 666 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATGAAGAAAA AAGCAAAAGT CTTTTGGTGT TGTTTTAAAA TGATTCGTTG GTTGATTTG	60
GCGGTCTTTT TTTTGTTGAG CGTATCAGAC GCTAAAGAAA TCGCTATGCA ACGATTTGAC	120
AAACAAAACC ATAAGATTTT TGAAATCCTT GCGGATAAAG TGAGCGCCAA AGACAATGTG	180

ATAACCGCCT CAGGGAATGC GATCCTATTG AATTATGACG TGTATATTCT AGCGGRTAAG	240
GTGCGTTATG ACACCAAGAC TAAAGAAGCG TTATTAGAAG GCAATATTAA GGTTCATAGG	300
GGCGAGGGCT TGCTCGTTAA AACCGATTAT GTGAAATTGA GTTTGAACGA AAAATATGAG	360
ATCATTTTCC CCTTTTATGT CCAAGACAGC GTGAGCGGGA TTTGGGTGAG CGCGGATATT	420
GCTAGCGGGA AGGATCAAAA ATATAAGATT AAAACATGA GCGCTTCAGG GTGCAGCATT	480
GACAACCCCA TTTGGCATGT CAATGCGACT TCAGGCTCAT TTAACATGCA AAAATCGCAT	540
TTGTCAATGT GGAATCCTAA GATTTATGTC GGCGATATTC CTGTATTGTA TTTGCCCTAT	600
ATTTTCATGT CCACGAGCAA TAAAAGAACT ACCGGGTTTT TATACCCTGA GTTTGGCACT	660
TCCMAC	666

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATGCTGGATT TTGATTTGGT TCTTTTGGC GCGACTGGGG ATTTAGCCAT GCGAAAGCTC	60
TTTGTTTCGC TTTATGAAAT TTATATTCA TTTATGGTTT TAAAAACGAT TCTAGGATTA	120
TCGCATCGGG GCGTAAGGAG CTATCCAATG AAGAGTTTT	159

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...327

(D) OTHER INFORMATION: /note= "alkylphosphonate uptake genes A through Q"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATGCAAGATT TACCCCCATG CCCTAAACGC AACGACGCCT ACACCTACCA TGATGGCACG	60
CAGTTCGTTT GCTCTAGCTG TTTGTATGAA TGGAATGGAA ATGAAATTAG TAATGAAGAA	120
TTGATCGTTA AAGATTGCCA TAATAATCTT TTACAAAATG GGGACTCGGT CATTCTCATT	180
AAAGATTTAA AGGTTAAAGG CTCATCTTTG GTGCTTAAAA AAGGCACTAA AATCAAAAAT	240
ATCAAGCTTG TCAATAGCGA TCACAATGTG GATTGTAAAG TGGAAGGGCA GAGCTTGTCT	300
TTAAAATCTG AATTCCTTAA AAAAGCT	327

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...219

(D) OTHER INFORMATION: /note= "outer membrane 30.2K protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GTGGATGGGG CTATCATAAC AGGGAATTAT GCCTTGCAAG CAAAACCTCAC CGGAGCCTTA	60
TTTTTCAGAAG ATAAGGACTC GCCTTATGCT AATCTTGTAG CCTCTCGTGA GGATAATGCG	120
CAAGATGAAG CGATAAAAGC GTTGATTGAA GCCTTACAGA GCGAAAAGAC CAGGAAATTC	180
ATTTTGGATA CCTATAAGGG GGCGATTATC CCGGCTTTT	219

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GTGTTTYCCA TGCTGGTGTT GGTGTTGAGC GATAATTTTT TAGGGCTTTT CATTGGCTGG	60
GAAGGGGTGG GGCTATGCTC TTA CTGCTC ATTGGCTTTT GGTATCATAA AAAAAGCGCG	120
AATAACGCTT CTATTGAAGC CTTTGTGATG AATCGAATCA CGGATTTAGG CATGCTCATG	180
GGGATTATTT TGATCTTTTG GAATTTTGGC ACCCTCCAGT ATAAAGAAGT CTTTAGCATG	240
CTCAATAACG CCGATTATTC CATGCTCTTT TACATTAGCG TGTTTCTTTT TATTGGCGCT	300
ATGGGGAAGA GTGCTCAATT CCCTATGCAC ACATGGTTAG CCAACGCTAT GGAGGGGCCT	360
ACCCCTGTAT CCGCTCTCAT CCATGCARCG ACGATGGTAA CCGCTGGGGT GTATCTAATC	420
ATCAGAGCCA ATCCTTTGTA TAGTGCGGTG TTTGAAGTGG GTTATTTTAT CGCATGCTTA	480
GGAGCGTTTG TGGCTCTTTT TGGAGCGAGC ATGGCTTTAG TCAATAAGGA TTAAAACGC	540
ATCGTGGSYT ATTCCACGCT TTCTCAATTA GGGCTATATG TTTGTAGCGG CCGGGCTTGG	600
GGCTTATGCG ATCGCGCTTT TCCACCTCTT TACGCATGCG TTCTTCAAAT CCCTCCTTTT	660
CTTAGGCTCA GGCAATGTCA TGCATGCGAT GGAAGACAAT CTGGATATTA C	711

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```
ATGATGATAA CCAAACAATC GTATCAAAGA TTCGCTTTAA TCGGGGTTTT TGTGTTTTTCG      60
CTTTTCGGCGT TTATTTTAA CACCACGGAG TTTGTCCCTG TTGCACTTCT GTCAGACATT      120
GCGAAAAGCT TTGAAATGGA GAGCGCAACA GTGGGGCTTA TGATCACTGC TTATGCATGG      180
GTGGTGTCTC TTGGCTCATT GCCCTTGATG CTGCTTAGCG CTAAAATTGA AAGGAAACGC      240
TTATTGCTTT TTCTTTTCGC TCTTTTATT TTCAGCCATA TCCTTTCGCG T                291
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(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 840 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```
ATGAAACTGA GAGCAAGTGT TTTAATCGGT GTGGCAATTC TGTGCTTAAT TTTAAGTGCG      60
TGCAGTAACT ATGCGAAAAA AGTGGTGAAA CAAAGAACC ATGTTTATAC GCCTGTGTAT      120
AATGAACTGA TAGAGAAGTA TAGTGAGATC CCCTTAAATG ACAAACCTCA AGACACACCA      180
TTCATGGTGC AAGTGAAGTT GCCAAATTAC AAGGACTATT TGTGAGATAA TAAACAAGTT      240
GTACTAACTT TCAAACTTGT TCACCATTCT AAAAAGATTA CGCTCATAGG CGATGCCAAT      300
AAGATCCTCC AATACAAGAA TTAATTCCAA GCTAACGGGG CAAGATCTGA CATTGATTTT      360
TACTTGCAAC CCACTTTGAA TCAAAAGGGT GTGGTGATGA TAGCGAGTAA CTACAATGAT      420
AATCCCAACA ACAAAGAAAA ACCACAGACC TTTGATGTGT TGCAAGGAAG TCAGCCAATG      480
CTAGGAGCTA ACACAAAAAA CTTGCATGGC TATGATGTGA GTGGAGCAAA CAACAAGCAA      540
GTGATCAATG AAGTGGCAAG AGAAAAAGCT CAGCTAGAAA AAATCAATCA GTATTACAAG      600
ACTCTCTTGC AAGACAAGGA ACAAGAATAT ACCACTAGGA AAAATAACCA ACGAGAAATT      660
TTAGAAACAT TGAGTAATCG TGCAGGTTAT CAAATGAGGC AGAATGTGAT TAGTTCTGAG      720
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ATTTTAAAGA ATGGCAACTT GAACATGCAA GCCAAAGAAG AAGAAGTTAG GGAGAAGCTA	780
CAAGAAGAAA GAGAGAATGA ATACTTGCGC AATCAAATCA GAAGTTTGCT CAGTGGTAAG	840

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGTGGTTAG ATCACATCGC TAAAGAGATC AGAAGTTTAG TGGAAAACGA TATTGAAGTG	60
GGTATTGTGA TTGGTGGAGG CAATATCATT AGGGGGGTTA GCGCGGCTCT AGGGGGGATC	120
ATTAGGCGCA CCAGTGGGGA TTATATGGGC ATGTTAGCCA CCGTGATTAW GCGG	174

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...372
 - (D) OTHER INFORMATION: /note= "variable antigen from Treponema"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GTGCATAACT TCCATTGGAA TGTGAAAGGC ACCGATTTTT TCAATGTGCA TAAAGCCACT	60
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GAAGAAATTT ATGAAGGGTT TCGGACATG TTTGATGATC TCGCTGAAAG GATCGTTCAA	120
TTAGGACACC ACCCCCTAGT CACTTTATCC GAAGCGATCA AACTCACTCG TGTAAAGAA	180
GAAACTAAAA CGAGCTTCCA CTCTAAAGAC ATCTTTAAAG AAATTCTAGA GGACTACAAA	240
CACCTAGAAA AAGAATTAA AGAGCTCTCT AACACCGCCG AAAAAGAAGG CGATAAAGTT	300
ACCGTAACTT ATGCGGACGA TCAATTAGCC AAGTTGCAA AATCCATTTG GATGCTAGAA	360
GCCCATTAG CT	372

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...270
 - (D) OTHER INFORMATION: /note= "HYPERSENSITIVITY RESPONSE SECRETION PROTEIN"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATGAATAAAA CCATAAAGC CGCCGCCCTA GCCTATAACA TGGGGCAAGA TCATGCCCCA	60
AAAGTGATCG CAAGCGGGGT GGGCGAAGTG GCTAAAAGGA TCATTCAAAA AGCTAAGGAA	120
TACGATATAG CGCTCTTTTC TAACCCCATG CTGGTGGATT CGCTCTTAAA GGTGGAATTA	180
GACTGCGCGA TACCTGAAGA ATTGTATGAA AGCGTGGTGC AAGTGTTTTT ATGGCTCAAC	240
AGCGTGGAAG ATAACGCGCA AATGTCCAAG	270

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 633 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...633
 - (D) OTHER INFORMATION: /note= "sensor protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ATGGGGAAAA TTTCAGCGCA TTTAGCCCAT GAAATCAGAA ACCCCGTAGG CTCTATCTCT	60
CTTTTAGCTT CGGTGTTATT AAAGCATGCG AACGAAAAAA CTAAACCCAT TGTGTGTAGAA	120
TTGCAAAAAG CTTTATGGCG CGTAGAAAGG ATCATTAAAG CCACCTTGCT TTTTCTAAA	180
GGCATTCAAG CCAACCGCAC CAAGCAAAGT TTGAAAACGC TAGAGAGCGA TCTCAAAGAA	240
GCCCTAAACT GCTACACTTA CTCTAAAGAC ATTGATTTTC TTTTAAATTT TAGCGATGAA	300
GAAGGGTTTT TTGACTTTGA TTTAATGGGG ATTGTGTTAC AAAATTTCTT GTATAACGCC	360
ATTGATGCGA TTGAAGCCTT AGAAGAGAGC GAACAAGGTC AGGTCAAAAT TGAAGCGTTC	420
ATTCAAAATG AATTTATTGT CTTCAACCAT ATTGATAATG GCAAGGAAGT GGAAAATAAA	480
AGCGCTTTAT TTGAGCCTTT TGAAACCACT AAATTAAAGG GGAATGGCTT AGGGTTAGCC	540
CTGTCTTTGC AAGTCGTTAA AGCCCATGAA GGGAGCATTG CGCTATTAGA AAATCAAGAA	600
AAAACCTTTG AAATTAAGAT TCTTAACGCT TCT	633

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 636 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GTGTCAGAAT TTCATCAAGT TTATGaCCCT TTGGGTAATA TTTGGCTGAG CGCTCTTGTG	60
GCCTTATTGC CGATTTTGTG ATTTTCTTA TCTTTAATGG TTTTAAACT CAAAGGTTAT	120
ACAGCGGCCT TTTTGAGCGT GGCCTTATCA GCCATTATTG CGGTTTTAGT GTATAAAATG	180
CCTGTTAGCA TGGTGGGTTC AAGCTTCCTT TATGGCTTTC TTTATGGCCT ATGGCTATTC	240
GCTTGGATCA TTATTGCCGC GATTTTTTTA TACAACTCA GCGTTAAATC CGGCTATTTT	300
GAAATCTTAA AAgAAAGCGT TCAGTCCATC ACTTTAGATC ACCGCATTTT AGTGATTTTG	360
ATTGGCTTTT GtTTTGGCTC ATTTTtagAA GGGGCGATCG GCTTTGGAGG GCCTATTGCC	420
ATCACAGCGG CGATTTTAGT GGGGTTGGGg TTAAGCCCTT TGTATTCTGC TGGGTtATGT	480
TTGAtCGcTA ACACCGCTCC TGTGgCCTTT GGcgCGGTGG GTATCCCTAT AAGCGCGATG	540
GCgAGCGCGG TAGGGGTGCC AGCGAtCTTA ATTTcAGCCA TGACGGGTAA AAtCCTCTTT	600
TTTGTGAGCT TGTTAGTgCC GTTTTTTATT GTGTkT	636

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 546 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...546
 - (D) OTHER INFORMATION: /note= "INVOLVED IN PENICILLIN
TOLERANCE-has signal peptide seq."
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ATGGAAATTA AAATGGCTAA GGATTATGGT TTTTGTTTTG GCGTCAAAAG AGCGATACAA	60
ATCGCTGAAA AAAATCAAAA CAGCTTGATT TTTGGCTCGC TCATTCATAA CGCTAAAGAA	120
ATCAATCGTT TGGAAAAAAA TTTCAATGTG AAAATTGAAG AAGATCCTAA AAAATCCCT	180
AAAAATAAGA GCGTGATCAT AAGAACCCAT GGCATTCCTA AACAGGATTT AGAATACTTG	240
AAAAATAAGG GGGTTAAAT CACTGACGCG ACTTGCCCGT ATGTGATCAA ACCTCAGCAA	300

ATTGTGGAAT CCATGAGTAA AGAAGGGTAT CAAATCGTGC TTTTGGGGA CATTAACCAC	360
CCTGAAGTCA AGGGCGTGAT CAGCTATGCC ACTAACCAGG CTTTAGTCGG CAATTCGTTA	420
GAAGAATTGC AAGAAAAAA ATTGCAACGG AAAGTGGCTT TAGTCTCTCA AACCACCCAA	480
GCAAACCCCA AAACCTCTGC AAATCGCTTC TTATTTGGTG GARGRTGCAC TGAAGTGCCT	540
ATTTTT	546

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ATGGATCATG AGTTTTTGAT TACCATGCGT TTGAGCTTTT CTTTAGCTTT GATTACCACC	60
CTTATTTTAC TCCCTATAGG GATTTTTTTA GGCTATTTTT TAAGCCTTAA ACGCAATCTT	120
TTAACGAGCT TAACAGAAAC GCTTGTGTAT ATGCCTTTAG TTTTACCCCC AAGCGTGCTA	180
GGGTTTTATC TTCTTTTAAT CTTTTCGCCT TCTTCTTTTT TGGGAGCGTT TTTACAAGAT	240
GTGTTAAATG TGAAACTCGT TTTTAGTTTC CAAGGGCTTA TCTTAGGGAG CGTGATTTTT	300
TCCTTGCCCT TTATGGTAAG CCCTATTAAA AGCGCGTTAA TTTCTTGCC CACTTCTTTA	360
AAAGAAGCCA GTTATAGCTT GGGTAAAGGG GAATACTACA CCCTTTTTTT TGTCTACTC	420
CCTAACATCA AACCCAGTGT GTTGATGGCT ATCATTACAA CTTTATGCA CACTATAGGT	480
GAATTTGGCG TGGTGATGAT GCTTGGGGGT GATATATTAG GGGAAACAAG AGTGGCTAGC	540
ATTACGATCT TTAACGAAGC TGAAGCACTC AATTATTCTA AAGCCCATCA ATACGCCTTA	600
ACGCTCACGC TTATTAGTTT TAGCCTCTTG TTTGTTACCC TATTTTTAAA TAAAAACAA	660
AGCTCGTTTT TA	672

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ATGCATCCTA TAATGTTTGC CTATATCGCT AACGCGCTCG CTCAAGCTAG AAAGATCAAC	60
GGAACACTTT GCATGGCGTT TCAAAAAATA TCTCAAGTCA AAGAATTAGG CATTGATAAA	120
GCAAAGAGTT TGATAGGCAA CCTTTCTCAA GTGATTATCT ACCCCACAAA AGATACTGAT	180
GAATTAATAG AATGTGGCGT CCCATTAAGC GATAGTGAAA TCAATTTCTT ACACAACACG	240
GACATGAGAG CCAGACAAGT GCTAGTAAAA AATATCGTTA CAAACGCTTC AGCTTTTATT	300
GAAATTGATT TAAAAAAGAT TTGCAAGAAC TACTTTATAT TCTTGATAGC AATGCTGGTA	360
ATAGAAAAAT CCTCAATGAT CTTAAAAAAG CAAACCAAGA AACTTATAAG GAAGAGTATT	420

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATGTGCCTGA CAGGCGGCTT GATGCGTTGG CTCAAATCGG TAAAGCCTGA ACGAATCTTG	60
CATTCTGTGG TGGAATTTGT GGATATTGCC GGATTGATTA AGGGGGCGAG CAAGGGGGAG	120
GGTTTAGGCA ATCAGTTTTT AGCCAATATC AAGGAATGCG AAGTGATCTT GCAAGTGGTG	180
CGCTGTTTTG AAGATGACAA TYATCACGCA TGTGAACGA	219

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATGCATGTTG CTTGTCTTTT GGCTTTAGGG GATAACCTCA TCACGCTTAG CCTTTTAAAA	60
GAAATCGCTT CCAAACAGCA ACAGTCCCTT AAAATCCTAG GCACTCATTT GACTTTAAAA	120
ATCGCCAAGC TTTTAGAATG CGAAAAACAT TTTGAAATCA TTCCTGTTTT TGAAAATATC	180
CCTGCTTTTT ATGACCTTAA AAAACAAGGC GTTTTTTGGG CGATGAAGGA TTTTTTATGG	240
TTATTAAAGC AATTAAAAAA CATCAAATCA AACGTT	276

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ATGAAAAGA AGCCATTGAT GTGGCGTATC TGTGCGTTAA GGAGACTTCT TCTAGGGTTC	60
AAGAGAGAGA GAGAGTTATT AAGCTTCGCT AAACATTGGA ATATCCCAAC GATTGTCGTT	120
TTCACACACA CTCAAGCCGA AGCCGGCGAT GCGTTTGTCC AAGAAACTAA AGGGATCATA	180
GACGAAGAAT GGGGGTTTAA AGGTTTTGTC AGAGCCTATG TGAGGGTCAA TTCCGTTGCC	240

TTTTCATTTA GGGGGTTGAA AGTCCCTGTT GAAGGTTTAG AAGAATTGGT AGATGAAACG	300
AAAAAATGCC TTTCAGACGC TGAAAAAAT AAGAAAAGGC ATTTCTTGAG TATTCAAAGA	360
GTTAAGATTTC AAGAAAGAAA ACAGGCTATG ATAGAGGAAT GTAAAACCAT TATCCATGTT	420
GCATCAGGCG CTGCAGGAGT TGCTGGGCTT ATCCCCATAC CTTTtagCGA TCGCTCGCT	480
ATCGCACCCA TTCAAGCAGG GATGATCTAT AAAATGAATG ACGCTTTTGG AATGGATTG	540
GATAAATCTG TGGGCGCGAG TTTGGTCGCA GGATTGTTAG GCGTAAACTG TCGCGCAAGT	600
GGGGAGGACT CTCGT	615

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...123
 - (D) OTHER INFORMATION: /note= "chemotaxis protein cheW"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTGCTTGGCG TGTTYAATTT AAGGGGCAAT GTCTTCCCTT TGATCAGTTT GCGTTTAAAG	60
TTTGGCTTGA AAGCCGAAAA ACAAACAAA GAACTCGTT ATTTGGTGGT ACGCCATAAC	120
GAT	123

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 657 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTGAAAAGCG TTTTTCAGCGA AGAAAAAGAA ACGCCTGTTA CTAAAGAAAA CGGCTCTTAT	60
TTGATCGCTT ATGACCCCCT AGATGGGAGT TCAGTGATGG AGGCGAATTT CTTAGTAGGC	120
ACGATTATAG GGGTTTATGA AAAGGATTAT AAGGCGCAAA ATTTAGTTGC AAGCCTTTAT	180
GTGGTTTTTTG GGCATAAAAT AGAATTGGTG GTGGCTTTAG AAGAAGTTTA TCGTTACGCT	240
TTTTATCAAA ACAAGTTTCA TTTTATAGAA ACCATCGTTT TAGAAAATAA GGGTAAAATC	300
ATCGCTAGCG GAGGCAATCA AAAGGATTTT TCYTTGGGCT TAAAAAAGGC TTTAGAAGGG	360
TTTTTTGCAG AAAATTACCG CTTGCGATAC TCAGGATCTA TGGTGGCTGA TGTCCATCAT	420
GTGTTGGTTA AAAAGGGCGG AATGTTTTCC TACCCGCAAA AGAAATTGCG AAAGCTTTTT	480
GAAGTCTTTC CTTTAGCCTT GATGGTTGAA AAAGCTAAAG GGGAAGCGTT TTATTTTGAT	540
AAGGGGGTTA AAAAGCGTTT GCTAGATCAA AGCGTAGAAA GCTACCATGA AAAAAGCGAA	600
TGCTATTTAG CCAGCCCGCA TGAAGCTCAG ATTTTAGAAA AACATTTAAA GGGAGAA	657

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 564 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATGAAAAGCA TTGGAGAAGT GATGGCGATA GGGGGCAATT TCTTAGAAGC CTTACAAAAA	60
GCGTTATGCT CTTTGGAAAA CAATTGGCTA GGGTTTGAAT CGTTAAGCAA AGATTTAGAG	120
GCGATAAAAA AGGAAATCCG CCGGCCCAAT CCCAAACGCT TGCTCTATAT TGCTGATGCG	180
TTCAGGTTGG GCGTTTCTGT GGATGAAGTG TTTGAATTAT GCCAGATTGA CAGGTGGTTT	240
TTATCTCAAA TTCAAAAAC AGTCAAAGCA GAAGAGGGCA TCAATTCTAG CGTTTTAACG	300

GACGCCAAAA AATTGAGAGG GCTTAAAAAT TTAGGCTTTA GCGATGCCAG GATTGCCACT	360
AAAATCAAAG AAAATGAAAA TTTAGAGGTC AGCCCTTTTG AAGTGGAATT AGCTAGATCT	420
AATTTACAAA TCGCGCCCCA TTTTGAAGAA GTGGACACTT GCGCGGCGGA GTTTTATCG	480
CTCACGCTTA TTTGTATTCC ACCTATGCCC CTAACCCTTT GCCCCTATT GGAAACAAAC	540
AAGAAAAACA AGAAAAGAAA ATCC	564

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 693 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...693
 - (D) OTHER INFORMATION: /note= "transmembrane receptor"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATGTTTGGGA ATAAGCAGTT ACAGCTTCAA ATCAGTCAAA AAGATTCTGA GATTGCGGAG	60
TTAAAAAAG AAGTCAATCT CTATCAAAGC CTTTTAAATT TGTGCTTGCA TGAGGGTTTT	120
GTAGGTATTA AAAACAATAA AGTCGTTTTT AAAAGCGGGA ATCTTGCAAG CTTAAACAAT	180
TTAGAAGAAC AAAGCGTTCA TTTTAAAGAA AACGCAGAAA GCGTTAATTT ACAAGGGGTT	240
TCTTATTCTT TGAAAAGCCA AAATATTGAC GCGGTGCAGT ATTTTTCATT GGCTAAAAAA	300
ACAGGGGGTG TGGGGGAATA CCATAAAAAT GATTTGTTTA AGACTTTTTG CACGAGCTTA	360
AAGAGGGGCT TAGAGAACGC GCAAGAAAGC ATGCAGTATT TCCATCAAGA AACAGGCTTG	420
CTCTTGAATG CGGCTAAAAA TGGCGAAGAG CATTCTAATG AAGGATTAAT AACCGTTAAT	480
AAAACGGGTC AAGACATTGA ATCGCTTTAT GAAAAGATGC AAAACGCCAC TTCGTTAGCG	540
GACTCCCTCA ACCAACGGAG CAATGAAATC ACTCAAGTCA TTTCTTTGAT TGATGATATT	600
GCAGAGCAAA CCAATCTCTT AGCCCTAAAC GCCGCTATTG AGGCCGCACG AGCGGTGAAC	660

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ATGTGGATTA TGTCTTCACT TTCTAGTTCA TTCTTTCATT CGCTCTTCTT CATCAAATCA	60
AACCCTGGCC AACTCTTAAA AGGTTGGGGT TCAAAAATCT TTTTCATAAA TAGAAAGTTT	120
GTTTTAGCAC AGTATAATCC TAGCGTTTCA ATTTTTATTT TACTCAATAG GGTGTTTGGT	180
GTTGGCGTT	189

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...459
- (D) OTHER INFORMATION: /note= "Outer membrane 30K protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GTGGGCGCTA ACCCTGTGCC GCATGCGCAA ATCTTGCAAT CAGTTGTGGA TGATTTGAAA	60
GAGAAAGGGA TCAAATTAGT GATCGTGTCT TTTACGGATT ATGTGTTGCC TAATTTAGCG	120

CTCAATGACG GCTCTTTAGA CGCGAATTAC TTCCAGCACC GCCCTTATTT GGATCGGTTT	180
AATTTGGACA GAAAAATGCA CCTTGTTGGT TTGGCCAATA TCCATGTGGA GCCTTTAAGA	240
TTTTATTCTC AAAAAATCAC AGACATTAAA AACCTTAAAA AAGGCTCAGT GATTGCTGTG	300
CCAAATGATC CGGCCAATCA AGGCAGGGCG TTGATTTTAC TCCATAAACA AGGCCTTATC	360
GCTCTCAAAG ACCCAAGCAA TCTATACGCT ACGGAGTTTG ATATTGTCAA AAATCCTTAC	420
AACATCAAAA TCAAACCCCT AGAAGCTGCG GTTATTGCC	459

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATGGGGCTTG TTGCGAGCGG CATTAACGAT GAAGAGCTTT TAAAATGGCT TCAGGCTTTT	60
GGGTAA AAAA TGGGTCTTTG TTTCAAGTG CTAGATGATA TTATAGACGT TACACAAGAT	120
GAAAAAGAAA GCGGTAA AAC CACGCATTTA GACAGCGCTA AAAACAGCTT TGTGAATTTA	180
TTGGGGCTAA AAAAGGCAGC GGTTACGCCC AA ACTT	216

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 627 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...627
- (D) OTHER INFORMATION: /note= "integral protein in
inner membrane"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGGGGTTTA ACCGCTTGGT GGATAGAGAC ATTGATAAGG ATAACCCAAG GACGAAAAAC	60
CGCCCGAGCG TGGATGGTAG GATCAGCGTT AAAGGCATGG TCATTTTCTAG CGTTTCAAAC	120
GCTCTTTTGT TCGTGGGAGT GAGTTATTTT ATCAACCCTT TAGCTTTCAA GCTTTCGTTA	180
CCTTTTTTAA TCATTTTAGG GGGTTATTCG TATTTCAAGC GCTTTTCTTC TTTGGCGCAT	240
TTTGTCGTGG GTTTGGCTTT GGGTTTAGCC CCCATTGCAG GAAGCGTGGC GGTTTTAGGG	300
GATATTCCTT TATGGAATGT CTTTTGGCY TTAGGGGTGA TGTTGTGGGT GGCTGGGTTT	360
GATTTGCTCT ATTCTTTACA GGATATGGAG TTTGATAAAG AAAGGGGCTT GTTTTCATT	420
CCTAGCCAAT TAGGGGAAAA ATGGTGCTTG AATCTTTCAA GGCTCTCGCA CCTGTGGCA	480
CTGATCTGCT GGCTTTGTTT TGTGAAATGC TATCATGGGG GGCTTTTTC GTATTTGGGC	540
TTAGGGGTTT CAGCCTTGAT CTTACTCTAT GAGCAGATTT TAGTGGCCAG AGATTATAAA	600
AACATTCCTA AAAGCCTTTT TTGTGAG	627

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GTGGAGCAAA ATAAATCAT TAAACTCTT ACTGTGGCGA CTATGGCGAT GATGCCCCC	60
ACATTGATTG GCACGATTWA TGGCATGAAT TTAAATTCA TGCCGGAGTT AGAATGGCAA	120
TACGGGTATC TTTTTCGCT GATTGTCATG GCGATTTCTA CGATTTTGCC GGTGATTTAT	180
TTCAAAAAGA AAGGTTGGT TGTAGCCTT CATGGAATTT TTATCCTCAC TCTTAGACGC	240

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

ATGTTGATT CAATCGTTTA TTTTTCAAT AAGAGCGGGT TTGTTACCAC GCTTGTTT	60
GTTTGGATTT CGCTTTATTT GGTGATGACT TTATGGGTCT TTTTGTATAA AAGCATTGTA	120
TTAAAGATTG AACTCAGGCG CGAGATGCAA TCTTTGTCTA ACATTCTTAA TGGAGCGCAA	180
GACGCTCCAG AGCATTTTAT GTTTAATAAA AAAAGAAATG ATGAGACCAA AAGGTATTCT	240
AATGAATTGT TGCAGGSCTT GGAAACACCA GGTCT	276

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATGGCGATGC TYTATTGCAT GCGTTATTG ATGCCGATTT TAGGAGCGAT TAAAGGGGGG	60
GATATTGGCG AATGGTTCCC TGATAATGAC CCCAAATACA AAAACGCCTC TTCTAAAGAG	120
CTTTTAAAAA TCGTGTTGGA TTTTCTCAA AGCATTGGGT TTGAATTGCT TGAAATGGGA	180

GCGACCATCT TTAGCGAAAT CCCTAAAATC ACTCCTTACA AACCGGCGAT TTTAGAGAAT	240
TTGAGCCAAC TTTTGGGTTT AGAAAAATCT CAAATCAGCT TGAAAGCCAC TACAATGGAA	300
AAAATGGGGT TCATTGGCAA ACAAGAAGGG CTGTTAGTCC AAGCGCATGT GAGCATGCGT	360
TATAAACAAA AACTT	375

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...3534
- (D) OTHER INFORMATION: /note= "cytotoxicity associated immunodominant antigen [*H. pylori*]"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ATGATACCAA ATTTAGATAT AGAAGGAGAA ACAATGACTA ACGAAGCCAT TAACCAACAA	60
CCACAAACCG AAGCGGCTTT TAACCCGCAG CAATTTATCA ATAATCTTCA AGTGGCTTTT	120
ATTAAAGTTG ATAATGTTGT CGCTTCATTT GATCCTAATC AAAAACCAAT CGTTGATAAG	180
AATGATAGGG ATAATAGGCA AGCTTTTGAG AAAATCTCGC AGCTAAGGGA GGAATTCGCT	240
AATAAAGCGA TCAAAAATCC TACC AAAAAG AATCAGTATT TTTCAAGCTT TATCAGTAAG	300
AGCAATGATT TAATCGACAA AGACAATCTC ATTGATACAG GTTCTTCCAT AAAGAGCTTT	360
CAGAAATTTG GGAATCAGCG TTACCAAATT TTTATGAATT GGGTGTCCCA TCAAAACGAT	420
CCGTCTAAAA TCAACACCCA AAAAATCCGA GGTTTTATGG AAAATATCAT ACAACCCCT	480
ATCTCTGATG ATAAAGAGAA AGCGGAGTTT TTGAGGTCTG CCAAACAAGC TTTTGCAGGA	540
ATTATCATAG GAAACCAAAT CCGATCGGAT CAAAATTCA TGGGCGTGTT TGATGAATCT	600
TTGAAAGAGA GGCAAGAAGC AGAAAAAAT GGAGAGCCTA ATGGAGATCC TACTGGTGGG	660
GATTGGCTTG ATATTTTTTT ATCATTTGTG TTTAACAAAA AACAATCTTC CGATCTCAAA	720

GAAACGCTCA	ATCAAGAACC	AGTTCCTCAT	GTCCAACCAG	ATGTAGCCAC	TACCACCACT	780
GACATACAAA	GCTTACCGCC	TGAAGCTAGG	GATTTGCTTG	ATGAAAGGGG	TAATTTTCT	840
AAATTCACCTC	TTGGCGATAT	GAACATGTTA	GATGTTGAGG	GAGTCGCTGA	CATTGATCCT	900
AATTACAAGT	TCAACCAATT	ATTGATCCAC	AATAACGCTC	TGTCTTCTGT	GTTAATGGGG	960
AGTCATAATG	GCATAGAACC	TGAAAAAGTT	TCATTGTTGT	ATGGAAACAA	TGGTGGTCCT	1020
GAAGCTAGGC	ATGATTGGAA	CGCCACCGTT	GGTTATAAAA	ACCAACGAGG	CGACAATGTG	1080
GCTACACTCA	TTAATGTGCA	TATGAAAAAT	GGCAGTGGGT	TAGTCATAGC	AGGTGGTGAG	1140
AAAGGGATTA	ACAACCCTAG	TTTTTATCTC	TACAAAGAAG	ACCAACTCAC	AGGCTCACAA	1200
CGAGCATTGA	GTCAAGAAGA	GATCCAAAAC	AAAgTggATT	TCATGgAATT	TCTTgCACAA	1260
AATAATgCTA	AATTAGACAA	CTTgAGCAAG	AAAGAGAAAG	AAAAATTCCA	AAATGAGATT	1320
GAAGATTTTC	AAAAAGACTC	TAAGGCTTAT	TTAGACGCCC	TAGGGAATGA	TCACATTGCT	1380
TTTGTTTCTA	AAAAAGACAA	AAAACATTTA	GCTTTAGTTG	CTGAGTTTGG	TAATGGGGAA	1440
TTGAGCTACA	CTCTCAAAGA	TTATGGGAAA	AAAGCAGATA	AAGCTTTAGA	TAGGGAGGCA	1500
AAAACCACTC	TTCAAGGTAG	CCTAAAACAT	GATGGCGTGA	TGTTTGTTGA	TTATTCTAAT	1560
TTCAAATACA	CCAACGCCTC	CAAGAGTCCT	GATAAGGGTG	TGGGTGCTAC	GAATGGCGTT	1620
TCCCATTTAG	AAGCAGGCTT	TAGCAAGGTA	GCTGTCTTTA	ATTTGCCTAA	TTTAAATAAT	1680
CTCGCTATCA	CTAGTGTCGT	AAGGCAGGAT	TTAGAGGATA	AACTAATCGC	TAAAGGATTG	1740
TCCCCACAAG	AAGCTAATAA	GCTTGTCAAA	GATTTTTTTGA	GCAGCAACAA	AGAATTGGTT	1800
GGAAAAGCTT	TAAACTTCAA	TAAAGCTGTA	GCTGAAGCTA	AAAACACAGG	CAACTATGAC	1860
GAGGTGAAAC	AAGCTCAGAA	AGATCTTGAA	AAATCTCTAA	AGAAACGAGA	GCGTTTGGAG	1920
AAAGATGTAG	CGAAAAATTT	GGAGAGCAAA	AGCGGCAACA	AAAATAAAAT	GGAAGCAAAA	1980
TCTCAAGCTA	ACAGCCAAAA	AGATGAGATT	TTTGCGTTGA	TCAATAAAGA	GGCTAATAGG	2040
GATGCAAGAG	CAATCGCTTA	CGCTCAGAAT	CTTAAAGGCA	TCAAAGGGA	ATTGTCTGAT	2100
AAACTTGAAA	ATATCAACAA	GGATTTGAAA	GACTTTAGTA	AATCTTTTGA	TGAATTCAAA	2160
AATGGCAAAA	ATAAGGATTT	CAGCAAGGCA	GAAGAAACAC	TAAAAGCCCT	TAAAGGCTCG	2220
GTGAAAGATT	TAGGTATCAA	TCCAGAATGG	ATTTCAAAAG	TTGAAAACCT	TAATGCAGCT	2280
TTGAATGAAT	TCAAAAATGG	CAAAAATAAG	GATTTTCAGCA	AGGTAACGCA	AGCAAAAAGC	2340
GACCTTGAAA	ATTCCATTAA	AGATGTGATC	ATCAATCAAA	AGATAACGGA	TAAAGTTGAT	2400
AATCTCAATC	AAGCGGTATC	AGTGGCTAAA	GCAACGGGTG	ATTTCAGTGG	GGTAGAGCAA	2460

GCGTTAGCCG ATCTCAAAAA TTTCTCAAAG GAGCAATTGG CTCAACAAGC TCAAAAAAAT	2520
GAAGATTTCA ATACTGGAAA AAATTCTGCA CTATACCAAT CCGTTAAGAA TGGTGTAAAC	2580
GGAACCCTAG TCGGTAATGG GTTATCTAAA GCAGAAGCCA CAACTCTTTC TAAAAACTTT	2640
TCGGACATCA AGAAAGAGTT GAATGCAAAA CTTGGAAATT TCAATAACAA TAACAATAAT	2700
GGACTCGAAA ACAGCACAGA ACCCATTTAT ACTCAAGTTG CTAAAAAGGT AAAAGCAAAA	2760
ATTGACCGAC TCGATCAAAT AGCAAGTGGT TTGGGTGATG TAGGGCAAGC AGCGAGCTTC	2820
CTTTTGAAAA GGCATGATAA AGTTGATGAT CTCAGTAAGG TAGGGCTTTC AGCTAACCAT	2880
GAACCCATTT ACGCTACGAT TGATGATCTC GGCGGACCTT TCCCTTTGAA AAGGCATGAT	2940
AAAGTTGATG ATCTCAGTAA GGTAGGGCTT TCAAGGGAGC AAAAATTGAC TCAGAAAATT	3000
GACAATCTCA ACCAGGCGGT ATCAGAAGCT AAAGCAAGTC ATTTTGACAA CCTAGATCAA	3060
ATGATAGACA AGCTCAAAGA TTCTACAAAA AAGAATGTTG TGAATCTATA TGTTGAAAGT	3120
GCAAAAAAAG TGCCTACTAG TTTGTCAGCG AAATTGGACA ATTACGCTAC TAACAGCCAC	3180
ACACGCATTA ATAGCAATGT CAAAAATGGA ACAATCAATG AAAAAGCGAC CGGCATGCTA	3240
ACGCAaAAAA ATTCTGAGTG GCTCAAGCTC GTGAATGATA AGATAGTTGC GCATAATGTG	3300
GGAAGTGCTC CTTTGTGAGC GTATGATAAA ATTGGATTCA ACCAAAAGAA TATGAAAGAT	3360
TATTCTGATT CGTTCAAGTT TTCCACCAGG TTGAGCAATG CCGTAAAAGA CATTAAGTCT	3420
GGCTTTGTGC AATTTTAAAC CAATATATTT TCTATGGGAT CTTACAGCTT GATGAAAGCA	3480
AGTGTGGAAC ATGGAGTCAA AAATACTAAT ACAAAGGTG GTTTCCAAAA ATCT	3534

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

ATGAAAGCGT TGAAGACTTT TTAAAAAAA TCCCTTATTC TGTTACTAGC AATTGCCTTA	60
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AACCACTTAA ACGCTGTGGC TATGATTGTG GATAATCCTA CGCAGAACGC TTGGAATGGT	120
GCTAAAAGAG CATGGGATGA AAGCAAGTGG GCTAAACATT TAGCCACTAT TACTGAAAGG	180
ATCAAGCTCG CTCAAGACAC ATTAGATAGG GCTAATCAGA CGCTTAATTC CATCAACAAA	240
GTGAATGATG TTTTGAACAA AACCAATCAA TTTCTAACAG GCAGTATTTT AAGCATCCCC	300
AATCCCATGC AGTATGTAGA AAAAATCCAA AGTTTTGCCA AGCAAGTTCA AGCCAATACT	360
GAAAGGATCA AAGAAAATGC ACAAACACTAT GATATACGCA ATCAAATTGC AGCCAAACGC	420
ATCTCTGAAA AATGCCCTGA ACTCAATTGG GATGTCAGTC AAGACGCGAG CCCTACAGAG	480
AAAAACTTAC ACCAATTTTT CACGAGCAAG GGGAAAGAAA GCGCTAACAC AAAGGCTCTA	540
AAGGATTTTG CTAACGCCAT AGGTAACACT CAAATCAGCA CGGCGAACGA TTTAGGAGCT	600
GGACTTAGAG GCAGAGCCTT ATTAGAATAC ATTTGCATTC AAAAAGGCAA TTTAGAAGCG	660
GCTAAAAAAA TCCAATTATT AGACAGCCAA ATGACTTTAG CTCTACTCAA TAACGACTAT	720
ACGGCTTATG AAAAAGCTTAG AGCTGAAAAA GAAGAATTAA AAAGACAAAT CGCTTCAAAT	780
GTGTATGCGA AAGTCAAACA GCTTGTTGTA GCTTCCCAAG ATAGAGCGTT TAGTCAAATG	840
GATAATGAGT TGGGCGTTAA AACTTTTGGG TTCAACGATG AGAATGTTAA AAAAGGTTAT	900
TGCAAGAAAG AAAACAGAAA TGGCAAAAGC GAGTGCATCC CTAACATGCT CAATGTTAAT	960
CGCTTAAAAG CGCAATTTGA TGAGCTTAAT TTAGATTATA GTAGGGATAT TGCTGGTAAA	1020
AAAGGTGAAG CAGCCGCTAA AGTGTTCAAT GACTACAAAC ACCGATTCCA ACAATTAAGC	1080
GTAGAACTG CTTTAGAAAT CGCTCAAAAT TTAAGTTTTA TGAATAAGAC GCTAGGTTTA	1140
ATGGTGCAAA TGCAAAGCTA TGCATTCAAG CAACAAATGG GCTATTTTGA AGATATTATT	1200
CCTGCTGACG CCCTAAAAGA TGACAAAGAG CATCAAGAAA ATCTTGAACA AAAACAACAA	1260
GAAATAGAGA AAGTCTATAG GGCTAAATTA GACGCTTATG GTTTCCTTAA TGGTAGTGTA	1320
GGAAAGGCAA GTGGCGTGAA TTCAAATAGT AATAATGAAG CCCCAAGCTC TGATAATATC	1380
CAGTCGTTTA ATCCGTAT	1398

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

ATGAATTTTT	TTGACACCCT	TATGGGTATG	TTTGTTGAGC	CATCTCAAAA	AGTAGCCAAA	60
AGTCTTGCTG	AACATGTGGG	TAGCTTTTTT	CATGCACAAC	TCATTTTAAA	CACAATTATT	120
ACTATTTTAT	TTATGATATG	GGCGTATAAG	CGTGTGAAAG	AGGGCGATAT	GTTTGAGTTT	180
AAAACCGCTA	TGGGTGTGGT	TGTATTTATA	GCGTTTGTAG	GATTTATCAA	TTGGGGGATT	240
AAAAATCCTA	ATGATTTTAA	CACTTATTTT	ATCAATACGA	TATTCTACCC	ATCTGAAAAA	300
CTAGCCATAC	TTATCGCTCA	AAGCCTAAAT	GATGGCTTAG	AAATCCCCAC	TAACACTAAT	360
TTAAGTCCTA	GTGAAATTTT	TAGCATAGGA	AATTTAGCCT	CAAGTGC GTA	TGCAATGATA	420
GTTAATCTGT	GGGATAATGC	TTTTGATGGT	ATTAACATGT	TTAATTGGCT	CACAATGATA	480

CCTAAAATAA TTATGTTTTT TTTAGTGATT TTAGGGGAAT TATTGTTTTT AGGCTTATTG	540
CTTATTATTG TGTTATTAGT TACAGCAGAA ATTTTATGT GGTCAGCATT AGGTTTAATT	600
GTATTGCCTT TAGGTTTAAT CCCCCAAACC AAAGGCATGT TATTTAGCTA TCTTAAAAAG	660
CTCATTTCCTT TTAATCTTTA TAAACCTTGT ATGATGTTAG TAGCTTTTTT TAATTATGGA	720
ATAATCTATA AAGTCAATAC TTTAATCCCC ACTAAACACG AAGTCACACA AGGCTTTTAT	780
GGCAATGCGG ATAAAATGGC AAATGAGGGA AAAATTATTG ATGTCTTTGG CAATGTCTTA	840
GAAGGAGATT GGAACCTCTTA TATAGCCCAT AGTTCTATTG TAGGCTTTTT AACCATTATT	900
GTTTTAGGTT CTGTGATTG TTTCTTTCTA GTCAAACGAG TGCCTGATTT TATCAATAAT	960
ATCTTTGGCA CAAGTGGAGG CGTGGGGGCA GTAACAGAAA TGATGCAAAA AATTGGCATG	1020
ACAATAGGCG GAGCTGTATT TGGGGGTAGT GCAGTTATGG TTGCTAATCA AGTTAAGCAA	1080
GCCTATCAGA GTGCTGGGGG CGGACTAGCA GGAATTCAAG CTGGAGCTAA AGCTTTTGGG	1140
CTTGGAGCAA TCAGTGGAGG GGCAAGTGCT ATGGCAAACC ACAGGAGTGT TAAAGCTGGG	1200
GTGAAACACT TTGTAGCAAG TGTAAAAAGT GGCTTTGGAT TTGATAATGA TAAAAATAAT	1260
AAA	1263

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...267
 - (D) OTHER INFORMATION: /note= "ARGININE TRANSPORT ATP-BINDING
[E.coli] & homology to Myco. leprae
U00013_12 abc2"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ATGGATGAAC CAGAAACCAG TTTAGAGCAA AACGCTCTTA TAAGACTATC AAATCTCATA	60
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AGCTTGCGCA ACACCCAACA ACTTACAAGT ATCATCGCCA CTCATGATCC TATTGTCTTA	120
GATAGTTGCG AATGGGTATT GCTCCTTAAG AATGGCAACA TTGCTCAATA CAAACCTTTA	180
AATTCTATAT TAAAATCTGT AGCTAAACT TTAACTTTA AAGAAAAACC AACCACAAAA	240
GACTTATTAG CGTTACTAAA GGATATT	267

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GTGAAACCT TAGGATTGTC TTCGCTTGGT GGGACTTTAG AATTTTACGA TTTTATCATC	60
TTTGTATTTT TTACAAGTAT CATTGCCAAA CACTTTTTCC CAAACACGCT TAGCCCTATC	120
TGGTCTGAAA TCAACACTTA TGGGATCTTT GCTGCAGGTT ATCTGGCGCG CCCGCTTGGT	180
GGCATAGTGA TGGCCCACTT TGGGGATAAA TTCGGTCGTA AAAACATGTT CATGCTCTCT	240
ATTTTATTAA TGGTAATCCC AACCTTTGCG CTAGCTTTGA TGCCAACTTT TAATGATTTG	300
GTGGGTTTTG GCGTGGATAG CATGGGGCTT ACCCCTAAAA ACGCTCATTA TCTTGGTTAC	360
ATAGCTCCTG TTTTTTTRGT RCTTGTTAGG ATTTGTCAAG GCGTCGCTGT GGGTGGTGAA	420
TTGCCTGGCG CTTGGGTTTT TGTCCATGAA CATGCCCCAC AAGGACAAAA AAACACTTAT	480
ATCGGTTTTT TAACCGCTTC CGTAGTTTCT GGGATTTTGC TTGGGAGTTT GGTTTATATC	540
GGGATTTACA TGGTTTTTGA CAAGCCTGTT GTTGAAGATT GGGCTTGGCG GGTTCCTTTT	600
GGGCTTGGAG GAATTTTGG TATCATTTCT GTGTATTTGA GGCCTTTTTT AGAAGAACT	660
CCCGTTTTTC AGCAAATGAA GCAGGGACGA TGCCTTAGTC AAATTCCCGC T	711

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1413 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ATGCGCAAAT TTTTGGATGG GGCAAAAAGT GAGGTTTTAA AATACGATGT GATTTCCTTTT	60
GATATTTTTG ATACCTCCT TCTAAGACCT TTCATTAAAC CCACAGATTT ATTTTTGTAT	120
ATTGAGACTA AATACAATAT TAAAGGTTTT CATCAAGCAA GGATCCTGGC AGAAATGCAA	180
TCCAGAAAAT TAAGTAAAAG ACAAGACATT ACTCTAGATG AAATTTATCA TCAAATCCCA	240
AAAGAGTTTC ATTCATATAA GGGAGTAGAA ATCGCTACTG AAAAAGAGGT GCTTGTTCCA	300
AACTTGGA GA TGTAGAACT CTATCGTTTC GCTAAAGAGA ACAATAAGAG AGTGATTATT	360
GTATCAGATA TGTATTTACC TTTAGAGGTT CTTGAAGATA TTTTAATTTT TAAGGGTTTT	420
GATGGTTATA CAAATTTCTA TCTTAGTAAC CATATAATGC TCACTAAACA TTCAAAGGAT	480
TTGTTTAAGC ATGTTTTAAA ACAAGAAAAT ATTACTAATA CGCAGATATT GCATATCGGT	540
GATAATTCTT GGGCAGATGA CGCTATGCCT AAAAGTTTAG GCATAGCAAC GCTATTTAGA	600
AAAAGCGTGT TGAAACAATT AGAAGAAGTT TTTCTTAAAT ACAAACATT TAATCCAACC	660
AGTGTTGCGC AAAGTTTTAT TTTAGGATCT TTATGCGTTT TTTATAAAAA TTATATTCAA	720
AAACATGAAA AATTTGATTA TTGGTTTCTT TTAGGAGCGA TGCAGGCAGG AATTGCAGCC	780
GTTGCTTATT GCCAGTTTAT CTATAAGGAG ATTCACAAAA GAAATATTGA TACTTTAGTG	840
TTTGTTGCGC GAGATGGTTA TTTATTGCAA AAAATTTTTT ATATTTTATA TCCAAATTCA	900
TATAAACTA CTTATGTCTA TGCTCCCAGA ATTTTAAAAA AAGCGGTATT TTTAGAAGTC	960
GTAGAGGGCG AGAGTTTGA AATTTTGCGT ATTTTAGAAG GCGAAGAAGA AGTTAAAAAG	1020
AAGCAAATCA CCACCAACCA ACAGGCGTAT GTATATCTCT ATAGCAATTT TGAACATTGC	1080
CGCCATTTAG CGTTAAAATG TTTAGATAAT TACAGAAAAT ACTTGTTTTT ATCAAATTTA	1140
GAAGGAAATA TCGCTATTGT AGATACGATT ACTTTAGGCT ATTCTTCGCA AGGGTTAATC	1200
CAAAAAGCTT TAAATAAAGA AGTTTTTGGG TGCTATGTGG ATCTCCTAAG AATTTTAAAT	1260
TATGATTGCG TGAGTTTCTT ACCTTTTTCA CACCCTAAAC CCGTTTATTT TCATAATTGG	1320

GATTTTATGG AGTTTTTGCT AACAAAGCCCT GAATACCCTA TTTTAAATGT AGAAAATGGC	1380
GTTCCAATCT TATCAAAAAG ACGTTTCATC TTG	1413

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GTGTTGAAAT TCTTTGAAGA TTCCAAACAG CTTAGCACGC CTATGGGAAA GAGCGCGGTG	60
GGGATTTTGA TTTTCCAAGA TATTGCAGCC ATTCCCATGC TTTTAATTTT GACGATTCTA	120
GGCAGTAAGG ATTCTCATGT CAATTTGCTC ATTCTTAAAA CCCTTATTTC AGCGGGGATT	180
ATTTTAATTC TTTTATTATT GCCTGGAAAA AAAGGGGCTA ATCTCATCTT AGAGCAAGCG	240
AAAGACACGC GCTTGCCTGA AATCTTTATA GGCACGGATT TTAGTGATTG TTTGCAGCGC	300
GGCGGGGTTG AGCCATTTTT TTGGGTTTTT TATGTCTTTG GGGGCGTTCA TTGTGGGCAT	360
GGCGATTTC	369

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

ATGATTTTAG CCCTTTTGAT TTCTAAAGAA AAAACGCATT TAGAAGCGTT GTATTATTTG	60
AGCTATGGCG TGCTTTTAGG GGGCGTGGCT CAAATCTTAT TACACTTTTA TCCTTTAGTA	120
AAATTAGGCT TATGGGATTT ATTATTTAAA GGGTTGTTGG GTTTTAAGAC TAAAAATACA	180
AACAAAAAAG AATATCGTTT GAATAGGGCT AAAAAGGATC TAAAAGCGTT TTTCAAGCAA	240
TTCTTCCCCA GCGTCTTAGG CAATTCTAGC GCTCAGATCG CTTCTTTTTT AGACACCACA	300
ATCGCTTCTT TTCTGGCGAG CGGGAGCGTG TCTTATTTGT ATTACGCCAA TAGAGTCTTC	360
CAGCTCCCTT TAGCCTTATT CGCTATCGCT ATCTCCACAG CTCTTTTCCC TAGCATTGCG	420
ATCGCGCTTA AAAACAACCA GCAGGATTTA ATCTTACAAC GCTTGCAAAA GCGTGGGTTT	480
TTTTTGGTGG GGGTTTTGCT TCTTTGCAGC ATTGGGGGGA TAATGTTAAG CAAAGAAATC	540
ACCGAACTTT TATTTGAAAG GGGGCAATTT AGCCCTAAAG ACACCCTAAT CACTTCGCAA	600
GTCTTTTCGC TCTATCTTTT AGGCTTGCTC CCTTTTGGGC TAACCAAACCT CTTTCTTTA	660
TGGCTTTATG CGAAATTAGA GCAAAAAAAA GCGGCTAAAA TCTCTTTAAT TTCGCTTTTT	720
TTAGGTTTAG CGGCTTCTTT GAGTTTAATG CCTTTGTTAG GGGTTTTGGG TTTGCGT	777

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GTGCTAAAT ACCCTACRRT GTTCATGTGT GCGGATGCGG TCATTATCAG TAAGGCGGAC	60
ATGATTGAAG TGTTTAATTT TAGGGTTTCT CAAGTCAAAG AAGACATGCA AAAATTAAAG	120
CCTGAAGCGC CCATTTTTTTT AATGAGCTCC AAAGACCCTA AAAGCTTGGA AGATTTTAAA	180
AATTCCTTT TAGAAAAAAA GCGTGAAAAT TACCAATCCA CGCATTCGTT T	231

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ATGCTGCTTT GCGCGGAAG GAATGAGACT TTAAAAAAG CGGTGCCTAT TGGTGTGGGC	60
TTGATAGAGA GCGCGATCAA TTTAACGAGA ATGTGCCTTA AAAACCCTGA TACAGAAAGC	120
CTTATTTTTA TAGGGAGCGC GGGGAGTTAT AGCCCAGAAA CGGAGATTTT GAGCGTGTTC	180
GAAAGCATTG AAGGCTATCA AATTGAAGAG AGTTTTAGCC ATTTAAACAG CTACACGCCT	240
TTGGATAATT TCATTACAT AGAAACTAAA GAGCAGGCTC TTTTGTAAAG GGTGCGTGTG	300
AATAGCAGTA ACTACATCCA CACCAGCGAA ATGTTTGCTA AAAAAATGGT TCAAAAGGGC	360
GTTTTATTAG AAAACATGGA GTTTTTTAGC GTCTTAAGCG TGGCTAAAAT TTTTCTTTA	420
AAGGCTAAAG GGATTTTTTG CGTGAGCAAT CATGTAGGGC TTAACGCGCA TAAGGAATTT	480
AAAGAAAACC ACGCCAAAGT CAAACAGATT CTAGAAAACA TCATTGATAG TTTGATAGTT	540

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...639
- (D) OTHER INFORMATION: /note= "FLAGELLAR M-RING PROTEIN"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTGTATGAAG AAAGGATCAC TCTGGCTTCT CAAGGGATCC CTAAAACGAG TAAAGTGGGC	60
TTTGAAATCT TTGACACTAA AGACTTTGGG GCGACTGATT TTGATCAAAA CATCAAACCT	120
ATTCGCGCCA TTGAGGGGGA ATTGTCGCGC ACGATTGAAA GTTTAAACCC CATTCTTAAA	180
GCCAATGTGC ATATTGCAAT CCCTAAAGAC AGCGTGTTTG TGGCTAAAGA AGTCCCTCCT	240
AGCGCTTCAG TGATGCTCAA GCTTAAGCCT GACATGAAGC TTTCACCCAC TCAAATTTTA	300
GGGATTAAAA ATTTAATCGC TGCAGCTGTG CCTAAACTCA CGATAGAAAA CGTGAAAATC	360
GTGAATGAAA ATGGCGAATC AATAGGCGAG GGCGATATAC TAGAAAACCTC CAAAGAATTA	420
GCCTTAGAGC AATTGCGCTA CAAACAAAAT TTTGAAAACA TTTTAGAAAA TAAGATCGTC	480
AATATCTTAG CCCCTATTGT GGGGRGTAAA AACAAARGTRG TCRCAARRGT CAATRCGGAG	540
TTTRATTTCA RCCAAAAGAA AAGCACCAAA GAGACTTTTG ATCCCAATAA TGTCGGTAAG	600
GAGCGAGCAA AATTTAGAAG AAAAAAAGA AGGCGCTCC	639

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GTGATAARGA AAGGCTATAT AAGAGGAGAT CTTATGCGTA TAGTTAGAAA TTTATTTCTT	60
GTATCGTTTG TGGCGTATAG TAGTGCGTTC GCAGCGGATT TAGAAACCGG AACCAAAAAC	120
GACAAAAGA GCGGTAAAAA ATTTTACAAA CTCCATAAAA ACCATGGCTC AGAAACCGAG	180
ACTAAAACG ATAAAAAGCT TTATGATTTC ACTAAAATA GCGGATTAGA AGGCGTGGAT	240
TTAGAAAAAA GCCCTAACCT TAAAAGCCAT AAAAAAGCG ATAAAAAGTT TTATAAACAA	300
CTCGCTAAAA ACAATATCGC TGAAGGGGTG AGCATGCCGA TTGTGAATTT CAATAAAGCC	360
CTATCTTTTG GGCCTTATTT TGAAAGGACT AAAAGCAAAA AAACCCAATA CATGGACGGC	420
GGGTTGATGA TGCACATCCG TTTT	444

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...843
- (D) OTHER INFORMATION: /note= "spoIIIE gene product"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTGATGATCG ATCCCAAAAT GGTGGAATTT AGCATTATG CGGACATCCC TCATTTACTC	60
ACGCCCATTA TCACTGACCC TAAAAAGCT ATCGGGGCTT TGCAAAGCGT GGCTAAAGAA	120
ATGGAGCGCC GATACTCTTT AATGAGCGAA TACAAGGTTA AAACCATTGA TTCTTATAAT	180
GAACAAGCCC AAAGTAACGR CGTTGAAGCG TTCCCCTATT TGATTGTGGT GATTGATGAA	240
TTAGCGGATT TGATGATGAC AGGGGGCAAA GAAGCGGAGT TTCCTATCGC TAGAATCGCT	300
CAAATGGGGC GAGCGAGCGG CTTGCACCTC ATTGTGGCGA CCCAACGCCC GAGCGTGGAT	360
GTCGTAACCG GCTTGATTAA AACCAACTTG CCTTCAAGGG TGAGTTTTAG GGTAGGCACT	420
AAGATTGATT CTAAAGTGAT TTTAGACACC GATGGGGCGC AAAGCTTACT AGGAAGGGGC	480
GATATGCTCT TTACCCCCC AGGAACAAAC GGGTTAGTGC GCTTGCATGC CCCCTTTGCC	540
ACTGAAGATG AAATCAAAAA AATCGTGGAT TTTATTAAAG CCCAAAAAGA GGTGGAATAC	600
GATAAAGATT TCTTGCTAGA AGAATCGCGC ATGCCTTTAG ACACCCCTAA CTATCAAGGC	660
GATGACATTC TAGAAAGGGC TAAAGCGGTG ATTTTAGAAA AAAAGATCAC TTCTACGAGC	720
TTTTTACAAC GCCAATTAAA AATCGGCTAC AACCAAGCCG CCACCATTAC TGACGAATTA	780
GAAGCTCAAG GCTTTCTATC CCCAAGAAAC GCCAAAGGCA ACAGAGAGAT TTTGCAAAAT	840
TTT	843

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 432 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

 (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

ATGAATTTTT TTAAATCCT TTAATGGAG TTAAGAGCCA TTGTTTCTCA TAAGGGCGTT	60
TTATTGATCC TTATAGGCGC TCCTTTAATC TATGGCTTGT TATACCCTTT GCCTTATTTG	120
AAAGACATCG TAACGCAGCA AAAAATCGCC CTTGTAGATG AAGACAATTC CTCCTTTTCT	180
AGGCAATTAG CCTTCATGGT GCAAAGCTCC AACGAGTTAG AAATCGCTTT CTTTAGCCCC	240
TCTATGCTGG AAGCCAAAAA GCTTTTAAAA GAAGAAAAAA TTTATGGGAT CTTACACATT	300
CCCTCTCATT TTGAAGCCAA TATTTATAAA CAAAGTGCCT GTAACGATAG ATTTTATGC	360
GAACGCCAAT TACTTTTTGA TTTATGGTGC GTTAGCGAAT GCGGTGGTGG GGAGCATCAA	420
CGCCTTAAAC GA	432

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 219 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

 (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTGGGGGGCT TAGCCATGCT GGGCTTTTTT TATAATATTG AAAAAATTTC GCTCGCCACA	60
GCGACGGCTT TCTCGCAATG CGCGCCTAWT TATACGGTGC TCCTTTCCCC TTTGCTTTTG	120

AAAGAAAAGC TCAAAAAGAAG CGCGTTAATT TCCGCATGCA TCGGGCTAGT GGGGGTGGTG	180
TTGATTTTCAG ATCCTAGCGT GGAAAATGTA GGACCTAGT	219

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 933 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GTGTGCTGGA CGGATTTGAT TCAAGGGCTT TTGATGATGA GCGCTTTAAT CGTGGTGCCG	60
ATTGTTATGA TAATCCATCT TGGAGGGATT GGAGAGGGGA TTAAAATCAT TAGAGAGATC	120
AAGCCTGAAA ACCTWTCTTT CTSGCAAGGC TCTAGCGTAG TCGCTATTAT TTCAAGCCTT	180
GCTTGGGGGT TAGGCTATTT TGGGCAACCC CATATTTTAG TCGCTTCAT GTCTATCCGC	240
TCCATTAGAG ATGTGCCTAA AGCGACCACT ATTGGGATTT CTTGGATGGT TATTTCTTTA	300
ATTGGGGCAT GCGTTATGGG GCTTTTAGGC GTTGCTTATG TACATAAATY TGACTTGAGT	360
TTAGAAGACC CTGAAAAGAT TTTCATTGTA ATGAGTCAAT TGCTCTTTAA CCCTTGGATC	420
ACAGGCATTT TATTGAGCGC GATTTTAGCG GCGGTGATGA GCACGGCCAG TTCGCAACTG	480
CTTGTAAGCT CTTCTACCAT TGCTGAAGAT TTCTATGCGA CGATTTTCAA TAAAAACGCC	540
CCCCAAAAT TAGTGATGAC GATTTCTAGG CTTTCGGTTT TAGGGGTGGC TTGCATCGCT	600
TTTTTCATTT CAACGGATAA AAACGCTAGC ATCCTCAGCA TCGTGAGTTA CGCATGGGCT	660
GGCTTTGGCG CGAGTTTTGG CTCTGTGATT TTGTTTTCAC TTTTTTGGTC AAGAATGACG	720
CGCATTGGCG CGATTGCTGG CATGCTCTCT GGGGCTAGCA CGGTGATTTT ATACGATAAA	780
TTTGGCAAAA GCTTTTTTGA TATTTATGAA ATCGTTCCGG GCTTTATTGT AGCGAGCGTA	840
GCTATTGTTG CGTTTAGTTT GTTTTCTAGC GTGCGATCAG GCACTAAAGA GGCCTTTGAA	900
ACCATGCTTA AAGAAATTGA GAGCTTAAAG CAT	933

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GTGGGGCTTT TTATCGTTTT GTTTTAAATT ATAATGAAGC ACCAAACCTC CCCCTATGCT	60
TTCACGCATA ATCAAGCCCT TGTCAC TCA ACCCCCCCT ATTTACGCA ACTCACTATC	120
CCTAAACCAA ATGACGCTTT AAGCGCGCAT GCGAGCTCTT TAATCAGCTT GCCTAACGAC	180
AATCTTTTGA GCGCTTATTT TAGCGGCACT AAAGAAGGGG CAAGGGATGT GAAAATCAGC	240
GCGAATCTTT TTGACAGCAA GACTAATCGC TGGAGCGAAG CCTTCATTCT TTTAACCAAA	300
GAAGAGCTTT CTCATCATTC GCATGAATAC ATCAAAAAA TTAGG	345

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 600 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...600
 - (D) OTHER INFORMATION: /note= "flagellar biosynthesis protein flhF"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATGCTTGTAG GGCCAACAGG CGTGGGGAAA ACGACGACTT TGGCTAAATT AGCCGCACGC	60
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TATTCTAGAA TGCTGGCTAA AAAATACAAG GTGGGCATTA TCACTTTAGA CAATTATCGC	120
ATTGGGGCTT TGGAGCAATT GAGTTGGTAT GCTAATAAAA TGAAAATGAG TATAGAAGCG	180
GTGATTGACG CTAAGGATTT TGCTAAAGAA ATTGAAGCTT TGGAATACTG CGATTTTATT	240
TTAGTGGATA CGACAGGGCA TTCGCAATAC GATAAGGAAA AAATTGCCGG TTTGAAAGAG	300
TTTATAGATG GGGGTTATAA TATTGATGTA TCCTTAGTGC TTTCGGTTAC CACTAAGTAT	360
GAAGACATGA AAGATATTTA TGATTCTTTT GGGGTGTTAG GGATTGACAC TTTAATCTTT	420
ACGAAATTAG ATGAGAGTAG GGGGTTAGGG AATTTGTTTT CTTTAGTGCA TGAAAGCCAA	480
AAGCCTATCA GTTATCTTTC TGTCGGCCAA GAAGTGCCTA TGGATTTGAA AGTGGCTACT	540
AATGAGTATT TAGTGGATTG CATGCTAGAT GGCTTTAGTA ACCCTAATAA GGAACAAGCA	600

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 792 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...792
 - (D) OTHER INFORMATION: /note= "vacuolating cytotoxin Hpylori"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GTGGGAGGAG CGAGCTTTAT TTCTGGGGGC AATGGCACGC TTTATGGCTT GAATGTGGGC	60
TATGACCGAT TGGTTAAAAG CGTGATCCTT GGGGGTTATG TGGCTTATGG CTATAGCGGT	120
TTTAACGGGA ACATCATGCA TTCTTTGGCT AATAATGTGG ATGTGGGGAT GTATGCGAGG	180
GCTTTTTTGA AAAGAAACGA ATTCACTTTG AGCGCGAATG AAACCTATGG AGGCAATGCG	240
AGTCATATCA ATTCTTCTAA TTCCTTGCTC TCTGTGTTGA ACCAACGCTA CAACTACAAC	300
ACCTGGACAA CGAGCGTGAA TGGGAATTAC GGCTATGATT TCATGTTCAA ACAAAAAAGC	360
GTGGTGCTAA AACCTCAAGT GGGCTTGAGC TATCATTTCA TAGGCTTGAG CGGGATGAAA	420
GGTAAAATGC AAAATCCAGC TTACCAACAA TTCGTCATGC ATTCAAACCC TTCTAACGAA	480

TCGGTTTTTAA CGCTCAACAT GGGGTTAGAG AGCCGTAAAT ATTTTGGTAA AAATTCCTAT	540
TATTTTGTA A CGGCGAGGTT GGGTAGGGAT CTTTTGATCA AAGCTAAAGG CGACAATGTG	600
GTGCGTTTTG TGGGTGAAAA CACTTTATTG TACCGCAAGG GGGAAATTTT TAACACTTTT	660
GCGAGCGTGA TCACAGGAGG CGAAATGCAT TTGTGGCGTT TGATGTATGT GAATGCGGGG	720
GTGGGGCTTA AAATGGGCTT GCAATACCAA GATCTTAATA TCACTGGGAA TGTGGGCATG	780
CGAGTGGCGT TT	792

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGGACGGCT ATGGGTTTTAA AATGCAAGAC TTGGGGCCAAA AAACCTCAAGT TATCCAACAC	60
ATCTTTGCCG GGGATGATGT GAGCGCTTTA GAAGTCAAAG AAAATGAATG CGTTAAAATC	120
RTGACTGGAG CGATGGTGCC AAAGGGAATA GAAACGATTG TTCCCATAGA ATGCATGCTA	180
GAGAGTCATA AAGATTTTCG CCTAGCTCCT AAAGATTTTA AAATTCACGC TAATATCCGT	240
CAAAAGGGCG AGAACGCTTC TTAAACAGC GTTTTAGTCC CTAAAAATAC CCGTTTGAAT	300
TATGGCCATA TCGCGCTCAT TGCCTCTCAA GGGTTCAAAG AAATCAAAGC GTTTAGAAAA	360
TTAAAAATCG CTCTCTTTAG TAGCGGCGAT GAATTAGTGC CTTTAGGGCA AAACGCCCTA	420
GAGTGCCAGG TTTATGATGT TAATTCAGTG GGTGTTTTTA ACATGCTTAA AAACACAAC	480
ACGCATTTTC TAGGGGTTTT AAAAGATGAT AAAAATTTAC AGCTTAAAAT ACTTGAATTG	540
CAAGGCTATG ATGTCATCCT TTCAAGTGCG GGGGTGAGCG TAGGGGATAA AGACTTTTTT	600
AAAGACGCTT TGAAAGAAAG AAACGCCCTT TTTTATTACG AAAAAGTCAA TCTCAAACCT	660
GGAAAGCCGG TAACTTTAGC CCAACTCAAT CAAAGCATT AATTAGGCTT ACCGGGTAAT	720
CCTTTAAGTT GCTTACTGGT TTTACGAGTT TTGATTCTAC CTTATTGGA GCGCTTATCC	780

TTAAATAAAG ATTTTAAATT AAAACCCTTT AAGGCTCAAA TCAATGCCCC TTAAAGCTT	840
AATAACAAAC GGACGCATTT AATCTTAGGC AACTATTCAA ACCACCAATT CATTCCTTAC	900
AACAACCGCT ATGAATCAGG AGCGATTCAA GCCCTTGCGC AAGTGGATTC TATCRCTTTA	960
ATTGATGAAG GAGTGGGATT GGTTCAGGGC GAAATTGAAA TTTTAAGGTT TGAAAAT	1017

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 438 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

ATGCCATACG CCTTAAGAAA AAGATTTTTC AAACGCCTTT TATTGTTTTT TTAAATTGTT	60
TGTATGATAA ATTTGCATGC CAAAAGCTAT CTGTTTTCTC CTTTGCCCCC AGCGCACCAG	120
CAAATCATT AAGACAGAGCC TTGCTCTTTG GAGTGCTTGA AAGACTTGAT GCTGCAAAAT	180
CAAATCTTTT CTTTTGTATC CCAATACGAT GATAACAACC AAGATGAGAG CCTTAAAACT	240
TATTACAAGG ACATCTTAAA CAAACTCAAC CCCGTATTCA TCGCTTCTCA AACTCCAGCT	300
AAAGAAAGCT ATGAGCCTAA GATTGAATTA GCGATTTTAC TGCCTAAAAA GGTGGTGGGC	360
CGTTATGCGA TTTTAGTGAT GAACACCCTT TTAGCGTATT TTGAACACCA GAAACAACGA	420
TTTCAATATC CAAGTCTT	438

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ATGCCTATTA ACCCTCTCTA TCTTTTCCCC AATCTTTTTA CCGCTAGCAG TATTTTTTTA	60
GGCATGATGA GTATTTTTTA CGCTTCCAGT TACCAATTG TCATGGCGTG TTGGTTAGTG	120
GTGGCGAGTC TTATTTTAGA TGGGCTTGAT GGGCGTGTCT CAAGGCTTAC CAAACACCAC	180

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 699 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATGCTTTCAG CTTGCTTTC TAAAATGGGG ACTTACGCCT TATTACGCTT CTTGCTCCCCG	60
CTTTTTCCTG AACTTTCAGA AATTTATTTA ACCCCCATAG CCATTGTGGC GCTGTGCATG	120
ATCATTTATG GAGGTTTTCT AGCCTACGCT CAAAAAGATT TAAAACCCCT CATCGCTTAT	180
AGCTCTTCT CGCACATGGG AGTCGTGGTG CTTGGGGTTT TTTCTTTCAA TGTTGAAGGG	240
GTTTCAGGGG CGGTGTTTAT GATGTTTGCG CATGGCGTTA TCGTCATGGG ATTATTTTTA	300
CTCGCTGGTA TCTTGGAAGA ACGCGCCAGC AGTTTAGAAA TCGCTCGCTT TGGATCGATC	360
GCTAAAAGCG CTCCTGTTTT TGCAGCCTTT TTTATGATCG TTTTAATGGC GAATGTGGGC	420
ATGCCTTTAA GCATTGGTTT TGTGGGAGAG TTTTGTARCT TGTTAGGGTT TTTTGCCACT	480
TACCCTCTTT TGGCTATCAT TGCCGGGACA AGCCTCATTC TATCAGCGGT TTACATRCTC	540
ACTTCATATA AAGATGTGTT CTTTGGCAAC TTAAAAACCG GGAACAACCA AATCAGCGTG	600
TTTGAAGATT TAAACGCTCG TGAGGTAGGG GTTTTAAGCG TGATTTTAGC CTTTGATCTT	660
AATTTTAGGG ATTTATYCYA AAGCGCTTTT AAAACCGAT	699

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTGGAATTGA TTAGCAATAA CCCTAACGCC AGCCAACAAT CTATCGTTAT TCCTTTGGAG	60
ACTTTTGCCT TGGCGCGAGC GTTAAAGGGA ATCTTT	96

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGAAAATTT TTGGGACTGA TGGCGTGAGG GGTAAGCAG GGGTGAACT CACCCCCATG	60
TTTGTGATGC GTTTAGGCAT TGCTGCCGGA TTGTATTTTA AAAACATTC TCAAACGAAT	120
AAAATTCTAA TCGGTAAAGA CACCAGAAAG AGCGGCTATA TGGTAGAAAA CGCTTTAGTG	180
AGCGCTCTCA CTTCCATAGG CTATAATGTG ATCCAAATAG GGCCTATGCC TACCCCTGCG	240
ATCGCTTTTT TAACCGAAGA CATGCGCTGT GATGCGGGCA TTATGATAAG CGCGAGCCAC	300
AACCCTTTTG AAGACAATGG CATCAAGTTT TTCAATTCCT ATGGTTATAA ACTCAAAGAA	360
GAAGAAGAAA GAGCGATTGA AGAAATCTTT CATGATGAAG AATTACTGCA TTCTAGCTAT	420
AAAGTGGGCG AGAGCGTCGG TAGCGCTAAA AGGATAGACG ATGTGATAGG GCCGCTATAT	480

CGCGCATTG AAGCACTCTY TYCCCAAACA TTT

513

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GTGCGAGCCG TGTGTTGCTT TGGTTTGAAA GCGGCGTTTT GTATAGGGAT TTTTCTCTAT 60

GGCGCTTATT ATTCCTAGA TGAGTTTTTA ATCAAGCTC 99

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GTGAGGAGCG GTAAAAGATT AGGCTATACC AATCAAGTGA TCACCGATAT TGTCAATATC 60

GGTATTGGGG GGTCAAGTTT AGGCGCTTTA ATGGTTTGCA CCGCCCTAAA ACGCTACGGC 120

CACCCAAGAT TARRAATGCA TTTTGTGTCT AATGTGGAAT GGCACGCAGA TTTTAGACGT 180

TTTGGAAGAA ATCAACCCGG CCAGCGCGCT 210

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

ATGAATCTTG TCTTTTTGTG GGCCGCTCTA GGAGGGGCTA TAGGGAGCTC GTTAAGGTAT	60
TTTGTGGGCA AAATGATGCC CAGTAAATTT TTAATGTTTG AAAGTTTCCC TTTAGGGACT	120
TTTAGCGTGA ATCTCATAGG GTGTTTTATC ATCGGCTTTA TGGGGCATTG GGCCGCTAAA	180
AAAGTTTTTG GTGATGATTT TGGGATTTTC TTTGTAACCG GAGTTTTAGG GGGTTTTACG	240
ACCTTTTCTT CTTATGGGTT AGACACTTTA AAACCTCTGC AAAAATCCCA ATACCTTGAA	300
GCCATTTCTT ATGTCTTAGG CACTAACCTT TTAGGGCTTA TTGGGGTAGC TATCGGTTGG	360
TTTTTGGCTA AGAATTTTGT AGGCGTTAAT	390

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATGTTGGAAG AACTGATTGA AAGAGTGTTG TTTGCCACTC GTTGTTTGCT AGCCCCCTTA	60
TGCATTGCCA TGTCGTTAGT GTTGGTGGTT TTAGGCTATG GTTTCATGAA AGAGTTGTGG	120
CACATGCTCA GCCATTTARA CACCATTAGT GAAACGGATT TGGTTTTATC AGCCTTAGGT	180
TTAGTGGATT TGTTGGTTCA TGGCCGGGCT TGTTTTGATG GTGCTGCTCG CCAGTTA	237

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ATGCACTATC AATTAACAAG TTTCAATATA ATACAAGATC TTTTATAAC TTGTCATGTG	60
TTAAGGATCA AAATGCGCGT GTTTGTTTGC TTTTATAGGGG TTTTGTATC TAACGGCTTG	120
GCTCGTTTTG GCTATGTGGT TTTAATCCCC CTACTCATTT TATCAGGGAG TTTAACCCCA	180
CACCAAAGCT TCCAAGTGGG TATTGCGGTG CTAATGGGCT ATGTTTTTGG GAGCTTTTTA	240
ATCCAATTTT TAAGCCCGTT AATGTCATTA SAAAGCATCG CTAAAATCAG TTTTAAATTA	300
ACACTT	306

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTGGATATGA AAGACGCTGT AGGGACTTAT AAAC TAYTCA GGGCT	45
--	----

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3081 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

 (A) NAME/KEY: misc_feature

 (B) LOCATION: 1...3081

 (D) OTHER INFORMATION: /note= "mature-parasite-infected
 erythrocyte surface antigen"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GTGTGTTTAG ACCATCAGGT TGGAGCAGGC AAGACTTTGT GCGCTATAGC CAGCTGCATG	60
GAACAAAAAC GCATGGGATT AGTGAATAAA ACGCTCATTG CCGTGCCTAA CCATTTAACC	120
AAGCAATGGG GCGATGAATT TTATAAGGCT TACCCTAACG CTAATGTGTT AGTTGTTGAT	180
AGCAAGGACA CCACTGAAAA AGAAAGAGAA CTTTTATTCA ATCAAATCGC TAACAACAAT	240
TATGACGCTG TGGTTATCGC GCACACCCAT TTGGAATTAT TGTCTAACCC TAGAGGAATC	300
ATAGAAGAAT TGAAAGAAGA AGAGCTAGTG AATGCTGAAA AAAACTTTGA AAGGCAAGAA	360
TTAGCTTATA AAAATAACCC TAGAGAACT AAAAAACCCA ATGAAAGAGC CTTTAAAAAC	420
AAGTTGGATA AAATCCGTGC TAAATACGAT GCGATTTTAG AAAACAAGG CTCTCATATT	480
GATATTAGTC AAATGGGGAT TGACAATTTG ATTGTGGATG AAGCCCACTT ATTCAAAAAT	540
CTAGCCTTTG AAACCTTCTAT GGAAAAAATT GCAGGACTTG GTAACCAACA AGGCTCTAAT	600
CGCGCTAGAG ATTTGTTTAT TAAAACGCGC TACTTGCATC AAAACGATAA GAAAATCATG	660
TTTTTAACCG GCACGCCTAT AGCTAATTCC TTGAGTGAAA TGTATCACTT GCAACGCTAT	720
TTAACCCCTG ATGTGTTAAA AGAAAGAGGG TTAGAATTCT TTGATGATTG GGCTAAGACT	780
TATGGGGAAG TGGTGAATGA TTTTGAATTA GACTTCCG CTCAAAGTTA TAAATGGTT	840
AATCGCTTTT CTAAATTTAG CGATGTGCAA GGCTTAAGCA CCATGTATAG AGCTTTTGCG	900
GATATTGTCT CTAATGATGA TATTTTAAAG CATAACCCCC ACTTTGTGCC TAAAGTGAT	960
GGGGATAAAC CTATCAATGT GGTGGTGAAA AGAAGCGAAG AAGTGGCTCA ATTCATTGGA	1020
GTGGCTTTAG AAAATGGAAT ATATAATGAA GGCTCTATCA TTGATAGGAT GCAAAAATGC	1080

GAGGGCAAGA	AAAGCCAAAA	AGGGCAAGAC	AATATCCTTT	CTTGCACCAC	AGACGCTAGA	1140
AAAGTGGCTT	TGGATTACCG	CTTGATTGAC	CCTAACGCTA	AAGTAGAAAA	AGAATTTTCT	1200
AAAAGCTATG	CTATGGCAAA	AAATATCTAT	GAGAATTATT	TAGAAACTCA	TGCCACTAAA	1260
GGCACACAAC	TTGGTTTCAT	AGGGCTATCC	ACACCCAAAA	CCCATAGCCA	AAAAGTCAGT	1320
TTAGAAGCGC	TAGATAACGC	TCACGAAACT	GAAAATAAAA	ATCCCCTAGA	TAAAGCTCAA	1380
GAACTTTTAG	AAAGCTTGTC	TAGTTATGAT	GAAAAGGGCA	ATCTTATCGC	TCCTAGCAAG	1440
AAAGAATTAG	AGAACGAGCT	CAAAGAGAAA	GAAGCTAAAA	GCGTCAATTT	AGATGAAGAG	1500
ATAGCTAAAG	GCTGTTCGTT	TGATGTTTAT	AGCGATGTTT	TAAGGCATTT	AGTCCAAATG	1560
GGTATCCAC	AAAATGAAAT	CGCTTTCATC	CATGACGCTA	AAACCGAAGA	GCAAAAGCAG	1620
GATTTGTTTA	AAAAGCTCAA	TCGTGGCGGA	GTCAGGGTAT	TATTGGGCAG	TCCTGCTAAA	1680
ATGGGCGTAG	GCACTAATGT	GCAAGAAAGA	TTAGTCGCTA	TGCATGAATT	AGATTGCCCA	1740
TGGAGACCTG	ATGAATTGTT	GCAAATGGAA	GGGCGTGGGA	TAAGGCAAGG	CAATATTTTA	1800
CACCAAAATG	ATCCTGAAAA	CTTTAGAATG	AAAATCTATC	GTTACGCCAC	TGAAAAGACT	1860
TACGATAGCC	GTATGTGGCA	AATCATAGAA	ACTAAATCTA	AAGGCATAGA	GCAATTTAGA	1920
AACGCGCACA	AATTAGGCTT	GAATGAATTA	GAAGACTTTA	ATATGGGTAG	CTCTAATGCG	1980
AGCGAGATGA	AAGCAGAAGC	GACAGGCAAT	CCCTTGATTA	TTGAAGAAGT	CAAATTGAGA	2040
GCGGAGATTA	AAAGCGAAGA	ATCAAAAATAC	AAAGCCTTCA	ATAAAGAGCA	TTACTTCAAT	2100
GAAGAAAGCT	TAAAAAACAA	CGCTTCTAAA	TTGGATTATC	TAAAACAGGA	ATTGAAAGAT	2160
TTAGAAACGC	TTCAAAGATC	CGTAATAATC	CCCCTCATA	CAGAGATCAA	GCTCTATGAT	2220
TTGAAAAATG	AAGAAAGTAA	GGATTATGAG	CTTATCAAAG	TTAAAGAGGT	AGAGCCTTTA	2280
AAAGAAAACG	CCTCTATGAG	TGAAGAATTA	ACGCACAAGA	AACTCAAAGA	ACAAAACAAG	2340
CAAATAGCCG	AACAAAATAA	AGAAAAGCTA	GACGCTATTA	AAAAGCAATT	TGCAAGCAAT	2400
TTGAACACCT	TGTTTGTGAA	TGAAGAAGAA	GATTATAAGC	TTTTAGAATA	CAAGGGCTTT	2460
GTGGTGAATG	CTTATAAAAC	TAAGTATCAA	GTGGAGTTTA	GTTTAAGCCC	TAAAGACAAT	2520
CCCAATATTG	CCTATAGCCC	TAGCAATATG	GTTTATAAAA	ACGATACTAT	CAACATGTTT	2580
AGCTCTTATA	ATTTCTGCGC	TGAGATCAAG	TTTGATGGGT	TTTTAAAAAG	GTTGGATAAC	2640
GCTATCACTA	AACTCCCTGA	AAAAATCAAG	GAATTAGAAA	ACTCCATTGA	AATCACGAAA	2700
AAAAATATCG	CTAAATACAC	AAGATTAGTG	GAGCAAAAAC	CTTCTTACCC	ACGACTAGAA	2760
TACCTGCAAG	CTTTAAAATG	GGATCATAAA	ACTCTAATAG	ATGATTTAGC	TAAAATGAGC	2820

AAAGACAGAA ATTATAAGCC TCGGTTCAAC CCTAAATCTA AAGAAGTCTT AAAGAATTTG	2880
AACGCTGAAA AAAGAGCGAG TTTAGAGAAT GAGAGGGAAG AGCAAGGGGT TAAGGGGAAC	2940
ACAAAGAGTC ATGATGAAAT AGAGCCAGCT ACAGAACAAG TGATTGAAAA AGAAATAGAA	3000
AAAGGAGATG AAATCGCTAA TAATGTTGAT TACTACGAGA ACGAACAAGA AGTGGAATT	3060
ACTAAATCAA TGGGTAGAAG A	3081

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

ATGGCCGAAG AAGAAAAGAC CGAACTCCCT AGCGCGAAAA AAATCCAAAA AGCCAGAGAA	60
GAAGGCAATG TGCCTAAAAG CATGGAAGTG GTGGGGGTTT TTAGGGTTAT TGGCTGGGCT	120
AATGAGTATT TTTGTTTTTT TTATATGGTG GGTGGGATGG CTTTAGCGAG ATGTATCGCC	180
ATGTGT	186

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 711 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

ATGAAAACAC TCGTGAAAAA TACCATATAT TCTTTTTTGC TATTGTCTGT TTTGATGGCA	60
GAAGATATAA CAAGCGGCTT AAAGCAACTG GATAACACCT ACCAAGAGAC CAACCAACAA	120
GTGCTCAAAA ACCTAGATGA GATTTTTTCA ACCACTAGCC CTAGCGCTAA TAATAAAATA	180
GGTCAAGAAG ATGCTCTAAA CATCAAAAAA GCGGCCATTG CTTTGAGAGG AGATTTAGCG	240
TTATTGAAAG CCAATTTTGA AGCGAATGAG TTATTTTTCA TCTCAGAAGA TGTGATTTTT	300
AAGACTTATA TGTCTAGCCC TGAACTTTTA TTAACCTATA TGAAAATCAA TCCCTTAGAC	360
CAAAAGACTG CTGAGCAACA ATGCGGAATA TCCGATAAAG TTTTAGTTCT TTATTGTGAG	420
GGGAAGCTGA AAATCGAGCA AGAAAAACAA AATATAAGAG AGCGTTTAGA AACTTCTCTA	480
AAGGCATATC AGAGCAACAT TGGAGGTACA GCTTCCTTAA TCACTGCTTC ACAGACGCTT	540
GTAGAAAGCC TAAAAAATAA AAATTTTCATC AAAGGAATCA AAAAGCTTAT GTTAGCTCAC	600
AACAAGGTCT TTTTAAATTA TTTAGAGGAG TTGGACGCAT TAGAAAGATC CCTAGAACAA	660
AGTAAGCGAC AATACCTACA AGAAAGGCAA TCAAGTAAGA TCATTGTTAA A	711

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GTGAGCGAAA AAGACAGGGC GTTTCCTTTA GCGAGCTTGT CTTGCGTGGA TTATGTTGTG	60
GTGTTTGGAG AAGACACGCC CATAAAATTG ATTCAAGCCC TAAAGCCTGA TATTTTAGTC	120
AAGGGAGCGG ACTACCTCAA TAAAGAAGTC ATAGGGAGCG AGTTGGCTAA AGAAACCCGT	180
TTGATAGAAT TTGAAGAAGG TTATTCCACA AGCGCTATCA TAGAAAAAAT TAAAAGGACA	240
CATAATGAT	249

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

 (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

```
GTGTATGACA AATCCTTGTG TAAGACCATG GCGCTAGCGT TGAAGGCTTT AGGCGTTAAA      60
AGGGCGATGG TGGTTAATGG AGGGGGGACA GGTGAAATCG TGTTGCATGA CATTACGCAT      120
GCGTGCGAAT TGAAAAATAA CGAAATTTTA GAGTATGATT TGAGCGCTAA AGATTTTGRT      180
TTRCCCCCCT CA                      192
```

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 684 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...684
 (D) OTHER INFORMATION: /note= "D-XYLOSE TRANSPORT ATP-BINDING
 PROTEIN"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```
ATGCTAGTAG AAATAGAGAA TTTGACTAAA ACTTATGGGA GTTTAAAAGC GCTAGACAAT      60
ATCAGTTTGA AACTACCCAA ACAGCAATTT ATAGGGCTTT TAGGGCCTAA TGGGGCGGGT      120
AAAACCACTC TGTTAAAAAT TTTAGCCGGA TTGAATTTGA ACTATCAAGG GGAAGTGAAA      180
ATTTTAAACC AAAAGATTGG TATAGAGACT AAAAAAAGCG TGGCGTTTTT AAGCGATGGC      240
```

GATTTTTTAG ATCCTAAATT AACGCCTTTA AAAGCGATCG CTTTTTATAA GGATTTTTTTT	300
AGCGATTTTG ATGAATCAAA AGCCCTAAAT TTGTAAAAAC GCTTCAGCGT GCCTTTAAAAA	360
AGAGAGTTCA AAGCCCTTTC AAAAGGCATG AGGGAAAAAT TGCAGCTGAT TTTAACCCCTA	420
TCACGAAACG CTTCTTTGTA TCTTTTTGAT GAGCCGGTGG CTGGGATTGA CCCTATTGCA	480
AGAGAAGAGA TTTTGTAGTT AATCGCTAAG GAGTTTAGCC AAAACGCAAG CTTGCTAGTC	540
TCTACGCATT TGGTGGTGGA TGTGGAAAAG TATTTAGACA GCGCGATTTT TTTAAAAGAA	600
GCTAAAGTGG TGGCTTTTGG GGATGTGGGG GAATTAAAAA AAGGGTATAG CAGTTTGGAG	660
GCAGCGTATA AAGAAAGGTT GAAA	684

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112: ○

ATGAACAAGC TTTTTTTAGC TTTTATTGTT GGGGGAATGC TTTTAAGTGC TGATGCTTTA	60
AACGATAAGA TTGAGAATTT AATGGGGGAG CGATCCTACC ACATGAACAA GCTTTTTTTTA	120
GAGCGTTTGT TTAAAAATCG TAAGGATTTT TATGAAATGG GCGGTTTGGA TTCCTTAAAA	180
CTACTCAACA CTCTCAAAGA AAACGGGCTT TTATCGTTTA ATTTTGACAA ACCAAGCGTG	240
TTAAAAATCA CTTTCAAGGC TTCAAGTAAT CCCCTAGCGT TTGCCAAAAG CATCAACAAT	300
TCTTTGAATA TGATGGGGTA TTCGTATGTT TTGCCTATTA GAATGCAAAG CTCTTCAGGC	360
GAGAATGTTT TTTCATACGA GCTTAAAACG GAATACGTTT TAGACCCTAA CATTTTGATA	420
GAGACGATGA AAAGGCATGG TTTTGATTTT ATGGATATTA GACGGGTGTC TTAAAGGAG	480
TGGGAATACG ACTTTGCCTT ACAAAGATC AAGCTCCCTA ACGCGAGAGC CTTAGTTTTG	540
AGTAGCGATC CTGTGGAGTT TAAGGAAGCG AGCGGGAAAT ATTGGCTGAG CGTGAATCAA	600
AACGCGTATT TAAAAATAAG CTCCAATAAC CCTTTGTGGC AACCCAAAAT CATTTTTTAT	660

GATGAAACT TAAAGATCAT TCAAATCATT GCTAAAGAAA ACAGACAACA AGAAATCGCT	720
CTTAACTTGC TTGATGGCGT GCGTTTTATC CATATCACTG ACGCAAAAAA CCCTATCATT	780
TTAAAAAATG GGATTAGCGT GGTTTTGTAT GCGATGCCT	819

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...45
 - (D) OTHER INFORMATION: /note= "H.influenzae lic-1 operon
licA-licD genes"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GTGTCTCGCC CGTTCAAAC GATCAAAAAA CCCCCACAAC CCCCT	45
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(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

ATGATCGCTG TATTACCGCC CTTGTTTCT ATGGGGAGCT TTGATGAGTG GATTTATAGG	60
GGGCTTGTGG CTTTAATGGT GAGCTGTCCT TGC GCGTTAG TGATTCTGT GCCTTTAGGG	120

TATTTTGGAG GCGTGGGAGC GGCGAGCCGA AAGGGGATTT TAATGAAAAG AGTGCATGTT	180
TTAGAGGGTG CTTACCCAAA C	201

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 969 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GTGCAACACT TCAATTCCT CTATAAAGAT TCTTTATTTT CTATCGCTTT ATTCACTTTC	60
ATTATCGCTC TTGTGATTTT ATTAGAACAG GCTAGAGCGT ATTTACCCG AAAGAGAAAC	120
AAAAAATTTT TGCAAAAATT CGCCCAAAAT CAAAACGCCT ATGCGAGCAG CGAGAATTTA	180
GACGAGCTTT TAAAGCATGC TAAAATTTCC AGTTTGATGT TTTTAGCTAG GCGTATTCT	240
AAAGCGGATG TGGAAATGAG CATTGAAATC TAAAAGGGC TTTTGAATCG CCCCTTAAAA	300
GATGAAGAAA AAATCGCTGT TTTAGATTTA TTGGCTAAAA ATTATTTTAG CGTGGGGTAT	360
TTGCAGAAAA CAAAAGACAC CGTGAAAGAA ATTTTGCGCT TTTCCCAAG GAATGTGGAA	420
GCGTTGTTGA AGCTTTTGCA TGCGTATGAA TTAGAAAAAG ATTATTCAAA GGCTTTAGAA	480
ACTTTGGAAT GTTTGGAAGA ATTAGAGGTG CCTAAAATTG AAACGATTAA AAATTACCTC	540
TATTTAATGC ATTTAATAGA GAATAAGGAA GATGCGGCTA AAATCTTGCA TGTTTCAAAA	600
GCGTCGTTAG ATTTGAAAAA AATCGCTCTG AATCACTTAA AATCGCATGA TGAAAATCTT	660
TTTTGGCAAG AAATTGATAC AACCGAACGG CTAGAAAATG TGATCGATCT TTTATGGGAT	720
ATGAATATCC CTGCTTTTAT TTTAGAAAAA CATGCCCTTT TGCAGGACAT CGCGCGATCT	780
CAAGGGTTGC TTTTGGATCA CAAACCTTGC CAAATTTTTG AATTAGAGGT TTTACGCGCT	840
CTATTGCATA GCCCTATAAA AGCGAGTCTG ACTTTTGAAT ACCGCTGCAA GCATTGCAAA	900
CAAATCTTTC CTTTGTGAAAG CCATAGGTGT CCTGTGTGTT ACCAGTTAGC GTTTATGGAT	960
ATGGTGGCT	969

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ATGGAACACC TTACAAGGGG AATTAAGCAC

30

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GTGGTTATCT TAGGCTCRCA TGGCAAGGAA GAGTATTACG CTAGCAAGAT TGCAGCCCCC
ATTTTTAAAG AAATCACCGA AATTTTAGTG CGTTACAATT ACCTATCGCC CTCTATTGCG
ATTCAAAACG CTTTGGAAAA AAACCGCTTA AAA

60

120

153

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ATGAAAAAGG TTATTGTGGC TTTAGGCGTT TTGGCGTTTCG CAAATGTTTT AATGGCAACC	60
GATGTTAAGG CTCTTGTAAG AGGTTGTGCC GCTTGCCATG GGGTTAAGTT TGAAAAGAAA	120
GCTTTAGGTA AAAGCAAAAT CGTTAACATG ATGAGCGAAA AAGAGATTGA AGAGGATCTT	180
ATGGCTTTTA AAAGCGGTGC CAACAAGAAT CCTGTCATGA CCCGCAAGCT AAAAAAT	237

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...285
- (D) OTHER INFORMATION: /note= "influenzae type B
lipooligosaccharide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ATGGGGATTG CAACCAGTCT CATCAGTGAG GTTTCTAAGT TTTATTACGC TTTAAAATAC	60
CATGCGAAAT TTATGAGCTT GGGGGAGCTT GGGTGCTATG CGAGCCATTA TTCGTTGTGG	120
CAAAAATGCA TAGAGCTCAA TGAAGCGATC TGTATTTTAG AAGACGATAT AACCTTGAAA	180
GAGGATTTTA AAGAGGGCTT GGATTTTSTA GAAAAACACA TCCAAGAGTT AGGCTATGCG	240
CGTTTGATGC ATTTATTGTA TGATGCCAGC GTGAAAAGTG AGCCT	285

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 462 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATGCACCTTA AAAGTGGGGC TGTTTTTATC TCTGATGCGC ATTTTTTGCC CAAAAGCCCT	60
CATTTAATCC ATACGCTTAA AGAACTTTTA AGCGCCAAAC CCCCACAAGT CTTTTTCATG	120
GGCGATATTT TCCATGTTCT TGTGGGCTAT TTACCCCTAG ATAAAGAGCA GCAAAAAATC	180
ATTGATTTAA TCCATGCGTT GAGCGAAATT TCACAAGTCT TTTACTTTGA AGGCAACCAT	240
GATTTTTTCCA TGCGTTTTGT ATTCAATTCC AAAGTAATGG TTTTGTAGCG CCAAAACCAA	300
CCCGCATTAT TCCAGTATGA TAACAAACGC TTTTGTCTAG CCCATGGGGA TTTATTCATC	360
ACTAAAGCGT ATGAATTTTA CATCACGCAG CTCACTTCCA CTTGGGCTAG ATTTTTTTTA	420
ACTTTTTTAA ATTTATTAAG TTTTAAAACC TTATACCCTT TT	462

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 939 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GTGCAACCGA TGAAATCTAA AAAACTTTAT TTAGCTTTAA TCATAGGGGT TTTATTAGCG	60
TTTTTAACCC TATCTTCATG GCTAGGTAAT AGCGGTTTAG TGGGGCGTTT TGGGGTGTGG	120
TTTGCCGCAA TCAATAAAAA ATATTTTGGG TATCTTTCAT TGATTAATTT ACCCTATTTG	180

GCGTGGGTTT TATTCCTTTT ATACAGGGCT AAAAACCCCTT TTACAGAAAT CGTTTTAGAA	240
AAAACTTTAG GGCATCTATT AGGCATTTTA TCTTTACTCT TTTTGCAATC TAGCCTGTTG	300
AATCAAGGGG AAATCGGCAA CAGCGCGCGT TTGTTTTTAC ACCCTTTTAT AGGGGACTTT	360
GGGCTTTATG TGCTGATAAT GCTTATGGTA GTTATCTCTT ATTTAATTTT ATTCAAAC TG	420
CCCCCTAAAA GCGTTTTTTA CCCTTATATG AACAAAACAC AAAGCCTTTT AAAAGAGATT	480
TACAAACAAT GCTTGCAGGC CTTTAGCCCT AATTTTAGCC TGAAAAAAGA GGGTTTTGAA	540
AACACCCCAT CAGATTCTCA AAAAAAGAA ACCAACAACG ACAAAGAAAA AGAAAACCTC	600
AAAGAAAACC CTATTGATGA AAACCACAAC ACCCCTAACG AAGAATCGTT TTTAGCGATC	660
CCTACCCCT ATAACACGAC CTAAATAAT TCAGAGCCGC AAGAAGGCTT AGTCCAAATT	720
TCCCCACACC CCCCTACCCA TTACACCATT TACCCTAAAA GAAACCGATT TGATGATTTG	780
ACTAACCCCA CTTTAAAAGA ACCTAAGCAA GAAACCAAAG AAAGAGAACC CACGCTAAAA	840
AAAGAAACGC CCACCACACT CAAACCTATC ATGCCCATAT CCGCATCCAC ACAGAAAATC	900
ATGACAAAAC RGAAAACCAC AAAACCCCTA ACCACCCCA	939

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GTGATGTTAA GTAGAGACAT TGTCCAATAT TCCAAGATCC GCACCGAGTT ATACGCCTAC	60
CTCACTTATT TGTTTTTCGCA CAATATCCGC AACCACCTTC CTGAAATCAC TTTGGATTAT	120
TTAAACAGGC AAATCAGTAA GATGCAAGCT GAAATCAAAA TGGCAAAAAG TTTTTTTGTT	180
TTAGACGCTA AGGGCATGCT CATGCTTAAG CCAAGCCAAT TTAAAGAGCA GGGGCATAAG	240
GAAGGGCTAT TAGAGCATGA TTTAACAGAA GGGATTGAAT TAGAATCGCA TGTCAGTTTT	300
AGCGATAAGT ATTATTTTTTA TCAAGCCGTG AATGAAAAGC GTTGCATTTT AACCGACCCC	360

TATCCTTCTA	AAAAAGGGAA	CCATTGTTGTA	GTGAGCGCGT	CTTACCCGGT	GTATGATCAA	420
AATAACGATC	TAGCGTTTGT	GGTGTGCTTG	CAAATCCCTT	TGAGGGTGGC	GATTGAAATC	480
AGCTCGCCTT	CAAAGTATTT	TAAAACTTTT	AGCGAAGGGA	GCATGGTCAT	GTATTTTATG	540
ATTTCTATCA	TGCTCACTTT	AGTGTGCTG	CTTTTATTCG	TGAAATGCAT	TTCTAGCTTT	600
TGGACAGCGA	TCGTGCATTT	TAGCAGTTTT	GACATTAAAG	AAGTGTTC	CCCCATTGTG	660
CTTTTAACCC	TAGCTTTAGC	CACCTTTGAT	TTGGTCAAGG	CGATTTTGA	AGAAGAAGTG	720
TTGGGTAAAA	ATAGCGGGGA	CAACCACCAT	GCGATCCACC	GCACCATGAT	CAGGTTTTTA	780
GGCTCTATCA	TTATCGCATT	AGCCATTGAA	GCGTTAATGC	TCGTGTTTAA	ATTCAGCGTG	840
AGCGAGCCGG	ATAAAATCAC	TTATGCGGTG	TATTTGGCTA	TCGGCGTGGC	GGTGCTTTTG	900
ATCAGTTTGG	CGATTTATGT	TAAATTCGCT	TATAGCGTGT	TGCCCAAACG	AGAACGC	957

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

ATGTTTATAC	ATGAAAAAAT	CAAAAGCCGC	TTTTCTAGGA	ATTGGTCTTT	AAGGAATAGG	60
GGCAGGCATT	TTGCATCTTC	AAGCGTGTAT	TTTTTCTCAC	TTCTTGTCAT	TACAGCGGTT	120
AATAGAAGTA	GTGCAGTTGC	TTGGTTATTG	ATGCCTGAAC	ATTTGATTGG	GTGGTTTTTG	180
ATTTCTTTTA	GTGGGGAATT	TGTAGCAGAC	ATGGCGTTTG	GCAAAAAAAG	TAAGATTTTT	240
AAAACCCGCT	TTGGAATTC	TATTGTGAGC	GGCGTTTCAC	TATTGCTTGG	CGCTTACCAG	300
CGCTTTTATT	TTTTGTATGG	TTTGGCTTTA	TTAATTGGTG	GGCTGTCTTT	TTTA	354

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ATGTTTAAAA GCAGATTAAA TTCATGGATT TTATTAGGGA TTTTAGGGGT TTTAGTGGTG	60
GTTTTTTGGG ATGTCATAAA ATACAAAATA GAAGATTTC AACATGATCA TTATCTATCA	120
CAAGTGAAAG AAAGGGAAGA ATATTATAAA AACCACATAG AAGAAGCTTT GAAAAAGGAT	180
AGCGAATGCT TTGAAAAAGG AGGCGATAAA GTGGATTGCT CGGCTGCTAT GAGAATAGCT	240
GCTGGTGAAA GAAATAGAAG AATGTTAGAG ATTAAA	276

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 414 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ATGGTATTTT GGGGCGCTGT TTTCTTTTTA TGGGATCGAA CGGCATGGAA GCGCTTAATG	60
GTGTTTTTGA ACAGCTTGAW TTYCATGCTT GCGGCCTTGA GTTTGGGGTC GTTTTATAGG	120
GCATGGATCA AAAATGAAGC CCACACCACT CAAATCGTTT TGATTTCTTC TTTGCCCTTG	180
ATTTTTATGA TGGGTTTTGT GTGGCCTTTT GAATCCTTGC CCTCTTATTT GCAAGTCTTC	240
GTTCAAATAG TGCCTGCTTA TCATGGGATC AGTTTGCTCG GGCGATTGAA TCAAATGCAT	300
GCGGAATTTA TAGATGTTTC TATCCATTTT TACGCGCTTA TTGCGATTTT TATCGTGAGT	360
TTTATAGGGT GCGTGTTCAA ACTCAGCTCT TTAAAGAAAG CTTGTGAAAA CGCT	414

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ATGCATGAGC AAGGTTCTAT AAGCTTTRTA GGCGRACAGG GAGCTAAAAG ATTATTATAC	60
ATACTCTACA AGCTCGCATT TAATGCTAAG TCTAATAAGA TTGCCCTAGA TAGACATTAC	120
GCCAAAATGT TTTTGCAAGT TGTAGCAAGA ACTCTAATAA AGAATGTCAA TATATTAGAA	180
GAGCAAGGTT TTATTGAAGT CATTAAAGGA AAACAAAGAT ACTTGTATGT GTATCTTAAA	240
GATTACAGAG AATTAGAATG CTTAGTGAAG AGCAAGATGG CTAAGTATGT GATGTATTTA	300
AGACAATTCT TTGATTATTT GGATAGAAAA AGGCGTTATG GCTTTGATTT TACGCTTAAA	360
AACCTAGCCT TTGCTAAGAC CAAAGAAAGC TTACCCAGAC ATTTAAACGA TAAAGACTTA	420
AAGAGTTTTT TAAAAACACT CTTAGACTAT AAGCCAGCTA CAAGCTTTGA AAAACGCAAT	480
AAGTGTATTC TACTTATTGT AATACTTGGG GGACTTAGAA AATGCGAAGT GTTAAACATA	540
GAATTAAAC ACATTCAAGT AGAAGAGCAA AACTACTCTA TTTTAATTCA AGGTAAAGGT	600
AGAAAAGAGA GAAAAGCTTA TATTAAAAAG AGTTTGTTAG AACCAAGCTT GAATGCTTGG	660
ATTAGTGATG ATTACAGACT AAAATATTTT AATGGAGCAT ATCTCTTTAA AAAGGATAAG	720
CAAAAATCAC AAAATTCTTT AACGCTTTAT AATTTATCCC CT	762

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GTGGTCTTTA AAATTTTAAG TTTATGGTTA GGGGTGTTTT GTTTCCTTAG GGCTACGCAT	60
TTATACTTAG GCGAAGAACC CAAATATAAA GACAATTTC ACGCATTTTGA ATACGCTAAC	120
CCTAACGCTA GAAAAGGCGG TGTTTTGAGA AATGACGCTA TAGGGACTTT TGATAGCCTT	180
AACCCTTTTG CGCTTAAAGG CACTAAAGCC GAAGGCTTGG ATCTCATTTA TGACACTTTA	240
ATGGTGCAAA GCTTAGACGA ACCTTTTGCA GAATACCCCT TAATCGCTAA AGACGCCGAA	300
GTGGCTAAGG ATAACAGCTA TGTGATTTTT ACCCTAGATA AAAGAGCGAG ATTCAGCAAT	360
AACGCTCCCA TTTTAGCGAG CGATGTGAAG TTTAGCTTTG ATACGATAAT GAAATTAGGA	420
TCGCCCCTTT ATAGGCAGTA TTACCAAGAT GTTAAAAGG CGGTTATCTT AGACAAGCAC	480
CATGTTAAAT TCATTTYCAA AACCCTGAA AATAAGAAT TGCCCCTCAT TTTAGGGCAG	540
TTGCAGATCT TTTCC	555

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GTGGCCATGA TAGATTGCGC GATTATTGGA GGTGGTCCTG CAGGTTTGAG TGCGGGGCTT	60
TATGCCACTA GAGGCGGTGT TAAAAACGCC GTTTTATTTG AAAAAGGAAT GCCTGGGGGG	120
CAAATCACTG GCAGTAGTGA GATTGAAAAT TATCCGGGCG TTAAGGAAGT GGTGAGCGGA	180
TTGGATTTC A TGCAACCA	198

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GTGGGGAAAA GCTTGAGATA CAGCTTGAAT TTAGATCTCA ATCAAAAAGC CGATTGTGTTT	60
TTCACCGAAT TAGAGCCAAC AGGTCTCACG CTCTCCCCCA TCATGAAACG CTTTACTATC	120
AAAGGCGATT TTGATTCAGG GCTAAAATCC TATGACATGA GCTACATGTA TGCGAGCCTT	180
CAAGCTATAA GCGCGATCAG GAGATTACCC TTAGGGCTTT ATGATGGGGT GCATGTCTAT	240
TCTAAAACGC CCATGAAGGA TATTGAAAAA TTACGCAACG CTTTAAAAAC AATCAACCAC	300
CATGGCATAG GCATTGAAGG GTGGTGGCAA CAAAACGGGA ATTTTTTCTC GGCGATGGAA	360
TTGGAAAAAA GAGCGTTATT CATTGTGCTC ATGCTCATTA TTTTAATGGC GTCTTTGAAT	420
ATCATCAGCT CGCTTTTAAT GGTGGTGATG AACAGGCGTA AAGAAATCGC CCTACTCTTT	480
AGCATGGGGA GCAGTCAAAA AGAAATCCAA AAAACCTTTT TTTATTTGGG TAATATCATT	540
AGTTTA	546

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

ATGAAAAAAAA CTTTTTTGAT CGCTTTAGCG CTTACGGCTT CTCTTATAGG CGCTGAAAAC	60
ACCAAATGGG ATTATAAAAA TAAAGAAAAT GGCCCGCACC GCTGGGACAA ATTGCACAAA	120
GATTTTGAAG TGTGCAAAAG CGGTAAAAGC CAATCGCCCA TCAACATTGA GCATTACTAC	180
CACACGCAAG ATAAAGCCGA TTTGCAATTC AAATACGCCG CTTCTAAACC TAAAGCGGTC	240
TTTTTCACCC ACCATACTTT AAAGGCTTCG TTTGAGCCGA CTAACCACAT CAATTATAGA	300
GGGCATGACT ATGTGTTGGA TAATGTGCAT TTCCACGCC CTATGGAGTT TTTAATCAAT	360
AATAAAACCA GGCCTTTGAG CGCGCATTTT GTGCATAAAG ACGCTAAAGG GCGTTTGTG	420
GTGTTAGCGA TTGGTTTTGA AGAAGGGAAA GAAAACCCCA ACCTTGATCC TATTTTAGAA	480
GGCATTCAAA AGAAACAAAA TCTTAAAGAG GTGGCTTTAG ACGCTTTCTT GCCTAAAAGC	540
ATCAATTACT ACCATTTTAA CGGCTCTCTC ACCGCTCCTC CTTGCACAGA GGGGGTGGCA	600
TGGTTTGTCA TAGAAGAACC TTTGGAAGTT TCTGCCAAAC AATTGGCTGA AATCAAAAAA	660
CGCATGAAAA ATTCGCCCAA CCAACGCCCC GTCCAGCCTG ACTACAACAC CGTGATCATT	720
AAAAGCTCGG CTGAGACCCG C	741

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ATGAAAATTT CTTTATTGGG GCATGGAAAA ACCACTCTAG CCCTAGGGCG TTTTTTTAAA	60
AAAAACCATA ATGAAGTCAA ATTTTTTTGAT GATAAATTCC CTGCATTTTT TAAGGATAGC	120
GAGGGTTTTT TTTGCTACCC TAGTAAGGAT TTTAACCTTA ATGATTCCCA ACTAGAAATC	180
GTCAGCCCTG GCATTAGTTT CACGCACCCT TTAGTCATGA AAGCCAAGCA TTTAATGAGC	240
GAATACGATT ATATTGATAG TTTGTTTGAT CATTCTTTCA CGCCTACGAT GATAAGTATT	300
AGCGGCACTA ACGGGAAAAC CACCACGACC GAAATGCTCA CCACACTTTT AGAAGATTTT	360

AAGGCTGTGA GTGGGGGGAA TATCGGCACG CCCTTGATTG AATTGTTTGA AAAACGATCG	420
CCCTTGTTGGG TGCTAGAAAC AAGCTCCTTT TCTTTGCATT AACTAATAA GGCTTACCCT	480
TTAATCTACT TGCTCATCAA TGTGGAAGCC GATCATTTGA CTTGGCATTG CAATTTTGAA	540
AATTATTTGA ACGCTAAACT CAAGGTTTTA ACATTGATGC CTAAAACTTC GCTCGCTATC	600
CTCCCTTTAA AATTCAAAGA ACACCCTATT GTTCAAACT CGCAAGCGCA AAAAACTTTT	660
TTTGACAAAA GCGAAGAGGT TTTAGAGTGT TTAAAAATCC CTTCTAACGC CCTTTTTTTT	720
AAGGGAGCGT TTTTATTAGA CGCGGCTTTA GCCCTTTTAG TTTATGAGCA ATTTTTAAAA	780
ATAAGAATT TAAAATGGCA AGATTATAGA GAAAACGCCC TTAAAAGACT GAACGCTTTT	840
AAAATCGGCT CGCATAAAAT GGAAGAATTT AGGGATAAAC AAGGGCGTTT GTGGGTAGAT	900
GACAGCAAAG CCACGAATAT TGATGCCACC TTACAAGCCC TAAAAACCTT TAAAAACCAA	960
AAAATCCATT TGATTTTAGG GGGCGATATT AAAGGGGTCA ATTTAACCCC CCTTTTGTAA	1020
GAGTTTAAAA ACTATAAAAT AAGCCTTTAT GCCATAGGAT CAAGCGCTTC TATCATACAA	1080
GCCTTAGCGT TAGAATTTAA TGTTTCTTGT CAGGTTTGTT TGAAGTTAGA AAAAGCGGTT	1140
CAAGAAATTA AAAGCGTTTT ATTACAAAAT GAAGTCGCTT TGCTTTCACC TAGCGCGGCC	1200
AGTTTGGATC AATTTTCTTC GTATAAGAA AGGGGTGAAA AATTCAAAGC GTTTGTTTTA	1260
AAAGAT	1266

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...162
 - (D) OTHER INFORMATION: /note= "iron(II) transport system"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

ATGAAAGAAA TCATTGTCGC CCTTGTGGGC CAGCCTAATG TGGGGAAATC GTCCTTAATC	60
AACGCTTTGA GTAACSCCCA TTTRAAAGTG GGGAATTTTA CCGRGGTTAC CGTGGATAAA	120
ATGGAAGTGA GTTTGATCCA WAAAGATCAT CAARTSWYTM TC	162

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GTGCATCGTT TTTCTAGAAA CCCATGCGCA TCTTGCAATC GCGCTCGCTC TTGTTCGAGA	60
CTATCTCGCT CATTAGTGAG CGCGGTAAC TGGTGGTTGA GCTTGTCGTT TTCGGTGTT	120
AGTGCTTTAT TTTCTTTAGT CAGCTCGGTG ATTTTATGGG TTAGCTCGGT GTTTTCTCTT	180
TTTAGCCTTT CTTTTTCTGT TGTCAATTCT CTTTTTCTT CAGTCAGCCG ATCTCTGGCT	240
GCTAATAAGC GTGTGTTTTT TTAGCTAAA ATGTCTTTTT CCGTTTTT CAG TTCTGCTTTT	300
TCTTTAGTGA GCTTGTTATT GTTTTGCCAT AAT	333

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

ATGCAAAAAA TGGGCGTTGT CTCTTATTCC GTGTTTCAAG CGTTTGAAAA GGCTTTGAGT	60
CGGTTTAAAG AGGGCGTTGT TTTGATTGTG GATTCTTTAA GCGGTTTGAT TATGGGGAGC	120
GCTTCAGTTA AAGAATTGAG TGGGGTAATA GGCATTGTGG GGGCGTTAAG CCATGCCAAT	180
AGCGTGAGCA TGCTTTTGTG GTTTGGGGCG TTTTATCTA TCAATCTAGG GATTTTAAAT	240
TTATTACCCA TTCCAGCCTT AGATGGGGCG CAAATGCTAG GGGTCGTTTT TAAAAATATT	300
TTTCATATCG CTTTGCCAAC GCCCATACAA AATGCGTTGT GGCTAGTGGG GGTGGGGTTT	360
TTGGTTTTTG TCATGTTTTT AGGGCTTTTT AATGACATTA CTCGTTTGCT A	411

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GTGATGGCTT TGTTGAAAAT TAGTGTGGTA GTTCCTGAGG GGGAAGTTTA TACAGGAGAG	60
GTTAAAAGCG TTGTGTTGCC AGGAGTGGAA GGGGAATTTG GGGTGCTTTA TGGGCATAGC	120
AACATGATCA CCTTGCTTCA GCGGGGAGTG GTTGAGATTG AAACCGAAAA CAAAAAGAG	180
CACATTGCTA TCAATTGGGG TTATGCAGAA GTTACTAATG AACGGGTGGA TATTTTAGCC	240
GATGGAGCGG TCTTTATTAA AAAAGGATCA GATGACAGAG ATGATGCTAT CTCTAGGGCT	300
AAAAAGCTTT TAGAGGACGC AAGCTCTGAC AGGTTAGCGG TCTCTAGCGT GCTGGCTAAG	360
ATTGAGTCTC TT	372

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...258

(D) OTHER INFORMATION: /note= "UDP-N-ACETYLMURAMYL-TRYPEPTIDE
SYNTHETASE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

ATGTATTCTT	TGCTCTTAGA	TTTGAATAAA	AAGACCGCTC	TTTTAGGCAC	AAGAGGGTTT	60
TTTATCGACG	ACAAACACAT	CAAAGAAAAG	GGCTTGACCA	CGCCCACTCT	TTTAGAGCTT	120
TATAGCGATT	TGGAAGAAGC	GATTCGTTTA	AAATGCGAAT	ACTTCATTAT	GGAGGTGAGC	180
TCCCATGCGA	TTGTCCAAAA	CGCATCGCTG	GGCTTGATTT	CGCTCTTAAA	ATTCTCACCA	240
ATATCACAAG	CGATCATT					258

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ATGAAAACGA	ACTTTTATAA	AATTAAATTA	CTATTGCTT	GGTGTCTTAT	CATTGGCATG	60
TTTAACGCTC	CGCTTAACGC	TGACCAAAAC	ACGGATATAA	AAGATATTAG	TCCTGAAGAT	120
ATGGCGCTAA	ATAGCGTGGG	GCTTGTTTCT	AGAGATCAGC	TAAAAATAGA	GATCCCTAAA	180
GAAACCCTAG	AGCAAAAAGT	GACCATACTC	AATGACTATA	ATGATAAGAA	TGTTAATATC	240
AAGTTTGACG	ACATAAGTTT	AGGGAGTTTC	CAACCTAATG	ATAATCTAGG	TATCAATGCG	300
ATGTGGGGCA	TTCAAAATCT	TCTM				324

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ATGATTGATA SCCTTGATGG GGCAAAAGAT GCACAATTGA TAAAAAAGC TTACGCGTTT	60
TTGTGTTTAG GAGGCGATGG CACGATTTTA GGGGCTTTAA GAATGACGCA TGCTCACAAT	120
AAGCCATGCT TTGGGGTGAG GATTGGGAAT TTAGGGTTTT TGAGCGCGGT TGAATTGAAC	180
GGGTTGAAAG ATTTCTTACA AGATCTCAAG CAAAACAGGA TCAAATTAGA AGAGCATTTG	240
GCTTTGGAGG GCCGTATTGG AAACACTTCT TTTTATGCGA TCAATGAAAT CGTGATCGCT	300
AAAAAAAAG CTTTAGGGGT TTTAGACATC AAAGCGTGCG CGGGCCATAC GCCCTTTAAC	360
ACTTATAAAG GCGATGGGCT TATCATTGCC ACGCCCCTAG GCTCAACCGC TTATAATTTG	420
AGCGCTCATG GGCCCATTTG GCATGCTTTA AGCCAAAGCT ATATTTTAAC GCCCTTGTGC	480
GATTTTTCTT TAACGCAACG CCCTTTAGTG TTAGGGGCGG AATTTTGCTT GAGTTTTTGC	540
GCTCATGAAG ACGCTCTTGT GGTATTGAT GGGCAAGCCA CCTACGATTT AAAAGCCAAC	600
CAACCCCTAT ACATTCAAAA AAGCCCCACG ACCACCAAGC TCTTACAAAA AAATTCAAGG	660
GATTATTTTA AAGTGCTTAA AGAAAAGCTG TTATGGGGGG AAAGCCCTAA CAAAAAAGA	720

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

ATGATAGTGG GTTTGATAGG GGTGTGGAA AAAATCTCTG CTTTAGAAGC GCATATAGAA	60
GTGCAAGGGG TTGTTTATGG GGTGCAAGTT TCTATGCGAA CGGCTGCTTT GCTCCAAACG	120
GGCCAAAAAG CGCGTTTGAA AATCTTACAA GTGATTAAAG AAGATGCGCA TCTTTTATAC	180
GGGTTTTTAG AAGAGAGCGA AAAAATTCTC TTTGAAAGGC TTTTGAAAAT CAATGGGGTA	240
GGGGGGCGTA TCGCTTTAGC CATTCTTTCA AGCTTTTCGC CGAATGAATT TGAAAACATT	300
ATCGCTACTA AAGAAGTCAA AAGACTCCAG CAAGTCCCAG GCATAGGGAA AAAGCTCGCC	360
GATAAGATCA TGGTGGATTT GATTGGCTTT TTCATTCAAG ATGAAAACAG ACCCGCGCGC	420
AATGAAGTCT TTTTAGCCCT AGAGAGTTTG GGCTTTAAAA GCGCTGAAAT CAATCCAGTT	480
TTAAAAACCC TAAAACCCCA TCTCAGCATA GAGGCAGCGA TTAAAGAAGC CTTACAGCAA	540
CTGCGCTCT	549

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 462 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140

GTGGGGGTTT TGTRGCGTT GTTTTCTTT TATGCGAAAA ATAACCTTTT GGAAAACACC	60
CAAATACGCA TGCAATACAC CGCTGATGCG ATCGCTAAAA GCCTTTTAGA ATTAAATAAT	120
GCCTCTTCTT TAGAGCCTTT AAAAATCTTA GAAGAACGAT TCAAAAACAC CCCCTTTGTT	180
TTGTTGGACG CAGACAACAG AGTCAAGTTT TCTAATATCG GGGTGTTTGT GGCCTCTTTT	240
AAAAATGACG CCTTAATCAA AACCCCTTAT TTTGCGCTTA AAAAACAGGG CTTTACCTC	300
ACAGACAGCG CCCCAACTAA CCGCTTAGGG GTTCTAAAA TCATTATTGC AGAAGAAGAA	360

ATTCAAAAAA TCTTTATCCC CCTTTATAAA ATGATAGGCT ATGTGTTTTT GGGCGCGAGT	420
TTGTTTGTCTG CGCTAATAGC CATGTGGCTT TATAAAATCC CA	462

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 864 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GTGGTAATAA TGATTTTAGT CTGCTTTTTA GCTTGCTCGC AAGAGAGCTT TATCAAAATG	60
CAAAAAAAG CCCAAGAGCA AGAAAATGAC GGCTCTAAAC GCCCCAGCTA TGTGGATTCTG	120
GATTATGAAG TCTTTAGCGA AACGATTTTT TTACAAAACA TGGTGTATCA GCCTATAGAG	180
GAAAGAAACG CTTTTTTCCA ACTGACTAAA GATGAAGACA ATTCTTTTAA CCCTGAAAAT	240
TCCGTGATTT TACTGAATGA GCCAAGCGAT AATAGTGAAA AAAACCTACT CTCATACCCA	300
AACGATCCCA ATAACAATGA AGACAACGCT AATAATAGTC AAAAAAATCC GTTCCTTTAC	360
AAGCCCAAAA GAAAAACAAA AAACCCAAAA CTCATTGAAT ATTCCCAACA AGATTCTTAC	420
CCCCTAAAAA ATGGGGATAT TATCATGAGT AAAGAAGGGG ATCAATGGTT GATAGAAATC	480
CAATCCAAAG CCTTGAAGCG TTTTTTAAAA GATCAAAACG ATAAAGATCG CCAGATCCAA	540
ACTTTCACCTT TTAATGACAC TAAAACGCAA ATCGCGCAAA TTAAGGGCAA AATTTCTTCG	600
TATGTTTATA CCACCAATAA CGGTAGCTTG AGTTTAAGGC CYTTTTATGA ATCGTTTTTG	660
TTAGAAAAAA AGAGCGATAA TGTTTATACG ATAGAGAATA AGGCTTTAGA TACTATGGAG	720
ATTTCAAAGT GTCAAATGGT GTTAAAAAAG CATTCAACCG ATAAATTAGA CAGCCAGCAT	780
AAAGCCATCA GTATTGATTT GGATTTTAAA AAAGAGCGCT TTAAGAGCGA TACGGAACTC	840
TTTTTAGAAT GTCTTAAGGA AAGT	864

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ATGGCCGCTC CACTACTTGC TCTGCCCTTT CTTTCTAACC CTTTAGTGCT TGGTGCTTTA	60
GCTGT CATAG GAGTGGGTGC T TACTTGTAT CCCAATAAGC AAGATTCTTT AGTTGTGCAA	120
GCAGATGGGC TTTATAGTGA AATTCTTGGG TTTTTCATTT CGTTTTCTAG CAAGATCTTG	180
AAAGGAATTG GTGAGCCTTT AGCCAATGTT ATCCAACCTT TTGGTATGGT TTTAGGAATG	240
CTTTTAATCC TTTTGTATTC CTTTAAACGC TATCAAAACA ATGATTTATT TGAAATCAAA	300
ACCTTTTTAA TGCTTTTGT GTTTGTAGGA TACCTTTCTT TGTACCATTA TGCTTTTAAA	360
TCTGATGGTT CTAGTAGCGG TAATGGTCGC TCCAGTTTTG CCTTTCAAAA TCATGTAACA	420
GAAATTTTTG ACACGCCTGC TAACTTGCTA AATGCTGGGA TTTCTAATGT GGTAAAGGAA	480
TATCAACAA ATAGTGCAAG AGAACACAAG AATATAGACA CGCACCACAG TATCACTAAC	540
GCTAATATTT CATTCCATGT CAGACAAATT TTAACGAGTT TGAATAAACT ATATGAAGAC	600
TTCAAAATTA ATAATGGACT ATCGCTAAAA ACCCTTATTG CAGCTGTTTT GTTATTAGTT	660
ATTTTAGGAT TAGAATTGTT TTTATTGTTT AAAGTTTTCT GTTATGTTTT TATGACTTAT	720
TTAGAAAAAA TTATTTACTT GTCTTTGGTT ATTTTCATGC TACTGCTAGG GTTTTTTCAG	780
CAGACTAGAG GTTTTTTAGT GTCTTATGTG AAAAAAATTA TTTCATTGAC TTTTACATG	840
CCTTTGTTGT TGCTATTAGT GTTATTCAAC TCTTTTGCAT TACAATACGC AATCAAAGTG	900
GGAGGGAGCA ATGAAATAGT GGCTAAATTT GGCATTATTG TAGCAATAGG AATTTCACTG	960
ACATTTATTC AAAAAGTCCC CGAAATGATT AACGCTATCT TTGGCACACA AGGTGGTCTA	1020
ACGGATGCTA AAAGCTTCAT ATATCAAGGT GTGCAAATGG CTAGTGCTGG AGCTGGAGCC	1080
ATAGCTGGAA GTCTTAAGAG TGTGGGTCGT TCAGCATTTG GTAGAACGCT AGAAGCTTAT	1140
AAAGACGCAA AATCTACGAT AAACAGCACT ACGGCTAACA TGAGAGACAT GCCAGGACAT	1200
CCTGGTGTTA GAGTGGGTGT GGAGACGATT GAACTTCCCA AGTCTCATAG AGCTAGCAAA	1260

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GTGTTAAAT TTCAAAAT ACCCTTATTG TTTGTTTCCA TTCTTTATAA TCAAAGCCCT	60
TTATTGGCTT TTGATTATAA GTTTAGTGGG GTAGCGGAAT CTGTTTCTAA AGTGGGGTTT	120
AACCATTCCA AACTCAATTC CAAAGAAGGG ATTTTCCCTA CAGCCACCTT TGTAACCGCC	180
ACGATCAAGC TTCAAGTGRA TTYCAAATCT GCTCCC	216

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ATGGGTAATC ATTTTCTAA ATTAGGATTT GTTTTAGCGG CTTTAGGGAG CGCGATAGGT	60
TTAGGGCATA TCTGGCGCTT CCCCTATATG ACTGGGGTGA GTGGTGGGGG TGCTTTTGTT	120
TTATTGTTTT TATTTTATC CTTAAGCGTT GGTGCGGCGA TGTTTATCGC TGAAATGCTA	180
TTAGGACAAA GCACGCAAAA AAATGTAACA GAAGCTTTTA AAGAGCTTGA CATTAACCCT	240
AAAAAACGCT GGAAATACGC AGGGATCATG CTTATTTCTG GACCTTTAAT ACTGACTTTT	300

TATGGCACTA TTTTAGGTTG GGTGCTTTAT TATTTGGTGA GTATTAGTTT TAATTTGCCT	360
AGCAGTATCC AAGAATCTGA ACAAATTTTT ACTCAAACCTT TGCAGTCTAT AGGGTTACAA	420
TCCATAGGGC TTTTAGCGT TTTATTCATA ACCGGATGGA TTGTTTCTAG GGGGATTAAA	480
GAAGGCATTG AAAAAGCTCAA TTTGGTTTTA ATGCCCTTAC TCTTTGCCAC TTTTTTTGGT	540
TTGCTTTTTT ATGCGATGAG CATGGATTCT TTTTCTAAAG CTTTCCATT CATGTTGATT	600
TCAAGCCAAA AGATT	615

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ATGGAAAAAG TTTGCGTGAG CGCATGGGGG TTGCCTAAGA TTTTAGAAGA AAGATTAAAA	60
GAAAAATATG GCGATGATTG GGAAAAACAT GTTAAGGCTA AAGCAATAAA CGAAGAAGAG	120
CTTGAAGAAC AAGTCAAAGC TAAAGCCAAA GAGCAACAAA AGACACAAAG AGAAAAAACA	180
CTCAATGGAT TTTTAAAAAA AGTTGGTTTA AAAAAGCGTG ATATGTTACA AAGCACTATG	240
TTATTTGATG AAGTCAAAGA AGCTGATGTG CTTTTTCAAG CAGAGCGTAA AATTGGCGAT	300
TGGATTTTTA GCAGTGCGGT GTTCTTTTTT GCTCTAGCCC TTATAGAAGC CATTATTATT	360
GTATGCTTAT TGCCGTAAAA AGAAAAAGTG CCTTATTTAG TAACCTTTTC AAACGCTACA	420
CAAAATTTTG CCATAGTCCA AAGAGCAGAC AAGAGCATCC GTGCTAATCA AGCGCTTGTTG	480
AGACAATTGG TAGCGTCTTA TGTTAATAAT AGAGAAAATA TTTCAAGTAT AAAAGAGCAA	540
AACGAAATAG CCCACGAAAC CATTAGGTTG CAAAGCGCAT TTGAAGTGTG GGATTTTTTT	600
GAAAACTGG TTTCTTATGA GCATAGCATT TACACTAATA TAAATCTAAC ACGAAAAATT	660
AGCATTATCA ATATCGCTTT AATCAGTAAA ACCCAAGCCA ATATTGAAAT ATCCGCACAA	720
CTTTTTCATA AAGAAAAGTT AGAAAGCGAA AAGCGTTATA GAATAATTAT GACCTTTGAA	780

TTTGAACCTA TTGAAATTGA TACAAAATCT GTTCCCCTAA ACCCTACAGG CTTTATTGTT	840
ACAGGTTATG ATGTAAGTGA AATTGCGATT TTTAAAGATT TAGATGAGAA AAATAAAGTC	900
AAAGATGATG GTGTGAAATC TAGGATTATC CATGTCGAGA AAAAAGACCC TCATATGAGC	960
CAGTATAAAG ATGTTAAGGA GCAA	984

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ATGCTGCATA AGGCTAAGGT GGGCATCGTG TTTCAGGCGC TTTTAGGGAT TTTTGCCTG	60
TTTTTATTGT TGTCTTACTT GAGCGCGTTT TTAATGGTGG CTTTAAAGA CACTAAACGC	120
ATGTTTATAA GCGTTTAAAT AGGGAGCGTG GTGTTCTTT GGAGCGATCT ATTGGTCTTT	180
GTAGGGTTTA AAAATATCAG CTTTGTTTTG GATATTGGTT ATGAAATC	228

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ATGCCGTTTT TGAAAACTG GATCTGGAGT TTAAAGATGG CTTTGAGCGC GATTAGTGGG	60
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GCTAGTGGGG	TGGGGAAAAAG	CGTCCTTATT	GCGAGCCTTT	TAGGGGCGTT	TGGGCTTAAA	120
GAGAGCAACG	CTTCAAACAT	TGAAGTGGAA	TTGATCGCGC	CTTTTTTTAGA	CACGGAAGAA	180
TACGGCATT	TTAGAGAAGA	TGAGCATGAA	CCCTTAGTTA	TTAGCGTGAT	TAAAAAAGAA	240
AAAACACGCT	ATTTTTTTAAA	CCAAACAAGC	CTATCTAAAA	ACACGCTCAA	AGCGTTATTA	300
AAGGGGCTTA	TTAAACGCTT	ATCTAACGAC	AGATTCAGCC	AGAATGAACT	CAACGATATT	360
TTAATGCTCT	CCTTATTAGA	TGGCTATATC	CAAATAAAAA	ATARGCGTTT	AGCCCCCTTT	420

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ATGCCACAAA	ACCAGCTTGT	GATCACCATC	ATTGATGAAT	CAGGCTCTAA	GCAACTCAAA	60
TTTTCTAAAA	ATTTAAACG	CAACCTCATC	ATTTCTGTTG	TCATTCTTTT	ATTGATCGTG	120
GGGCTTGGCG	TGGGGTTTTT	AAAATTTTTA	ATCGCTAAAA	TGGATACGAT	GACAAGCGAG	180
AGGAATGCGG	TTTTAAGGGA	TTTAGGGGT	TTGTATCAAA	AAAATTACGC	CCTAGCGAAA	240
GAGATTAAAA	ACAAGCGAGA	AGAGCTTTTT	ATTGTGGGGC	AAAAGATCCG	TGGGCTAGAA	300
TCCTTGATTG	AAATCAAAAA	GGGGGCTAAT	GGGGGAGGGC	ATCTCTATGA	TGAAGTGGAT	360
TTAGAAAATT	TGAGCTTAAA	TCAAAAACAT	TTAGCACTCA	TGCTCATTCC	TAATGGCATG	420
CCCCTAAAAA	CTTATAGCGC	TATCAAACCC	ACTAAAGAAA	GGAACCAACC	CATTAAAAAG	480
ATTAAGGGCG	TTGAATCCGG	GATCGATTTT	ATCGCGCCAT	TGAACACGCC	TGTGTATGCG	540
AGCGCTGATG	GGATTGTGGA	TTTTGTGAAG	ACTCGTTCTA	ATGCGGGGTA	TGGGAAC TTG	600
GTGCGCATTG	AACATGCGTT	TGGTTTCAGC	TCCATTTATA	CGCACTTAGA	TCATGTCAAT	660
GTGCAGCCTA	AAAGCTTCAT	CCAAAAAGGG	CAGTTGATTG	GCTATAGCGG	GAAGAGCGGT	720
AATAGCGGCG	GCGAAAAATT	GCATTATGAA	GTGCGGTTTT	TGGGTAAAAAT	TTTAGACGCA	780

GAAAAATTCC TAGCATGGGA TTTGGATCAT TTTCAAAGCG CTTTAGAAGA AAATAAATTT	840
ATTGAATGGA AGAATCTGTT TTGGGTTTTA GAAGACATCG TCCAGCTCCA AGAGCATGTG	900
GATAAAGACA CCTTAAAAGG TCAG	924

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: phosphomannomutase

ATGATCACTG GCTCTCACAA CCCCAAAGAA TACAACGGCT TTAAATCAC GCTCAATCAA	60
AACCCGTTTT ATGGCAAGGA CATTCAAGGCT TTAAAAACA CGCTTTTAAA CGCAAAGCAT	120
GAAATAAAGC CCCTAAAAGA AACGCCAGAG AAAGTCAATG CCCTAGAAGC GTATCATCGC	180
TATTTGATCA AGGATTTTAA GCATTTAAAA AATCTTAAAT ACAAATCGC CCTGGATTTT	240
GGTAATGGCG TGGGGGCGTT AGGATTAGAG CCGATTTTAA AGGCTTTAAA CATTGATTTT	300
AGCAGCCTTT ATAGCGATCC TGATGGGGAT TTTCTAACC ACCACCCAGA CCCTAGCGAA	360
GCGAAAACT TAAAGACTT AGAAAAACAC ATGCGAGAAA ACGCTATTTT AATAGGCTTT	420
GCTTTTGATG GCGATGCGGA TAGGATTGCG ATGCTAAGCT CTCATCATAT CTATGCGGGC	480
GATGAATTAG CGATTTTATT CGCTAAACGC TTGCATGCTC AAGGCATCAC CCCTTTTGTG	540
ATCGGCGAAG TCAAATGCTC TCAAGTGATG TATAACGCAA TCAATACTTT TGGTAAGACG	600
CTCATGTATA AAACCGGGCA TAGCAATTTA AAAATCAAGC TCAAAGAAAC TAATGCGCAT	660
TTTGCGGCTG AAATGAGCGG GCATATCTTT TTAAAGAAC GCTATTTTGG CTATGATGAC	720
GCTCTTTACG CATGTTTAAG GGCTTTGGAG TTATTGCTTG AACAAAGTCC AAGCGACTTG	780
GAAACACCA TAAAAACCT CCCCTATTCC TACACCACGC CTGAAGAAAA AATCGCCGTG	840
AGCGAAGAAG AAAAATTTGA AATCATTCGC AACTTACAAG AAGCGCTTAA AAACCCGCCA	900

AGCCATTTCC CTACAATCAA AGAAATCATC AGCATTGATG GCGTGAGAGT GGTTTTTGAA	960
CATGGCTTTG GGCTTATTCG CGCAAGCAAC ACCCACCCCC TATTTAGTCA GCCGCTT	1017

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 621 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ATGTCCAAGA ACCTTCAAAA GAAGAATCCA AAGAAGAGTT TYCCACAAGC CCAGAAAGCC	60
ATAAGGGAGA TGAAAATGTT TGAAACCATT GCYTTTTTATT TCTTTGCGAT CCTTACTTTA	120
AGCATGGCGT TAGTGGTGAT CACAACCACA AATATCCTCT ATGCCATTAC CGCTCTCGCT	180
AGTAGCATGG TTTTATTTTC TGCTTTTTTTC TTTTACTGG ACGCTGAGTT TTTGGGCGTG	240
GTGCAAATCA CGGTGTATGT GGGTGCGGTC ATTGTGATGT ATGCGTTTGG CATGATGTTT	300
TTCAACTCCG CTGCAGAAGT AGTTGAACGC AAGCAAAGCC CTAAAATCTT GTGCGTTCTT	360
TCATTTGGCG TGGCGCTGTT GCTCACCTTG ATTTTAAGCG CTCCTAGCAT TGSSGAAAAC	420
CTTTCTAAGC AAGTCAATTC CAACGCTATT GATGCGCAAA TYCCYAACAT TAAAGCGATT	480
GGTTATGTGC TTTTCACCAA TTACCTCATT CCCTTTGAAG CGGCGGCTTT AATGCTTTTA	540
GTCGCTATGG TTGGAGGCAT CGCTACAGGG ATTCAAAAAA TCCATGGGAA AAATCACACG	600
CAATTTATAA AGGAATCTCT A	621

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 753 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

ATGGGTGCAA TTTTATCTAT TTAAAACTT GAAATCAAAT CTTATCTCAC CAATACAAGC	60
GCGCTATTTT GGACTTTTAT TTATCCTATT TTAATGCTCC TATTACTAAT TTTTGTTTTT	120
TCAAAAATA CCACTGAAAT TTTTACTTT AATAACATTA TAGGTCTAAT GGGACTTCTT	180
ATTATTTCTA GCGCGATCTT TGGTCTCACA CAAGCTATAA CAAGCTCTAG ATCGCATAAT	240
ATATTCTTAT TCTACATGCT ATCACCAGCA ACTTTCAAAC AAATAACTCT AGCATTAATC	300
GCTTCAAGAC TAATCGTTGT AATCCTATAT GCTTTTATCT TTATTGTTCT CTCTTTTTAT	360
GCGCTCAATA TCATCACTAT TCTTAATTTT AAAGCGCTTA TTTTGGGGTT TATTAGCATT	420
TTTTCAAGCG CATTGTTTTG TTTTGCTTG GCAATTTTGG TAGCTAGAAT TTTTCAAAAC	480
GAACAAAGCA TCTTAGGATT TTGTAATATC ATCAATCTCT ATGCGCTAAT GTCTTGTAAT	540
GTTTTTGTTT CTTTAGAATA CCTACCTAAT ATTGGTCAAT TATTTATCAA AACATCTATT	600
TTTTACTACC TTAATCAACT TCTAATCAAA GCTTTTCAAG GGATTGATAC TATACTGGTT	660
TTAGCAACTT CAACATTTTT CATTATTGGT GGCATTATTT TATTTTTACT AAGCGCTAAT	720
CGCATGTTAC TAACACCAAA AGAACGCATG CGT	753

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ATGGCAGGCA CACAAGCTAT ATATGAATCA TCTTCTGCAG GATTCTTATC GCAAGTCTCC	60
TCAATCATCT CAAGCACAAAG TGGTGTCGCA GGGCCATTG CAGGAATAGT AGCGGGCGCT	120

ATGACAGCAG CGATTATTCC TATTGTTGTG GGATTCTACTA ATCCGCAAAT GACCGYTATY	180
ATTRACCCAA TAYAATCAAA GCATCGC	207

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...336
 - (D) OTHER INFORMATION: /note= "spoIIIE gene product"
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:153:

GTGAGCCGTA TTTTAGGCTT GAGCGATGAT TTAGCGATGA CTTTATGCGC TGAATCCATC	60
CGCATTCAAG CCCCTATCAA AGGTAAAGAT GTCGTTGGTA TTGAAATCCC TAACAGCCAA	120
AGCCAAATTA TTTATTTAAG AGAAATTTTA GAAAGCGAAT TGTTTCAAAA ATCCAGCTCG	180
CCTCTAACCC TAGCTTTAGG CAAAGACATT GTGGGTAACC CTTTCATCAC GGATTTAAAA	240
AAGCTCCCCC ACTTGCTCAT CGCCGGCACG ACAGGGAGCG GTAAGAGCGT GGGCGTGAAT	300
GCGATGATTT TATCCTTACT TTATAAAAAA CCCCCC	336

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ATGGATGAAA GSCTCGTTTA TGGGGTGATT TGCATGCCCA GTCAGGTTTT TGCCAACACC	60
GGCACTAACG TGAGCATCAT CTTTTTTCAA AAAACGCCAA GCGCAAAGGA AGTGATCTTG	120
ATTGACGCTT CCAAACCTCGG CGAAGAATAC ACCGAAAACA AAAACAAAAA AACGCGCTTA	180
AGGCCAAGCG ATATGGATTT GATTTTAGAA ACTTTCCTAA ATAAAGCCCC AAAATCGGAT	240
TTTTGCGCTC TGGTTTCTTT TGATGAAATT ACAGAAAAAA ATTATTCTCT AAACCCCGGG	300
CAGTATTTCA CTATAGAAGA CACGAGCGAG ACAATCAGCC AAGCGGAGTT TGAAAACCTG	360
ATGCAACAAT ATTCAAGCGA ACTAGCGAGC CTTTTTGATG AAAGCCAAAA TTTGCAACAA	420
GAGATTTTAG AAACTTTAAA AGGGGTAGG TTTGAG	456

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...339
- (D) OTHER INFORMATION: /note= "chemotaxis protein cheY"

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:155:

ATGAGAAGAA TTATTAAAAA CAACTTTTCA CGCTTAGGCT ATGAAGATGT TTTAGAAGCT	60
GAGCATGGGG TGGAAGCTTG GGAAAACTA GACGCTAATG CGGACACTAA GGTGCTTATT	120
ACGGATTGGA ACATGCCTGA AATGAACGGG TTGGATCTCG TTAAAAAGGT GCGTGCGGAT	180
AACCGATTTA AGGAAATCCC TATCATTATG ATCACCACAG AGGGCGGTAA AGCTGAGGTC	240
ATTACGACTT TAAAAGCGGG CGTGAATAAC TACATTGTGA AACCTTTTAC CCCCCAAGTT	300
TTGAAAGAAA AATTAGAGGT TGTTTTAGGG ACAAACGAT	339

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 549 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ATGGCAGAAG AACAAGAAAA TACCGCGCAA CAACCCCAAA AAAAAAGCAA AGCCCTTTTA	60
TTTGTCAATTA TTGGAAGCGT GCTAGTGATG CTTTATTGG TGGGGGTGAT TATCATGCTG	120
CTTATGGGGA ATAAGGAAGA ATCTAAAGAA AACGCTTCTA AAAACACCCA AGAAGTCCAA	180
GCTAATCCTA TGGCGAACAA GAATCAAGAA GCCAAAGAAG GCTCTAATAT CCAGCAATAT	240
TTGGTGCTTG GGCCTTTGTA TGCGATTGAT GCGCCTTTTG CGGTGAATTT GGTCTCTCAA	300
AATGGCAGAC GCTACCTTAA GGCTTCTATT TCGCTAGAAT TGAGCAATGA AAAGCTTTTG	360
AATGAAGTCA AGGTTAAAGA CACGGCGATT AAGGACACGA TTATAGAAAT TCTATCGTCT	420
AAAAGCGTGG AAGAAGTGGT TACTAACAAA GGCAAAAACA AGCTTAAAGA TGAAATTAAG	480
AGCCATTTGA ATTCGTTTTT GATTGATGGC TTTATTAAAA ATGTCTTTTT CACTGATTTT	540
ATTATCCAA	549

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ATGGGGTGTT TTAGCACCAT TTGTTGTAAG GGTTTAACGC TTAGCGTTGG TGGATTTTTG	60
GTGATGATGA GATTCTTAAT ATTCAAAGAT TTTTGCAAAG ATTTT	105

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2106 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...2106
 - (D) OTHER INFORMATION: /note= "VirB4 homolog"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GTGGCGCGTC TTGTGGTTAA AAGGCGTAAA ATTGATTATA AACAAAGCAT TCAATCTGAC	60
TCTCAATACT TGCAAGCGAS CTTGAATCAG TTTGAAAATA AAGAAGTGTA TGAGAATCAG	120
TATTTTTTTAG TTTTAGAAAG CACTCACTCT TTGCATGGCG TTTTGAGCA TAAGAAAAAA	180
TCTTTCATGC ACGCTAATAG AGAAAATTTT AAGGATATTC TCTCTTATAA AGCGCATTTT	240
TTGCAAGAAA CTTTAAAAAG CTTAGAAATC CAGCTCAAAA ACTATGCCCC CAAACTCTTA	300
AACTCTAAAG AGGTTTTGAA TTTTATGCA GAATATATTA ATGGGTTTGA ACTCCCTTTA	360
AAACCCCTAG TAGGGGGGTA TTTGAGCGAT AGCTATATCG CTAGTTCTAT CACTTTTGAA	420
AAAGATTATT TCATTCAAGA AAGCTTTAAT CAAAAACCT ATAACCGCTT GATTGGCATT	480
AAAGCTTATG AGAGCGAAAG GATCACTTCT ATAGCGGTGG GAGCGCTTTT ATACCAAGAG	540
ACGCCTTTGG ATATTATCTT TTCCATAGAG CCTATGAGCG TCAATAAAAC GCTGAGTTTT	600
TTAAAAGAGA GGGCCAAGTT TAGCATGTCT AATCTTGTTA AAAACGAGCT ATTAGAATAC	660
CAAGAATTAG TCAAAACCAA ACGATTATCC ATGCAAAAAT TCGCCCTAAA CGTTCTTATC	720
AAAGCCCCCA GTTTGGAGGA TTTAGACGCT CAAACCAGCT TAATTTTAGG GCTTTTATTT	780
AAAGAAAAC TAGTGGGCGT TATAGAAACT TTTGGCTTGA AAGGGGGGTA TTTTTCCTTT	840
TTCCCTGAAC GCATCCATTT AAACCACCGC TTGCGTTTTT TAACCTCTAA AGCCCTAGCG	900

TGTTTGATGG TGTTTGAAAG GCAAAATTTA GGTTTAAAGG CTAATTCATG GGGGAATAGC	960
CCTTTGAGCG TGTTTAAAAA TTTGGATTAT TCCCCTTTTT TATTCAATTT CCACAACCAA	1020
GAAGTGAGCC ATAATAACGC TAAAGAAATT GCCAGAGTGA ATGGGCATAC TTTAGTTATA	1080
GGGGCAACCG GAAGCGGTAA AAGCACGCTG ATTAGCTATT TAATGATGAG CGCTTTAAAA	1140
TACCAAAACA TGCGCCTTTT AGCTTTTGAC AGGATGCAAG GGTTGTATTC TTTCACCGAA	1200
TTTTTTAAAG GGCATTACCA TGACGGCCAA TCTTTTAGTA TCAACCCCTT TTGTTTAGAG	1260
CCTAATTTGC AGAATTTAGA ATTTTGTCAA TCCTTTTTTT TGAGCATGTT GGATCTTGCC	1320
CCTTCAAGGG ATAAAGAAGC CTTAGAAGAC ATGAATGCGA TTTCTGGCGC GATTAAGAGC	1380
CTTTATGAGA CCTTATACCC CAAAGATTTT AGTTTGCTGG ATTTTAAAGA AACGCTTAAA	1440
AGAACCTCAT CTAACCAATT GGGCTTGAGT TTAGAGCCGT ATTTGAATAA CCCCCTTTTT	1500
AACGCTTTGA ATGACGCGTT CAACTCCAAC GCTTTTTTTAA ATGTGATAAA CCTAGATGCG	1560
ATCACCCAAA ACCCTAAAGA CTTAGGGCTT TTAGCCTATT ACTTGTTTTA TAAGATCTTA	1620
GAAGAGTCTA GGAAAAACGA CAGCGGCTTT TTGGTTTTTT TAGACGAATT TAAATCCTAT	1680
GTGGAAAACG ATTTGTTAAA CACTAAAATC AACGCTTTAA TCACGCAAGC CAGGAAAGCT	1740
AATGGCGTGG TGGTGTGGC CTTGCAAGAC ATTTACCAAC TTAGCGGGGT TAAAAACGCC	1800
CATAGTTTTT TAAGCAACAT GGGGACTCTC ATTTTGTATC CGCAAAAAA CGCTAGGGAA	1860
TTGAAACACA ATTTCAATGT GCCTTTGAGC GAAACTGAAA TTTCTTTTTT AGAAAAACACC	1920
CCTCTGTATG CCAGGCAGGT TTTAGTCAAA AATCTGGGTA ACGGGAGTTC CAACATGATT	1980
GATGTGAGTT TGGAGGGCTT GGGGTGTTAT TTGAAAATCT TTAATTCAGA TTCCAGTCAT	2040
GTCAATAAAG TGAAAGCGTT ACAAAAAGAC TACCCTACAG AGTGGCGTGA GAAACTTTTG	2100
AAGAGT	2106

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 879 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...879
(D) OTHER INFORMATION: /note= "methyl-accepting chemotaxis protein; transmembrane receptor"

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:159:

ATGCAAGAAG ACTGGCAAGC CGTCCAAGAC ACCATTAAAG TGGTTTCAGA TGTGAAAGCG	60
GGGAATTTTG CGGTGCGCAT CACGGCTGAA CCCGCAAGCC CTGATTTGAA AGAATTGAGA	120
GACGCGCTAA ATGGGATCAT GSAYTATTTG CAAGAAAGCG TAGGGACTCA CATGCCAAGC	180
ATTTTCAAAA TCTTTGAAAG CTATTCTGGC TTGGATTTTA GAGGGCGGAT CCAAACGCT	240
TCGGGTAGGG TGAATTGGT TACTAACGCT TTAGGGCAAG AAATCCAAAA AATGCTAGAA	300
ACTTCGTCTA ATTTTGCCAA AGATCTAGCG AACGATAGCG CGAATTTAAA AGAATGCGTG	360
CAAAATTTAG AAAAGGCTTC AAACCTCCAA CACAAAAGCC TGATGGAAAC TTCCAAAACG	420
ATAGAAAATA TCACCACTTC CATTCAAGGC GTGAGCTCTC AAAGTGAAGC CATGATTGAA	480
CAAGGGAAAG ACATTAAAAG CATTGTAGAA ATCATTAGAG ATATTGCCGA TCAAACGAAT	540
CTATTAGCCC TAAACGCTGC TATTGAAGCC GCACGAGCCG GCGAGCATGG CAGAGGCTTT	600
GCGGTGGTGG CTGATGAGGT GAGGAAGCTC GCTGAAAGGA CGCAAAAATC CCTCAGTGAG	660
ATTGAAGCCA ATATTAATAT TCTCGTTCAA AGCATTTCAG ACACGAGCGA AAGCATTAAA	720
AACCAGGTTA AAGAAGTAGA AGAGATCAAC GCTTCTATTG AAGCCTTAAG ATCGGTTACT	780
GAGGGCAATC TAAAAATCGC TAGCGATTCT TTAGAAATCA GTCAAGAAAT TGACAAAGTC	840
TCTAACGATA TTTTAGAAGA TGTGAATAAA AAGCAGTTT	879

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ATGCCTAAAA GTTTCACCTT ACCGACTTTC GTGTGGTGTT TGTTTGTGGG GGTTATCTTA	60
AGGAACGCTT TGTCGTTTTT TAAAATCCAT AGCGTGTTTG ACAGAGAGGT TTCAGTTATA	120
GGGAATGTGA GCTTGAGCCT GTTTTTAGCT TACGCT	156

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...546
- (D) OTHER INFORMATION: /note= "HYPOTHETICAL ABC TRANSPORTER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GTGGGGCTTT TAAATTCTAA GCGTTCAAA CCCTACCGCA AGATTTTGCA AATGGTGTTT	60
CAAGACCCCT ACGCATCATT AAACCCTCGC TTAAGCATT C AAAGCATTTT AATAGAAGCT	120
TTGCGCTTTG CTTACCCTAA AGCTTCACAA CAAGAATGGC ACCATTTAGC TGAACTTTGC	180
TTAGAAGAAG TGTGTTTAAA CCCTGAATTG CTTAACTTTT ACGCTTATGA GCTCAGCGGA	240
GGGGAGCGCC AAAGAGTGGC GATCGCTAGA GCGATTGCCT TAAAACCTAG AATCATTCTT	300
TTAGATGAGC CAACCTCTGC TTTAGACAAA AGCATTCAAA AAAGCGTGTT GGAATTATTG	360
TTGAATTTAC AAGAAAAGCA GGATTTGAGC TATTTGTTTA TCAGCCATGA TTTAGATGTG	420
ATCAAAGCTT TTTGCGATAG GGTGTTAGTG GTGAGTGAGG GGAAAATCGT GGAAACAGGC	480
GCTATTGAAG AGGTGTTTGA CAACCCCAAA CACGCTTATA CCAAGCGTTT GTTGAATCC	540
AGGCTT	546

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GTGAGTTTGA TTAAAGTTAG TGGTGATAAA AAAGTGATTG AGGTTTCTAT TCCTTTAACT	60
TCCATTTTCAG GCAAAGCGCG TGTGAAAATC AGACATGCCT TTAGCGATTA TGGTATTTC	120
ACAGCGACTA GAAAAATCCC TTTTAGTTTA AAGCATTATG TAGAGTGGCA GATCGGTTAT	180
GATGTCCCCA TTAAAGATAA AGAAAAATTT GAACTCACTA CTTTAAAAGA TGAAAAATAT	240
CATTTTTTTAG GGGCTAATAA TAAAGTAAAA ACTCTTTATG AATTGAGCGA AATGATTTAT	300
TACGCTAAGC GATTGGGTTT AATCAGTTTA GAAAATTTAG AAAATACTTT AAAATTTTTA	360
GAAAAACAAA AACAATTTAT AGAAGATAAT TTTATGATTA CAAGAGAAAG ATTTAGATCG	420
CATCAATTTG GTGGCATGGA TTTTGAACTC TCACGCATTT CTTATCCTTT GCTCATTCAT	480
TCTTTTGATG ATAATGAGTT GAGCGAAATA GTTATTAAGG AACAACAATA TGGCTCTAAA	540
ACCCAAGCCA TGCTGTATTT TTGCTTTTCT ATTTTGGAGT TAAAAACCGC TACCCCTTA	600
TTAAACAGAA CCGCTATGCC CAAAGAACAT GCCCTTTTGA TTATCCATGA AACCAACGCT	660
CTTGTGTTTT TAGAAATGCT TAAAATTTTT GGACTTTTAA GCCAAGTGCA CCATAACGAT	720
GTGTTWAAGA TTTTWGAAAA AATACTTCAA AAT	753

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...120

(D) OTHER INFORMATION: /note= "major surface LPS-antigen"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```
GTGATCACGG CGTGTTTAA TAGYGAAAAA ACCATTGAAG ACACCATTCT TTCCGTGCTT      60
AATCAAACCTT ATAAAAACAT TGAATACATC ATTATAGATG GGGCTAGCGC GATAGCACTT    120
```

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

```
GTGTTTGTAG GGCTTTATCA TGGGGCAAGC ATCTTTGATT TAAAATTTGA AGTCTATCTT      60
ACTATGCTAA TCTCTTTAAT GCCCTTTGTG GCTACGATTT ATATCAATTT CCCAAAAACC    120
ACAGAACTT CGCATGGCTA TGCGAGATGG GCTAATGTTA AAGATATAGA ATGCTTTAAA      180
ATTTTGTAGCA AAGAGGGCTT TTGTAAAGTG GTGCATAGAT TAGGGGTGCA ATTTGATAAT    240
GGCTTTATTC TAGGTAAATT TGGTTTCCA AAGCTTAGAA ATGTGTGCTA TGACAAGCCC      300
TTAGGAACGA TGATTGTTGC ACCCCTGGT GCGGAAAAAC TGCATGTGTG GCTTTGCCAA    360
ATTATAT                                           366
```

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

ATGAAACGCC TTGCTGTTGC GCTTATTTTG GTGTTGGGAG TGGTGTGGGG GAAATCCTTG	60
CCTAAGTGGG CAAAAGATTG CTCAAAAGAG ATGCGGATTG AAAAGACCCA AACCAAAGAT	120
GAAAAAATTT TAGTGTGTGG GATGAGCGAT ATATTGCTTT CAGATATGGA TTATAGCTTG	180
TCCTCAGCCA GACAAAACGC CTTAGAGAAA GTGATGGAAG CTTTCAAGGG GGATAGAATA	240
GAGATTAAGG CTGGTGAGCT AAAGGCCACT TTTATTGATA CGGATAAAGT TTATGTGCTT	300
CTAAGAATCA CTAAGAAGCA TGTCGCTTTA ATGAATGAG	339

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1311 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ATGAACCCCC AGATTCAACC CGCCACTAAA AAACCCTTAA AATCCCTTTT AGCCGCTAGT	60
TCAGGCAATT TAGTGGAATG GTATGATTTT TACGCTTATG CGTTCCTTGC TCCTTATTTT	120
GCTAAGGAAT TTACCCACAC CAATGACCCT ACTCTAGCGC TCATCTCAGC TTTTTTAGTT	180
TTTATGCTAG GGTTTTTTCAT GCGCCCTTTG GGGAGTTTGT TTTTGGTAA ATTGGGGGAT	240
AAAAAGGGGC GTAAAACTTC CATGGTGTAT TCCATTATCC TTATGGCGCT AGGCTCTTTC	300
ATGCTCGCAT TGCTCCCCAC TAAAGAAATC GTAGGGGAAT GGGCGTTCTT GTTTTTATTG	360
TTAGCCAGGC TTTTACAGGG CTTTAGCGTG GGAGGAGAAT ATGGCGTGGT CGC CACTTAT	420
CTCTCTGAAT TAGGCAAGAA TGGTAAAAAA GGTTTTTTATG GCTCTTTCCA ATATGTAAC	480
TTAGTGGGAG GGCAACTCTT AGCTATTTTT TCGCTCTTTA TCGTTGAAAA CGTTTACACG	540

CATGAGCAAA TCAGCGCGTT TGCTTGGCGT TATTTATTCG CTTTAGAGGG TATATTAGCC	600
CTACTCTCGC TCTTTTTGAG AAATATCATG GAAGAACTA TGGATAATGA AGCGACTCCT	660
CAAAAAAGA CTAATGTAAA TAATACAAAA GAAACCCATA TCAAAGAAAC CCAAAGAGGC	720
AGTTTAAAGG AATTGCTCAA CCATAAAAAA GCCTTAATGA TAGTCTTTGG GCTAACTATG	780
GGAGGGAGTT TGTGCTTTTA CACTTTTACG GTGTATTTAA AAATCTTTTT AACCAACAGC	840
TCATCGTTTA GCCCTAAAGA AAGCAGTTTT ATCATGCTTT TAGCGCTCTC TTATTTTCATC	900
TTCTTACAAC CCTTATGCGG GATGCTTGCG GATAAAATCA AACGCACCCA AATGCTGATG	960
GTTTTTGCGA TCACAGGGCT TATTGTAACG CCTATTGTCT TTTATGGTAT CAAGCATGCC	1020
ACTAGCGTGT ATGAAGCCCT ATTTTATGAA ATACTCGCAT TGAGCAGCAT GAGTTTTTAC	1080
ACTTGCAATTG CTGGGGTTAT TAAGGCGGAA TTATCCCTG AACATGTGCG AGCGCTTGGC	1140
GTGGGTTTAG CCTATGCGAT CGCCAATGCG CTTTTTGGAG GGAGCGCGAG TTATATAGCG	1200
TTAGAGTTCA AACAGCATGG TTTTGAAGAG GGGTTTGTGG GCTATGTCAT GTTGAGTATT	1260
GTTATCTTTA TGGTTATGGT TATCATATTC CCTAAAAAA CCTATTTGGA G	1311

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...285
 - (D) OTHER INFORMATION: /note= "phosphoglucomutase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

ATGGACATTA GCATTTTTAG AGAATACGAT ATTAGAGGCA TTTACCCAC CACTTTAGAT	60
GAAAATACGG CTTTGTAGTAT CGGCGTGGAG TTGGGAAAA TCATGCGAGA ATACGATAAA	120
AGCGTGTTTG TAGGGCATGA CGCAAGGGTG CATGGGCGTT TTTGTTTGA AGTTTTGAGC	180

GCGGGGCTGC AATCAAGCGG CTTGAAAGTG TATGATTTAG GGCTAATCCC CACACCGGTA	240
GCGTATTTTG CGGCCTTTAA TGAAATAGAC AATATCCAAT GGCCC	285

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GTGTGCGACA TTTTTTCTGA TGGCGTTTTA TTGGACAAAG CGTTAGTGAT TTATTTCAAA	60
GGCCCCTATA GTTTCACCGG TGAAGATGTG TGCGAAATCC AATGCCATGG AAGCCCCCTT	120
TTAGCGCAAR ATATCCTTCA AGCTTGCTTG AATTTAGGGG CTAGGCTCGC TAAAGCGGGG	180
GAATTTAGCA AAAAAGCCTT TTAAACCAT AAAATGGATT TGAGCGAGAT TGAAGCGAGC	240
GTTCARCTCA TCCTTTGTGA AGRTGAAAGC GTTTTAAACG CTCTAGCCAG GCAGCTTCAA	300
GGGGGA	306

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ATGTTTAAAA AAATGTGTTT GAGCCTGCTA ATGATAAGCG GTGTTTGTGT GGGGGCAAAG	60
---	----

GATTTGGATT TCAAGCTGGA TTATCGCGCG ACTGGGGGGA AATTCATGGG GAAAATGACG	120
GACTCTAGTC TTTTAAGTAT CACTTCTATG AACGATGAAC CGGTGGTGAT TAAAAACCTT	180
ATTGTCAATA GGGGAAATTC AGTCGAAGCG ACTAAAAAG TAGAACCCAA ATTTGGCGAT	240
AAGTTTAAAA AAGAAAAACT CTTTGATCAT GAATTAAAT ACTCGCAACA GATATTTTAC	300
CGCCTGGATT GCAAGCCTAA CCAATTGTTA GAAGTTAAAA TCATCACGGA CAAGGGCGAA	360
TATTACCATA AATTTTCCAA A	381

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...1506
- (D) OTHER INFORMATION: /note= "SULFATE TRANSPORT ATP-BINDING PROTEIN CYSA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ATGACCTTGA AGCCATATCC AACCAAAGAG ACTGGTCTTG CTAGCCAATT ATCTGGGCAC	60
TGGTTTTTTC AGCTTTCGTT ATTTAATAAA ACAAACTTTA ATCCTAATAA AATTTGGATT	120
CCTTTAGAGT TCAATAAAAG ATCAAAAATA AAGTTTGATA AAGATTTAGA AATCTATTTT	180
GATAGTCATG AATCGTTCAA TATCTCTAAA AAATACTTGC AAGAAATAGA TCAAGAATCA	240
CTAAAAAAGA TCAACAATC AAAAGATTTT TTTTCAATTC AAAAAATAGA GAGTAAGCAT	300
GATAATAACG ATATACTGCA ACTTGAATTT TTTGAGAATG ATACAAGTTT TCTTTTGTCT	360
AAAGGAAGTT TTGCAGAAAT TTTAGAATAC AACATGCAAT TAAAAATAGA TTCTTTAATT	420
ACAAAAGAAT TTAATAAGCT TTTAGCGATC GTTCAAGATA GTCCCCAAGA TAGTTACCAA	480
TTAAAAATTC GTGTCCGACA TAACAATAAG CTCCTAGAG AGAAATATAC GGAACATGAA	540
ATAAACTTG AAGTTTATGA TTGCAGAAAA TCCCACGATC ACAATGAGCC AATCATCTTA	600

AGCCAGCAAA GCACCGGCTT CCAATGGGCG TTTAATTTCA TGTTTGGCTT TCTTTATAAT	660
GTGGGATCAC ATTTTAGTTT TAACCATAAT ATTATCTATG TCATGGACGA GCCAGCCACT	720
CATTTGAGCG TGCCAGCCAG AAAGGAGTTT AGGAAATTTT TAAAAGAATA CGCTCATAAA	780
AATCATGTTA CTTTTGTTTT AGCCACCCAT GACCCCTTTT TAGTGGATAC GGATCATTTA	840
GATGAAATAA GGATTGTGGA AAAGGAAACA GAAGGCTCTG TAATTAAGAA TCACTTTAAC	900
TATCCCCTAA ATAATGCAAG CAAAGACTCC GACGCTTTGG ACAAATCAA ACGCTCTTTA	960
GGAGTGGGCC AGCATGTTTT TCATAACCCC CAAAAACACC GAATCATTTT TGTAGAAGGC	1020
ATCACGGATT ATTGTTATTT GAGCGCTTTT AAATTGTATT TGC GTTACAA AGAATACAAG	1080
GACAACCCCA TTCCTTTCAC TTTCTTACCC ATTTCAGGGC TTAAAAACGA TTCAAACGAT	1140
ATGAAAGAAA CCATTGAAAA ACTTTGCGAG TTAGACAATC ACCCTATTGT TTTGACAGAC	1200
GATGACAGAA AATGCGTTTT TAACCAACAA GCAACGAGCG AACGATTTAA AAGAGCTAAT	1260
GAAGAAATGC ATGATCCCAT CACCATCCTA CAACTCTCAG ACTGCGATAG GCATTTCAAA	1320
CAAATTGAAG ATTGTTTCAG CGCAAACGAT AGAAACAAAT ACGCTAAAAA TAAGCAAATG	1380
GAATTGAGCA TGGCTTTTAA AACAAAGGCTT TTGTATGGCG GAGAAGATGC GATAGAAAAA	1440
CAAACAAAAA GAAATTTTTT AAAATTATTC AAATGGATTG CATGGGCTAC AAAC TTGATC	1500
AAAAAC	1506

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GTGTATTTTT TTCTGGCATT GAGCGGGGAA AAAGTCTTAC TGCCCGTCAT TGGCGGTTTA	60
GAAAAAAACG CGCTAGAAGC CGGGCTGTTA AAGGGGGATA GAATCCTTCT ATCAACCATC	120
AAAAAA	126

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1050 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

ATGGAAAATT TTAAACTCAT CAACTTTTTT ACCGGTCAAA ACATGCGGG TAAAACCAAT	60
CTTTTAGAAG CTCTTTATAC CAACACAGGC CTTTGTGATC CTACTGCCAA TCAAGTCAGT	120
CTTCCTCCTG AACATGCCGT GAATATTAGT GAATTCAGAA AAATCAAACG CGATGCCGAC	180
AACCTAAAAA CCTTTTTTTA TCAAGGAAAC ACCGCTAATC CCATTAGTAT CCGCACTGAA	240
TTTGAACATG CTACTATCCC TCTTACTATC CAATACCCCA CACAAACCAG TTACAGCAAA	300
GACATCAATT TGAATAGCGA TGATGCTCAT ATGACAAACC TTATAAACAC AACAAATACG	360
AAGCCACAGC TCCAATTTTC CTACAATCCA TCCCTTTCCC CCATGACAAT GACTTATGAA	420
TTTGAAAGGC AAAACCTAGG TTTAATCCAT TCTAATTTAG ATAAAATCGC TCAAACCTAT	480
AAAGAAAATG CGATGTTTAT TCCTATAGAA TTATCTATTG TTAATTCTCT TAAAGCATTG	540
GAAAATTTAC AATTAGCAAG CAAAGAAAAA GAATTGATTG AAATCCTACA ATGTTTCAAC	600
CCTAATATTT TAAATGCTAA TACAATAAGA AAGTCTGTCT ATATCCAAAT CAAAGATGAA	660
AACACACCGC TAGAAGAAAG TCCCAAAAGG CTTTTAAATT TGTTTGTTG GGGTTTTATC	720
AAATTCCTTA TTATGGTGAG CATTCTTATA GACAATCGTG TCAAGTATCT TTTTATTGAT	780
GAAATAGAAA GCGGTTTGCA CCATACAAAA ATGCAAGAGT TTTTAAAAGC TCTGTTTAAG	840
TTAGCTCAAA AATTACAGAT TCAAATTTTT GCCACCACGC ACAATAAGGA ATTTTTATTA	900
AACGCCATCA ACACGATATC CGATAATGAA ACGGGAGTTT TTAAAGACAT AGCCTTGTTT	960
GAGCTTGAAA AAGAAAGCGC TTCTGRCTTT ATCAGACACA GCTATTCTAT GCTAGAAAAA	1020
GCGCTTTATA GGGGTATGGA GGTAGAGGC	1050

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

 (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

ATGGATTTTA AAAAATGCCC TAATTTTGAA AAAAAATGTG CGTTTCTTTG TTTCTCAAAT	60
TTGGTTTTTAC TTATTGAAAT CCACTCTAAA GGA CTACACA TGCAAAAAA GAAACCCAAG	120
AACCCGCAAC CGAATTTATT TAGCATCTTA GATAAGGGCG ATGTTGCAAC AAACAATCCT	180
GTTGAAGAGT CAGACAAGGC CAATAAAATA CAAGAGCCAC TCCCTTATGT CGTGAAAACG	240
CAAATCAATA AAGCAAGCAT GATTTCTAGA GATCCTATTG AATGGGCAAA GTATTTAAGC	300
TTTGAAAAAC GAGTCTATAA GGATAATAGT AAAGAAGATG TCAATTTCTT TGCCAATGGT	360
GAGATAAAAG AAAGTTCTCG TGTTTATGAA GCGAATAAAG AAGGGTTTGA AAGGCGCATC	420
ACTAAAAGAT ACGATCTGAT TGATAGAAAT ATTGATAGAA ATAGAGAATT TTTTATAAAA	480
GAAATTGAAA TTCTAACCCA CACAAACAGC TTAAAAGAAT TGAAAGAGCA AGGGTTAGAA	540
ATCCAATTGA CCCACCATAA TGAAACGCAT AAGAAAGCCT TAGAAAATGG CAATGAAATC	600
GTAAAGAAT ACGACCATCT TAAAGATATT TACCAAGAAG TAGAAAGAAC AAAAGATGGT	660
GGATTGGTAA GAGAAATAAT CCCAGTATT TCTAGCGCTG AGTATTTCAA GCTTTACAAC	720
AAACTGCCTT TTGAATCAAT AAACAATGAA AATACCAAAC TGAATACTAA CGACAATGAA	780
GAAGTTAAAA AACTAGAATT TGAATTAGCT AAAGAAGTGC ATATTTTAAT CCTAGAGCAA	840
CAATTGCTTT CAGCAACAAA TTATTATTCT TGGATAGATA AAGATGATAA TGCGAATTTT	900
GCTTGAAAAA TGCATAGGCT TATCAATGAA AATAAACTCA AAGAAAACCA TCTCAGCGCC	960
AATAACGCTA ATAAGATTAA GCAATTTTTC TTTAATAATG GTTCTATTTT AGGCTGGACT	1020
AAAGAAGAAC AAAGCGCTAT ACAAGAAAAC AGAGATTATT CTTTAAGAAG CGCTCTTTTA	1080
AGTTTAGAAG AAATCGCTCA AGCAAAAATT GAATTGCAAA AATACTATGA AAGCGTTTAT	1140
GTTAATGGTG ATGGGAATAA AAGAGAAATC AAGCCTTTTA AAGAAATTTT AAGAGACACC	1200

AACAATTTTG AAAAAGCTTA TAAGGAGCGT TATGACAAAT TGGTAAGCTT GAGTGCAGCA	1260
ATCATTCAAG CTAAAGAGGG TGGTAATGAG CGACAAAATT CTAGTGCAAA TAACAATAAC	1320
CCTATTAAAA ATACAATAGA GACTAATACT TCTAACAATA TTATTCAAAA TAATGATAAT	1380
ATAATCATCC AAATT	1395

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

ATGGCGCTTG AAGTGGTTTT ATGGGATTTT GATGGCGTGA TTTTGTACAG CATGCATTTA	60
AAATATGAAG GGTTTAAGGC GTTGTTCAT AAGCATGGCA ACGATAGTAA AGAGGGTTTG	120
AAACAATTTG AAGTTTATCA CTATCAAAGT GGGGGGATTT CAAGGAATGA AAAGATCCAA	180
TATTTTTATA ACGAGATTTT AAAAACCCT ATCGCTCAAG AAGAAATAGA TGCATTAGCC	240
CTAGAGTTTG GCGCTATCAT AGAGCAAAAG CTTTTTGATA GGGGGCATTT GAATAGCGAR	300
GTGATGGCGT TTATTGATAA GCATTATCAA AATTATATTT TCCATATCGC TTCAGCGGCC	360
TTGCATAGCG AATTGCAAGT GTTGTGCGAG TTTTATAGGA TTACTAAGTA TTTTAAGAGC	420
GTTGAAGGGA GTCCGCCTGA TAAACCCAAG ATTATCGCTA ATATCATTCA AAAATACGCC	480
TATGACCCAA GCCGTATGCT AATGATAGCG ATAGCGTCAA TGATTATGAA AGCGCTAAGG	540
CTAATAAAGT GCGGTTTTTG GGCTATAACA GCAAGGTTT	579

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

ATGCTCAAAA AAAAGATTGA TTTGCATAAA GATTCTATTA GGAAGCTCTT TTTTATTAC	60
TTCATCCCTT TAGTTTTTTC TATGATCTCA CTTTCTACTT ACTCTATGGT AGATGACATG	120
TTTGTGGGCA AAAAAGTGGG TAAAGAAGCT ATCGCTGCGG TCAATATCGC ATGGCCTATT	180
TTTCCAGGAC TCATTGCGTA TGAATTGCTT TTTGGTTTTG GGGCAGCGAG CATTGTGGGG	240
TATTTTTTAG GTCAAAATAA AACCCATAGG GCTAGGCTTG TGTTTAGCAG CGTGTTTTAT	300
TTTGTGCTC TAAGCGCCTT TATTTTGAGC ATGGCGTTAT TGCCTTTTAG CGAAAATATC	360
GCGCAGTTTT TTGGGAGCAA TGACGCTTTA TTGAACATGT CAAACGCTAT ATTGAAATCA	420
TTT	423

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GTGAAATGTT TATTAATAAA AAAATCACTT CTATTTGCAC TGAAACCATT GCCGGACCTA	60
AAAACGACTA CCCCTATTTT AGCGCCTATG AGCGTGGTGG CTGGGAGGTT GRCTSCSCAT	120
TTAGTCCAGC ATTATTTACT GGCTTTAGAG CATGTTAAAG GGTTTATGGG TAAGGGGGTC	180
ATACTAGGGG GTTTGTGGG TGCSCAAAGG GCTAAAATCG TCGTAATTGG AGGCGGTGTG	240
GTTGGCATGG AGAGCGCGAA AGTCTTAARC CAAATGGGGR CTAAAGTAAC GATTTTAGAA	300
TTAGACTACG CTAAATTACA AAACCACCCT TATTATCATT TGTATGATTT AGAAGTCTTA	360

AGCGTGAATG AAGCCAATAT CATTCAAGCC TTAAACGGGR CGGTGGGGCT AGTGGGAGCG	420
GTRCTGGTTA CARCGAGCCA AACCCCTAAA GTGRTCTTAA GAAGGCATTT AAAATAC	477

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1128 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

ATGCTTGCAA AAATCGTTTT TAGCTCATTG GTTGCGTTTG GAGTTTTGTC GGCTAATGTG	60
GAGCAGTTTG GTTCATTTTT CAACGAGATA AAAAAAGAAC AAGAAGAAGT GGCCGCAAAA	120
GAAGACGCTC TTAAAGCTCG CAAGAAGCTC TTAAACAATA CGCATGATTT CTTAGAAGAC	180
TTGGTTTTTA GAAAACAAAA AATCAAAGAG CTTGTGGATT ACAGAGCTAA AGTTCTTTTA	240
GATTTAGAAA ACAAGTACAA AAAAGAAAAA GAGGCTCTAG AGAAAGAGAC AAGAGGTAAA	300
ATCCTTACTG CTAAGTCAAA GGCTTATGGT GATCTAGAGC AAGCCTTAAA AGATAACCCT	360
CTTTATAAGA AACTTCTTCC TAACCCTTAT GCTTATGTTT TAAACCAAGA AACATTCACG	420
CAAGAAGATA AGGAGCGTTT GAGTTATTAC TACCCCAAG TGAAAACGAG CAGTATTTTT	480
AAAAAACTA CCGTACCAC TAAAGATAAG GCTCAGGCTT TGCTTCAAAT GGGTGTGTTT	540
TCTTTAGATG AAGAGCAAAA CAAAAAGCG AGCCGATTAG CTTTATCTTA CAAGCAAGCG	600
ATTGAAGAAT ATTCCAATAA CATTTCTAAT TTATTGAGCA GAAAAGAATT GGATAATATA	660
GATTATTACT TGCAGCTTGA AAGAAACAAA TTTGACTCCA AAGCAAAAGA TATTGCTCAA	720
AAAGCCACCA ACACGCTTAT TTTTAACTCG GAACGCTTGG CGTTTAGCAT GGCGATTGAT	780
AAGATCAATG AGAAATACTT AAGGGGCTAT GAAGCTTTTT CTAAGTTGTT GAAAAATGTC	840
AAAGATGATG TGGAGTTGAA TACTTTGACT AAAAAGTTCA CCAATCAAAA ATTGAGTTTC	900
GCACAAAAAC AAAAATTGTG TTTGTTGGTT TTAGACAGCT TCAATTTTGA TACCCAATCC	960
AAAAAATCTA TATTAATAAAA GACTAATGAA TACAATATCT TCGTAGATAG CGATCCTATG	1020

ATGAGCGACA AAACAACTAT GCAAAAAGAA CACTACAAGA TATTTAATTT CTTCAAAACA	1080
GTGGTTTCTG CATAACGGAA CAATGTTGCC AAGAATAACC CCTTTGAA	1128

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

ATGGATTTCG TAGGGTTTGA AGATTTAAAA TGCAAAGACA AAGAAAAC TC	60
TTTGTGATCC GTAACGATAA GTTAGGCGAT TTTATTTTAG YGATTCCCGC	120
CTCAAGCATG CTTTTTTAGA AAAAGGCGTA GAAGTGTATT TGGGCGTGGT	180
TATACCACCC CAATTGCTTT AGAATTCCTT TTCATTGATG AAGTTATCAT	240
CATTTAGCCA CCACCCYCAA AAACCGCTCC ATTGACGCTC TTATCTTTTT	300
TTTAAAAACG CCAAACCTCGC TTTCAGTTTG AGAAAATCCA TCCCTTATAT	360
AAGACCAAAA TCTATTCTTG GCTTTATCAA AAGAGAGTGC GCCAAAACCG	420
TTAAAAACCG AATACGAATA CAATTTGGAC TTAATCCATG CGTTTTGTAA	480
CTCCCTAACG CTCAACTTAA AAAAATCGCA TGGAAGCTTA AAGACAAATC	540
TCCATCATCG CTTCAAAACT CAACGCTAAT GTTGATCTAT TGTGGATTGG	600
CATAGCGGAG GCAGTTCGCC CGTATTGCCC GCTTCGCATT TCATTGAGTT	660
TTGCATGAAA AATTAAGTTG TGAGATCATT CTTATTTGCG GGCCAGGCGA	720
ACAGAAGAAC TCCTTAAAGA AGTCCCTTTC GCTCACCTCT ATGATACGAG	780
GTGGATTTAG CCAAATTGTG CGCGAATTTA AGCGTCTGTA TCGGGAACGC	840
TTGCATGTGA ACGCTTTATT TGACAACCAA TCTATCGGGT TTTACCCTAA	900
GCCTCTATTG CCAGATGGCG GCCTTTCAAC GAACAATTTT TAGGCATCAC	960
GGCTCAAACG ATATGGGTTT GATTGACATT CAAAAGAAA GCGAAAAGAT	1020

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GTGGGTGTCT TATCCCTCAA AATAGAGGCA ATTTCTAATT TTTATGGGTT ATGCGTTTTA	60
GGGGTGTGTG TAGCATGTTT TTATCTTTTA GACGCTTATT ATCTCATGCA AGAAAGGCTG	120
TTAGGGGAGC AATACCAATG GCTAATAAAA AACCGACTTA AAACCGATGA AAGGCTGTTT	180
GAAGTCTTCC CTATTCATCA AACTTGCCAA TCAACGCAAT TCTTATCGCC ATGCGTTCGT	240
TTAGTCTTTT CCCCTATTGG GCGT	264

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ATGTCTTTAG GGGCAGTGGT CAGCTCACTC CTTTGCCATA AGTTAGAGGG GGCAATATTA	60
GATCTGAGAG CGTATCGTTS RARAGCTTAT TATCACGAAA ATAAAGATAC YTTGCTTATT	120
AAAGGCAAAA AACGCCTTCT TTACAATTAT ATTAAAGCCC ATATTGYTTT AAACCTTGCTA	180
TGGACAATTA GAAATCGCAC GTRATCATTG GGAAAATTTA CTCAAAATCC AACCGAACAA	240

CCGCCCCACGA ATAACCACAC CATTCAATGG AAAAACRGAA AACATTCTAA TGGACAGAAT	300
TTTAGTGATT GGTAT	315

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

ATGAAAAAAAA CAACCCTCTT TGTATTGGGC TTATTATTCA ATAGCTCTTT AAGCGCTGTT	60
GATGGGATTT CTCAAACCGA GCCTTCTTCT TTGAATTTGG CTGAAGATAG CCTGCCTTTG	120
AACCATTCTA ACGCCCCAAA ACTCTCTTTA AAAAACGCAT GGAATAGGGT GTTGTCTAAT	180
CATGAAGGCT TGCATGCGCA GAATACGCCA TTAAGCGAGC GAGTAAAA	228

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

GTGAAAAAAG TAGAATCCAT GAATGTGGTG CCTTTCATTG ACATCATGCT TGTGTTGTTA	60
GTGATCGTGC TCACAACGGC GTCTTTTGTG CAAACTTCAA AGCTTCCTAT TAGCATTCCT	120
CAAGTGGATA AGGATAGCAC TGATTCTAAA GATGTGTTGG ACAAAAAACA AGTTACGATC	180

GCTATTTCTA ATAAGGGTTC TTTTATTTT GACGATAAAG AAATCAGCTT TGAAAATTTA	240
AAACACAAGG TTTCCACTTT GGCTAAAGAC ACCCCTATTG TCTTTGCAAG GCGA	294

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

ATGGGATCTT ACACATTCCC TCTCATTTTG AAGCCAATAT TTATAAACAA AGTGCCTGTA	60
ACGATAGATT TTTATGCGAA CGCCAATTAC TTTTGTATTT ATGGTGCGTT AGCGAATGCG	120
GTGGTGGGGA GCATCAACGC CTTAAACGAT GAAATCAGGT TCAAACGCAA CGCCCCAAATA	180
GAAGAAGCTG AATTAGGGAC AGACGGGATT AAGATTAAGC CTATCGCTTT GTATAACCCCT	240
AGTGAGGGGT ATTTGAATTA CGCGCTCTCT AGCGTGTTTA TTTTCATCTT ACACCAGGTG	300
ATGCTCATTG CAAGCAGCAT GTTTACTAGC TCCAGGCGTT TGGAATTGGC CCTTTTAGAC	360
AAGAAACAAA TCGCTTTAAG GCTGTGCGCA AGACTCTTGG TGTTTCATGGG GCGCTTTAGC	420
GTTTTTGTTT TATGGTATTT TGGGGCGCTG TTTTCTTTTT ATGGGATCGA ACGGCATGGA	480
AGCGCT	486

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GTGATTATGA CTAAGCTTGA TGGCACTTCT AAGGGCGGAG CGATTTTARG CGTGCTGTAT	60
GAGTTGAAAT TACCCATTCT TTATTTAGGA ATGGGCGAAA AAGAAGACGA TTTGATCGCT	120
TTTGATGAAG AACGCTTTAT AGAAGATTG GTTGATGCGG TGTTTGTGGA ACAA	174

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185

GTGTGTGGGG CTCATGGAAA GAGCAGTATC ACGGYCATGT TGAGCGCGAT TTGCCCCGCT	60
TTTGGASSGA TTATTGGGCG GCATTCTAAA GAGTTTGATT CCAATGTSSG AGAGAGCGCG	120
GATATGAGTT TGGTTTTTGA ASCCGATGAA AGTGATTCAA GTTTTTTTAT TTTCCAACCC	180
TTTTTGCGCG ATTGTGCC	198

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1...231
(D) OTHER INFORMATION: /note= "spoIIIE gene product"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GTGAATGAGT TAAAAAACTC TAAGCAAGTT TTAGGGAATG GGAAAGCCGA TCTGAGCAAC	60
GAAACACCA AGGTAAGGCA GACTAAAACA RATCTGACTG AAAAAAATCA AAGGCTAACC	120
ACAGAAAAAA CAGAATTAAA TAACAAGATT ACTGGGTTAG CCACAGAAAA AGAAAGGTTA	180
GCCGCAGACA AAGAAAACCT AACTAAAGAA AGCAGACAAA GAAAACCTAA C	231

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 555 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

ATGGATTAC AACAAATTGA TGAGCTAGAA AATAAGTTTG AAGAACAAGA AGAACAAGCC	60
CAAGATACCC CCCTAAAACA AGAGCCTAGC ACAAAGGAAG TAAAAATCCC TAAAAAAGG	120
GGGCGTAAAA AAAGCTTGTT AGATGAAGAT AAGAAAAAGA GCTTTAACAT TGCCTTTAGT	180
CCTTGTGTGA TAAAAGAACT TAATGAATTT TTGCTAGAAT TTGGCTCATT TAAAGAGACA	240
CGAAGCACTT TTATTGAAGA AGCGCTTATT AGGCATTTAA AACACAGAAA AAACACCCAA	300
GAGCAAAAGC TTTTAAAGCA ACTAGAAAGA TTACAAAACA AAGAAAAGGG AATAATGAAA	360
ACAATGAACT TGAATGAATT TTTTACGCAT AAGATAATCT ATAAAGACAC CCCTTTAAAG	420
TTTAAGGATA CACTAGAACA AGAAATCAGC CAAGCTAGTT TAGTAGAGAA GTTAATCTTA	480
GCTAATATCT TAGCCAATAT GGTGTTTGCT AAGATAAGCA ATGAGAATGC CCCTAAAATT	540
CTTATTTTCA CGGCT	555

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

ATGGGGTGCT ATGGGATAGG CATTAGCCGG TTGCTCAGCG TGATTTTAGA GCAAAAAAGC	60
GATGATCTAG RCTGTGTGTG GACGAAAAAT ACCGCTCCTT TTGATGTGGT GATCGTGGTT	120
TCTAACCTGA AAGATGAAGC GCAAAAAAAA CTCGCTTTTG AAGTGATGA AAGACTGCTC	180
CAAAGGGCG TTGATGCGCT GTTAGATGAC AGAGACGCTC GTTTTGGGGC GAAGATGAGG	240
GATTTTGAAT TGATTGGGGA ACGATTAGCC TTGATTGTTG GGAAGCAAAC TTTAGAGAGT	300
AAGGAATTTG AATGCATCAA ACGCGCTAAT TTAGAAAAGC AAACGATCAA AGACATAGGA	360
ATTAGAAGAA AAAATTTTAG AAATGTTAGC GAGCGAATAA GGGGAGGGAA TGGAAAAAYT	420
AGTGATTGGC TC	432

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

ATGGAAATAC AACAAACACA CCGCAAAATC AATCGCCCTT TAGTTTCTCT CGTTT TAGCA	60
GGAGCGTTGA TTAGCGCCAT ACCGCAAGAG AGTCATGCCG CCTTTTTCAC GACCGTGATC	120
ATTCCAGCCA TTGTTGGGGG TATCGCCACA GGCCTGCTG TAGGAACGGT CTCAGGGCTT	180

CTTAGTTGGG GACTCAAACA AGCCGAAGAA GCGAATAAAA CCCAGATAA ACCCGATAAA	240
GTTTGGCGCA TTCAAGCAGG AAAAGGGCTT	270

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 804 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

ATGTCAGAAA AAGAAAGACT GAATGAAGTG ATCTTAGAAG AAGAGAATAA TGGGAGTGGT	60
ACTAAAAAGG TGTTTTTGAT CGTGGCCATA GCCATTATCA TTTTGGCGGT GCTTTTAATG	120
GTGTTTTGGA AAAGCACCAG AGTCGCTCCT AAAGAGACTT TTTTACAAAC CGATAGTGGC	180
ATGCAAAAAA TAGGCAACAC TAAAGATGAG AAAAAAGACG ATGAGTTTGA AAGCTTGAAT	240
ATGGATTCTC CCAAACAAGA AGACAAGTTA GACAAAGTGG TGGATAATAT TAAAAACAA	300
GAGAGTGAAA ATTCTATGCC CATTCAAACC GATCAAGCTC AAATGGAGAT GAAAAACAAC	360
GAAGAAAAAC AAGAATCTCA AAAAGAATTA AAAGCTGTTG AGCCTATTCC CATGAGCACT	420
CAAAAAGAAT CTCAGGCTGT GGCTAAAAAA GAAACCCCCC ATAAAAAGCC TAAAGTAGCG	480
CCAAAAGATA AAGAAGCGCA TAAAGRATAA GCTAAGCATG CAGCTAARGA GCCAAAAGTC	540
AAAAAAGAAG CTCGTAAAGA AGTTTCTAAG AAAGCTAATT CTAAAACCAA TCTTACTAAA	600
GGGCATTATT TGCAAGTGGG GGTTTTTGCG CACACGCCCA ACAAAGCCTT TTTACAAGAG	660
TTTAATCAAT TCCCCATAA AATTGAAGAT AGGGGGGCTA CTAAACGCTA CCTYATAGGY	720
CCTTATAAGA GCAAGCAAGA AGCCTTAATG CATGCCGATG AAGTCAGCAA GAAGATGACT	780
AAACCGGTTG TCATAGAAGT GCGG	804

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...513
(D) OTHER INFORMATION: /note= "ferric enterobactin transport protein fepC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GTGGAATATT ATGCGTTTAA TTTCAGCGTG TTGGATTTTG TCTTAATGGG GAAAGCGACG	60
CATTTGAATC TGTTGCTAT GCCTAAAGCT AAGCACATTA AAGAAGCCAC GAGCGTTTTTA	120
GAGCGCTTGG ATTTAGAGTC CTTAAAAGAT CAAGGCATTA ACGATTTGTC CGGCGGTCAA	180
AGGCAGATGG TACTTTTAGC CAGAAGCTTG TTGCAAAGAA CGCCCTTATT GTTACTGGAT	240
GAGCCTACGA GTGCGTTAGA TTTAAAAAAC CAAGCCCTTT TTTTGTATGC GATTAAAGAT	300
GAGATGAAAA AACGAGAATT GAGCGTTTTTA GTCAATATCC ATGATCCCAA TTTGGTTGCC	360
AGGCACTCCA CGCATGTGGT CATGCTCAAA GATAAAAAAC TTTTGTGCA AGCTTCCACG	420
CCAATCGCTA TGAATTCACA CAATTTAAGC GCGCTTTATG ACACGCCCCCT ARAAGCGATC	480
TGGCATGATG ATAAGCTTGT GGTGTATGCG TTG	513

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

ATGATGGCAC ATTCACCTTAT TTTGGTTTCA AAAACATCAC TCTCCAACCT GCTTATTTTT	60
GTGGTTCAAC CTGATGGGAA ATTGAGCATG ACTGATGCCG CCATTGATCC TAACATGACT	120
AATTCAGGAT TGAGATGGTA TAGAGTTAAT GAAATTGCAG AGAAGTTTAA GCTCATTA	180
GACAAAGCCC TTGTAACAGT GATCAATAAA GGCTATGGGA AAAATCCATT GACAAAAAAT	240
TACAATATCA AAAACTATGG TGAATTGGAG CGTGTGATTA AAAAGCTCCC TCTTGTGAGA	300
GATAAA	306

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

GTGCTGAATG AAGAGCAAAA TTCATTAGAA GAAAAAGGGG GCGAAAACAA AAACGAAAAA	60
GAAACCCCCC TAAAGGGCAT TCATTCTAAA ATCCCCTCTT TGAAGCAGGC TTTGGAGCAG	120
ACGATTAGTA AAATCAAAAAG CTCTAAAGAG TTTTTCAAAC AGCTTCTACA CAATAAAAAA	180
AAGCTTTATA TCGCGCTTGG AATATTGCTT TCACTCATCG CGCTCATTGT GGCTTTGAGT	240
TTGTTACTAG GGCATAAAAA AGAAAATAAA CAACTTCTT TACAAACTAA TACCGCCACC	300
ACCAATAACG AAACGCCTAA CGACACCAAT AACGCAGAAG CCGAAGGGCA AATAGAAAAT	360
TTAGACTTGC CTGATTTAAT CGGCAAAGAC TCTTTGAAAA GAAACGATGA AAGCCAAGTG	420
GATGCGATGA TGCAAAAAGC GAGCCTTTTG TATGAGCAAG GGCAAAAAGA TGAAGCCTTG	480
CATTTGTTTG ATAAGATCGC TTCTTTCTCG CAAGGGATTG CGAGCCATAA TCTAGGGGTG	540
ATTAAATTCA AAGAAAAGGA TTTTAATGGG GCGTTGGATT TGTTTGATTG CAGTATCGCT	600
TCTAAAGAAA ACGCGAGCGT GRGCGCGATT GATGCGTTAG TTACGGCTTA TCATTGCAA	660
GATGCGGATT TGTATTATCA TTATCTAAAA ATTGTRAAGA GACACTTTGT A	711

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 675 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

ATGAATACAA GCTTATTGAC CCAAGCACAG GTTTTAAGCT CTAAAGAAAA TCAAATCCAT	60
CGCCTTTTGT TAGAGCTTTT AGAAGAGGCT AAGCTTCATT TTGAGCCTAA GCTTTATATC	120
ATTAACGCCC CTTACATGAA CGCTTTTGCG AGCGGGTGGG ATGAATCTAA TTCCCTTATC	180
GCTCTTACAA GCGCTTTAAT AGAGAGGTTA GATAGAGACG AATTAAAAGC CGTGATCGCT	240
CATGAGCTCA GCCACATACG GCACAACGAC ATCCGCTTGA CCATGTGCGT GGGGATTTTG	300
AGCAATATCA TGCTATTGGT GGCTAATTTT AGCGTGTATT TTTTCATGGG GAATCGCAAG	360
AATAGCGGGG CGAATTTAGC CCGAATGATT TTATGGGTTT TACAGATCAT CTTGCCTTTT	420
TTAACGCTCC TTTTGCAAAT GTATTTGAGC CGCACACGAG AATACATGGC CGATAGCGGG	480
GCGGCGTTTT TAATGCATGA CAATAAGCCC ATGATCAGAG CCTTACAAAA GATTTCCTAAC	540
GATTACACCA ACAACGATTA TAAAGAAATA GATAAAAATA GCACCCGATC AGCGGCCTAT	600
CTTTTAAACG CTGAAATGTT TAGCACCCAC CCTAGTATTA AAAATCGTAT CCAATCCTTA	660
AGAAAGCGTG TGATC	675

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1605 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

ATGTTTAATA	TTAAAAGGAC	TTTTTTAATA	ACGATCATAA	GTTTTTTTCT	CATTGTTTCCT	60
AATTGGTTGA	AAGCTATTGA	TTTGCCCAT	GTTTCAAATC	TCAAAATTTA	CCAAACAGTT	120
TATTGCATGC	TGATACCGAG	TTATGTTTTA	ACCAACAAAA	GTTTTGCAGA	TATTTTGACA	180
GGCTATACAT	CTATTGGTGC	ATCAGGGAGT	GGAAAGAGTT	CAGGGCAGGG	TGTGATCGAA	240
GCGCTTAGCA	CACCATTAGC	CACAAGTTTA	GCCGCTAGCA	ATCTGGTGAA	ATATTTGAAT	300
ACTTTAGGTC	CTTTATGGGG	ATCGGCGTGG	GCAAGTGTTG	CTACAGCTAT	ACAAGGTTTT	360
GCTCTAACGC	CATCAAGTGG	CTGTAATTTT	GGTTGGAACG	CATTGATAAA	TAAAAACATA	420
GATGTATCCA	TGGATAGCGT	ACTAGACAAT	TTGAGCAACA	AGATTCAGAA	TTTTACCAAA	480
GGCGGTGTTG	AGGACAATGT	GAAAGGCAAT	ATTCTTTTAC	AAATAATTGG	CTCAATAACC	540
GCTCAAGCTT	CTACGAATAT	TACAGCTGAT	GGTTTAATTT	GGCTGATTGG	TAAAGAATTC	600
ACTGCAAATA	AACTGCAAAA	CAACACTATA	GCCATGCTTG	CTTTTGCCGC	ATTAGAATCT	660
GTTGTCAAAG	GAGCGGACGC	TGCTGTTCTT	CCTGCATATG	GTGTAGTCAA	TCTGCCTGAT	720
ATTATCATAG	GGCAAGGGTC	ATATCTTGAT	TTTGTTTCTT	ACCTAATTTA	TATTGTTTTT	780
GGGATTTTTG	TTTTTATTTT	TTTTATGAAA	TTGAGAGATA	TTTCAAACGG	CATTCAGATT	840
AACATAGGTT	TTGAATACAT	GCGATTTGTT	GGGGGGACAT	TATTCAAAAT	GGCGATGGTC	900
TCTTTTATCG	CCTATGCAGG	TTTGTTTAT	CTTTATAAAA	TCTCTTATTC	TATTTATTTT	960
GGTTTAGCAG	GTGCTTTTGG	GCTGAATCAA	GTTCTTTTTT	GGGCTTTAGA	TTTAGTGCTG	1020
AATTACACTG	TTAATTCAAT	TTTACCTGCG	GTAAGAGCTG	TTTTTTCTAA	TGTTGGCAAC	1080
AACGCTCCTA	GTTTGTTACA	AGGCTTGCAA	GTGGCAGGTA	TTTCTTTATT	CGCTATTTTT	1140
ATGCAAGTAA	CTATCATTAT	GAGAATAAGC	ACTGTTGTTG	TGAAACCTTT	GATAGCGGGG	1200
GCTTTTAGCG	GTATTGTTTT	CCCTATTGCA	GTATGTTTGA	TCGTGCTAGA	TTGGTTCAAA	1260
GATTCTATGA	AAAACATATT	GATATGGTTT	ATTAATAATC	TGTTTATCTT	GGTTCTAGCT	1320
ATTCCTATTT	TGCTCTTTGG	TGTTTTGGCA	TTATTGGCAT	TCAATTTGAC	CATAACGCCC	1380
TCTGTTGCTA	TACAAAACAT	CAATCAAGGG	GGATTGGGTA	TCGATTCAAC	TATTGCGAGT	1440
TTGATCACTC	TATTTATTTT	AAAAGGTTTC	ATAGAGACGA	TTATTGAGAG	CGTCAATGCG	1500
ATCGTTAACA	CCATTTTCAG	CTCTGTCTCT	ATGGATGGTA	GCAGAATGGA	TAGAGAAAAGA	1560
GATGCCTTAA	TGGTGGGAAG	AGTTGGTGGA	TCTATGTTTA	AAGGA		1605

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

ATGGCGTTTT GGCAGGCTAT CCGGTGGTGG ATTTTAAAGT TACCCTTTAT GATGGGAGCT	60
ACCATGATGT GGATTCTTTC AGAAATGGCG TTTAAATCG CTGGYTYTAT GCGGTTTAAA	120
GAAGCGAGTC GTGCGGCTAA CCCGGTTTTA CTAGAGCCTA TGATGAAAGT GGAAGTGGAA	180
GTCCCTGAAG AATACATGGG CGATGTGATT GGCGATTTAA ACAGAAGAAG AGGGCAAATC	240
AATTCTATGG ACGATAGATT AGGTTTGAAA ATCGTGAATG CTTTCGTGCC GTTAGTGGAA	300
ATGTTTGGTT ATTCTACGGA TTTGCGATCA GCCACTCAAG GGCGTGGGAC TTA CTCTATG	360
GAGTTTGACC ACTATGGCGA AGTGCCTAGC AATATCGCTA AGGAAATCGT GGAAAAACGC	420
AAAGGC	426

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

ATGCAGAATT TGCCGGGTAT GCGGAGAGCG GCGATGCTAA CCACATCATC AGCCCCAGCC	60
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CCTGAGGGTG AAGGGGCTTT TAGAGCCATG AAAATGGCTT CAGAAATGGC GAAAGTGGAA	120
GTAGGCTATG TGAACGCCCA TGGGACAAGC ACGCATTATA ACGATTGGTA TGAAAGCATT	180
GCGTTAAAAA ATGTGTTGGC TCTAAAGAAA AAGTCCCTCC TGTTAGCTCC ACTAAAGGGC	240
AGATTGGGCT TGCTTGGGTG CTGCGGGGTT AGAAGCCGTT ATTCTATCAT GGCCATGAAY	300
CAAGGGATCT TACCTCCTAC CATTAATCAA GAAACGCCTG ACCCAGAATG CGAYCTGGAT	360
TATATCCCTA ATACAGCCAG AGAAAAGCAA GTGAATGCGG TGATGAGTAA CTCATTTGGT	420
TTTGGTGGCA CTAATGGTGT TGTGATTTTC AAAAAAGCC	459

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

ATGATACTAA AAAATTTGAT TTTGTTATTT TTAGCAAAGA GAAAACTTAT TTTCATAGAA	60
GCTAATTTTT ATACCATTAG TGGGAGCAAG CTTAATGAAG TCGCAAGATC CTATCAAGAC	120
TTAGCTTTAA AATTTGAAGC ATTCCTAAT TACGAATTTA TTTGGATAAC TGATGGCATA	180
GGTTGGCTAG ACGCTAAAAG CAAGCTCCAA GAAGCTTACA AATCTGTAGA AATCTATAAC	240
TTAAGCTATG TGAATGATTT TATATCAAAG GTGCAAAAA	279

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

ATGGAATCAC AACTCATGAA ACTCGCCATT GAAACTTATA AAATCACTTT GATGATTTCT	60
TTACCGGTAT TATTAGCGGG CTTAGTGGTG GGGCTGTTAG TCAGTATTTT TCAAGCGACC	120
ACCCAAATCA ATGAAATGAC TTTGTCTTTT GTGCCTAAGA TTTTAGCCGT GATTGGGGTG	180
CTGATTTTAA CCATGCCGTG GATGACGAAC ATGCTTTTAG ATTACACCAA AACCTTAATC	240
AAGCTCATTC CTAAATCAT AGGC	264

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

ATGAAATTTT TTACAAGAAT CACTGACAGC TACAAGAAAG TTGTAGTAAC TTTAGGGCTA	60
GTGGTAACAA CCAATCCTTT AATGGCGGTC ACCAGTCCTG CAACAGGCGT TACTGAGACT	120
AAAAGTTTGG TTATTCAGAT CATTTCTGTT CTAGCGATCG TAGGTGGTTG CGCTTTAGGG	180
GTCAAAGGCA TAGCAGATAT TTGAAAAATC TCTGATGACA TCAAAAGAGG TCAGGCGACT	240
GTTTTTGCTT ACGCGCAACC CATAGCTATG TTAGCGGTGG CAGGTGGCAT TATCTATTTG	300
AGCACTAAGT TTGGCTTCAA TATTGGCGAG AGTGGAGGAG CTAGC	345

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

ATGAAAAATC	CCCAAGCTAA	TGTTTTAAAA	CTCTTTTAA	ATCAAGTGGC	TGACCAAAAA	60
TACATAGATA	TGAATGATGA	AAAAAACTAT	GACCCAAGAG	AACCTGAACC	CCCTTATGGA	120
ACAAAAGGGG	CGTTAGATGA	GATTATAAGG	ACAGATGCTA	GGAGTTGGGC	AAACACTCCT	180
GATGATGAAT	TTGGGAGCAT	TATGTCTTCT	TTTAAGCGTT	TTATGTATGT	CTATAAAGAC	240
CCAAAAGTGC	GTGAAGCTAC	TTCTAAAATG	AGCTTTGATT	ATGAAGAATT	AAGAACGGGC	300
AATATCAGTA	TTTACATTGT	AATCGCTCAA	ATTGATATAG	GCACACTTTC	TTCTTTAGTA	360
AGAGCCTTTT	TAGAGAGTAT	TGCTAAAAAC	CTTATGGTCA	AAGAAAGCTC	TAAACCTGAA	420
GAGCGTATTT	TTATCATTGC	TGATGAATTT	GTTAGATTTG	GTAAGTTGCC	TTTCTTGTTA	480
GAAATGCCAG	CACTTTGTCT	CTCTTATAAT	GTTGTCCCCT	TATTCATCAC	GCAAGATTAT	540
GCTATGATTA	GAAATACTAT	AGCGATGATG	ATT			573

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1053 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

ATGATAAGTG	AGATTATTAA	GTTTCAATTA	AAAGGAATAA	AAATGATTAG	ATTAAAAGGT	60
TTGAATAAAA	CTTTAAAAAC	AAGCTTATTA	GCTGGGGTTT	TACTAGGTGC	TACTGCTCCC	120
TTAATGGCAA	AGCCTTTATT	AAGCGATGAA	GACTTATTGA	AACGAGTAAA	ACTACACAAT	180
ATCAAAGAAG	ATACGCTGAC	TAGCTGTAAT	GCTAAGGTGG	ACGGCTCTCA	ATACTTGAAT	240

AGTGGTTGGA ATTTATCTAA AGAATTTCCG CAAGAATATA GAGAAAAGAT TTTTGAATGC	300
GTAGAAGAAG AAAAACATAA ACAAGCCCTT AATTTAATCA ATAAAGAAGA CACTGAAGAT	360
AAAGAAGAAC TTGCAAAAAA AATCAAAGAA ATTAAGAAA AAGCTAAAGT TTTAAGGCAA	420
AAATTTATGG CTTTTGAAAT GAAAGAACAC TCTAAAGAAT TCCCAAATAA AAAGCAACTT	480
CAAACCATGC TTGAGAACGC TTTTGATAAT GGAGCTGAAA GTTTTATTGA TGATTGGCAC	540
GAACGCTTTG GGGGTATAAG TAGAGAGAAT ACTTATAAAG CACTTGGCAT TAAAGAATAT	600
AGTGATGAAG GAAAGATATT AGCCTTTGGC GAAAGAAGTT ATATTAGACA ATATAAAAAA	660
GATTTTGAAG AAAGCACTTA TGATACTAGA CAAACCTTAT CTGCTATGGC TAATATGAGT	720
GGCGAAAACG ATTATAAAAT TACTTGGTTA AAACCCAAAT ATCAGCTCCA TAGTTCAAAT	780
AATATTAAAC CCTTAATGTC AAACACAGAG TTGTTAAATA TGATAGAGCT AACCAATATC	840
AAAAAAGAAT ATGTTATGGG CTGTAATATG GAAATAGATG GTTCTAAATA TCCCATTCAT	900
AAAGATTGGG GATTTTTTGG TAAGGCAAAA GTCCCAGAAA CTTGGAGAAA TAAGATTTGG	960
GAATGTATTA AGAATAAAGT AAAGTCCTAT GACAACACTA CCGCTGAAAT AGGAATAGTT	1020
TGGAAAAAAA ATACTTATTC TATCTCTCAT CAC	1053

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

ATGGCTGATA TTTTAAGCCA AGAAGAAATT GATGCGCTTT TAGAAGTCGT TGATGAGAAT	60
GTGGATATTC AAAATGTCCA AAAAAAAGAT ATTATCCCCC AACGCAGCGT AACCTCTAT	120
GATTTCAAGC GCCCTAATCG TGTGAGTAAG GAGCAATTGC GCTCTTTTAG GAGCATCCAT	180
GATAAAATGG CTAGGAATCT TTCCAGTCAA GTCTCTTCTA TCATGCGTTC TATTGTAGAA	240
ATCCAGCTTC ATAGCGTGGA TCAAATGACT TATGGCGAAT TTTTGATGAG TTTGCCTAGC	300

CCTACGAGTT TTAATGTCTT TTCCATGAAG CCTATGGGGG GAACGGGGGT TTTAGAGATT	360
AATCCTAGCA TCGCTTTCCC TATGATTGAC AGACTATTAG GGGGTAAGGG GAGCGCGTAT	420
GATCAAAACA GGGAGTTT TAG CGATATTGAA TTGAATTTAT TGGATACGAT TTTACGCCAG	480
GTGATGCAAA TTTTAAAGA AGTGTGGTCG CCTGTGGTGG AGATGTATCC TACCATTGAC	540
GCTAAAGAAT CCAGCGCGAA TGTGGTCCAA ATCGTCGCTC AAAATGAAAT TTCTATCATG	600
GTGGTTTTTAG AGATTATCAT TGGGCATAGC CGTGGGATGA TGAATATTTG TTACCCGGTG	660
ATTTCCATTG AGAGCATTCT TTCTAAAATG GGGAGTAGGG ATTTTCATGCT TTCAGAAACG	720
AACTCCAAA AGAGCCGTAA TAAGGAATTG CAAGCACTAT TGAGCGGGGT GAGCGTGGAT	780
ATGATGGTGT TTTTGGGCGC GGTGGAATTG AGTTTGAAAG AAATGTTGGA TTTAGATGTG	840
GGGGATACTA TCCGGTTGAA TAAAGTCGCT AACGATGAAG TGAGCGTGTA TGTACATAAG	900
AAAAAGCGTT ATTTAGCGAG CGTGGGGTTT CAAGGGTATA GGAAAACCAT TCAAATTAAA	960
GAAGTGGTTT ATAGCGAAAA AGAACGCACT AAAGAAATTT TAGAAWTGCT WGAAGAACAG	1020
CGCAGGAGGC AAAGTTGGGC GRTGTTATGG AGC	1053

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

ATGCCACGA TGTTAGCGGT TGGTTTTTGG GTGTTGGTTT TTTTATCCAC GAGCAATGCG	60
GTGAATTTAA CCGACGGGTT AGACGGATTA GCGAGTGTGC CTAGCATTTT CACCCTCTTA	120
AGCCTTTCTA TCTTTGTGTA TGTGGCAGGG AATGCGGAAT TTTCTAAATA CTTGCTCTAT	180
CCTAAAGTCA TAGATGTGGG GGAATTGTTT GTGATTTTCG TAGCATTAGT GGGATCGCTC	240
TTTGGCTTTT TGTGGTATAA CTGCAACCCG GCAAGCGTGT TTATGGGCGA TAGCGGGAGT	300
TTGGCAATAG GAGGGTTTAT CGCTTATAAC GCTATTGTTT CGCATAATGA AATCTTGCTC	360

GTTTTAATGG GGTCTATTTT TGTAATAGAA ACTCTGTCTG TGATCTTGCA AGTAGGGAGC	420
TATAAAACCC GTAAAAACG CCTTTTTTTA ATGGCACCCA TCCATCATCA TTTTGAACAA	480
AAGGGTTGGG CAGAAAATAA GGTGATCGTG CGTTTTTGA TCATTTCTAT GCTGAGTAAT	540
TTAGTCGCTC TTTTGAGCTT GAAGGTGTGT	570

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GTGCGTTTTG AAAATTTTCAT CAACCGCCTA GCCTTTTACA TGGCCACAGG GAGCGGTAAA	60
ACGATCGTCA TTATCAAACCT GGTAGAGCTT TTAAGCGTGG CTATGGGAAT GGGTTTGATC	120
CCTAAGAAAA ATATCATGTT TTTTAGCGCG AACGAGCATT TAATCAAGCA ATTTGAAAAA	180
GAAATTGAAA AATACAACCG CAATAAGGAC TATTCCAAAC AAATTGATTT CAAAAACCTT	240
AAAAGCGTTA AGAATAAGGA TTTTATCGT GCTCCAAAG ATTCTTTAAT GAAAGAAATC	300
GCTCTTTTTT ATTACCGCGC AGATTTAATG AGCGATGAAG AAAGCAAGGA AAACCTTTTA	360
AATTATAAGG ATTGTTGGGA TAATGGGGAA AATTATGTGA TTTTAGATGA AGCGCATAAG	420
GGGAATAAGA CTGAAAGCAA AAGACAGGCG ATTTTITAGCC TGCTGTCTTT AAAAGGGTTT	480
TTATTCAATT TCAGCGCCAC TTCTACTGAA GAAAGCGATC TCATCACTGC GGTGTATAAT	540
TTGAGCGTGG GCGAGTGGGT GAAACTTGGC TATGGTAAAG AGTCTGTTTT ATTGAAGAAA	600
AACAACTTAA ACGCTTTTAA GGAATTGAAA GATTTAAACG ACAGGGAAAA AGAAATCGCT	660
CTTTTAAAGG CGTTATTGCT TTTAGGCATG CAAAAACGCT ATAAAGTAGA AGGCTATTTT	720
CATGACCCTT TAATGCTCGT GTTCACGCAT TCTGTGAACA TGGAAAACAG CGATGCGRAA	780
ATCTTTTTTA AAACTTTAGC GCGCGTGATT GAAAATGATG ATGAGAGCGA TTTTCAAAA	840
GCTAAAGACG ATTTATTAGA GGAATTAAAG AATCCGGAAT TCCTTTTTAG CGATGGCAAA	900

GATAAAGAAA AAGACTATAA AATTGAGGTC TTAAAGAGA GTTAAAGGG CATGGATTTT	960
AAAGGCTTAA AAGAAGCAGT TTTTATGCC AGTAATGGGC ATATTGAAGT CATCATTAAC	1020
CCTAAAAACA ACCAAGAAAT CGCTTCAAG CTCAACACGA GCGATAAAGT CTTTGCCTG	1080
ATTAGAATAG GCGATATTAC AGAATGGATC CGTGAAAAAT TAAAGAGCGT GAAGGTGGTG	1140
AGTAAGAATT TGAGCTTCAA AGAAGAGAGC TATTCAGCC AGATTGATAA GAGCAGTATC	1200
AATATCTTAG TGGGGTCTCG TGCTTTTGAC ACTGGGTGGG ATAGCACAAG GCCTAGCGTG	1260
ATTTTATTTT TAAATATAGG GCTTGATGAT GACGCTAAAA AGCTGGTGAA ACAATCTTTT	1320
GGCAGGGGCG TAAGGATTGA AAGCGTCAAA AACCAACGCC AAAGGTTAGC GTATTTAGAG	1380
ATAGATGAAG CCATTAAAGA ACAAGCTGAA ACCAAACGCT GCAATGCTGG AAATGCTTTT	1440
TGTGATACCT ACCAACCATG CAAGCCT	1467

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

GTGTTTAAAA ATTCCCTCTT TGGTATATCA ATCTCCATGC TTATCACTTG GGTTTTAACC	60
GCTTGTATTT TGATTTTAT CCTTTTGTC CCGAATTTTA CCCTTACGCA TCCAATTTT	120
CATTTCACTC CGTTTGAAAA AACCTATTTT CAAATTC TAGACTTGTTGG TATTGTAAGT	180
TCTATTATTT TCACCGGGT TTTGGCTGAT AAAATCAAAC CGCACAAAGT TTGCATGGCT	240
TTTAGCSCGA CCTTTGGGTT TTTGGCTTT TTATCTTTTA AGGAATTTTA TTCTAACGCG	300
CCAAGTTTAG TCAATACTAT AATTTTATAC TTTTAGCTT GCTTTTGCGC GGGCATTATG	360
AATTTTGCC CCATTTTCAT GAGCGATGTG TTAGCGCTA RAATCCGTTT TAGCGGGATT	420
TCCTTTGCTT ATAACATAGC CTATGCTATA ACCGCTGGCT TTACCCCTCA ACTTTCAAGC	480
TGGTTAAACG CAAAAGCTAT AGCAGTGCCT GAAAGTTTGC AAAGTTATGG TTTAAGCTTT	540

TATATCCTTA TAGTTTCTTT AATTGCTTTT ATTACATCGC TTTTAATGGC GCCAATTTAT	600
CACAAATCTA ATACCCAACA CGAAGTGTCTG CCCACGGCA	639

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

ATGAAAAGCG ATAAACCCTT TTTAGAACGC TATTTTTATG ACCCCACTCT TTTGCAAAAG	60
GGGTTGATTT TCGCGCTCTA TCCTTTTTCT TTAATCTATC AATGTATTGC CACAATTAAA	120
CGAAAAACCG CTAAAAAGCA TGATTTTAAA ATCCCCATTA TCAGCATAGG CAACTTGATC	180
GCTGGGGGAA GCGGTAAAAC GCCCTTCATT TTAGAAATCG CTCCAAGATA CCAAGAAGTG	240
GCGGTTGTTT CTAGAGGGTA TCAACGGGAT TCTAAAGGTT TAGTGGTGGT GAGCGTTAAA	300
GGAAACATTT TAGTTCCTCA AAAACAGCG GCGGATGAAG CCTATCTTTT AGCCTTAAAT	360
CTAAAACAAG CGAGCGTGAT TGTGAGCGAA AAAAGGGAGC TAGGCGTTTT AAAAGCCCTT	420
GAATTAGGAT CAAAGATCGT GTTTTATAGAC GATGGTTTTA GGTTTAATTT CAACCAATTC	480
AATGCGCTTT TAAAACCCAA AGTCCCCCCC TACTACCCTT TTTGTTTGCC TAGCGGGTTG	540
TATAGAGAAA ATATTAAAAG CTATAAGAA GCCCATTTAG TCATTACAGA AGATAAGGAT	600
TATCAAAGAA TCACCTCTAT CACTAACCCC ACCAAACGCA TGCTTTTAGT AACGGCTATC	660
GCTAACCTTA GCAGGCTTGA TGC GTTTTTTA CCCAAAGAAG TGGTTAAAAA ATTGTATTTT	720
AGAGACCATG CCCCTTTTGA TTTGAAGCTT TTAGAAAAAG AGTTTTATCA AAATAACGCC	780
ACCTCCTTAT TGGTTACTTC AAAAGATCTC GTCAAATTAC AAGATTGCAA ATTGCCTTTA	840
AGCGTATTGG ATTTAAAACT AGAAATTTGC CCTAAAGTTT TAGAGGAGAT TGATCGTTAT	900
ATCCTTTCTT ATCCTTGTA TATAAAAGAA CATCTA	936

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

```
ATGTCTTTAG GGGCAGTGAT CAGGCTTATT TTTTGTTATA AGTTAGAGGG GGTAATATTA      60
GATTTAAAGC GCATCAATTT CAAATCCTAT TACCCCAATA ATAAAAATGC ATTATTTATC      120
AACATAAGA AAAATCCATT ATCTAGTRCT TCAAAGTTCA TATTGCTT                      168
```

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 684 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...684
- (D) OTHER INFORMATION: /note= "cell division and sporulation protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```
ATGCTAGAAA CCACTATTGA TTTTCTCGT TACAGCAGCG TGAAAATCGG TGC GCCTTTA      60
AAAGTGAGCG TTTTAGAAAA CGATAATGAA ATCTCTCAAG AACACCAGAT CATAGGATTA      120
GCGAACAACC TTTTAATCGC TCCTGACGTG AAAAATCTCG CTTTATTAGG AAAAACTAC      180
GATTATATTT GCGATAAGGG TGAGTGGGTG GAGGTAGGGG GAGCGGCCAA TCGCTCTAAA      240
```


ATTTTAAATT ATTTTAGGGC GAATGATTTA GAGGGTTTAG AGTTTTTAGG GCAATTGCCT	300
GGCACTTTAG GGGCGTTAGT TAAAATGAAT GCTGGCATGA AAGAATTGA AATAAAAAAT	360
GTTTTAGAAA GCGCTTGCGT TAATGGCGAA TGGCTAGAAA AAGAAGCTTT GGGGCTAGAT	420
TATCGCAGCA GCGGGTTTAA TGGCGTTGTT TTGAGGGCTA GGTTTAAAAA GACGCATGGT	480
TTTAGAGAAG GGGTTTTAAA AGCGTGTAAG AGCATGCGCA AAAGCCACCC CAAATTGCCT	540
AATTTTGGGA GCTGTTTCAA AAACCCGCCT AACGATTATG CGGGCAGGCT TTTAGAGGGC	600
GTGGGCTTAA GGGGTTATTG TCTAAAAGAG TGGGCTTTGC CAAAGAACAT GCGAATTTTT	660
GGTGAATTTG GGGGGCGCAG AATT	684

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...267
 - (D) OTHER INFORMATION: /note= "chemotaxis protein cheY"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

ATGCTCAAAA ATGGCGATAA GATTCCGGAC GCTATTTTAG TGGATATTGA GATGCCTAAA	60
ATGGATGGCT ACACTTTCGC CTCTGAAGTG CGTAAATACA ATAAATTCAA AAACCTGCCC	120
TTGATCGCCG TTACCAGTCG GGTAAGTAAA ACGGACAGAA TGCGCGGCGT TGAATCCGGC	180
ATGACTGAAT ACATCACCAA ACCTTATAGC GGTGAATATT TAACCACCGT AGTGAAGCGC	240
AGCATTAAAT TAGAAGGAGA CCAATCG	267

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GTGTTTGAGC CGGTTATCGC TTACAAGCTT TTCCATTCTT TTGTGATTTT AGGGTGCGCG	60
ATTGAAACTT TAACGACTAA ATGCGTGGA GGCATCACGG CTAATGAAAA GATTTGCCAC	120
GATTATGTTT TTAACAGCAT TGGCATTGTT ACCGCGCTCA ACCCTCATAT CGGCTATGAA	180
AAATCCGCTA TGATCGCCAA AGAAGCCTTA AAAAGCGATC GCTCTATCTA TGATATCGCT	240
TTAGAAAAGA AAATCTTAAC CAAAGAGCAA CTGGACGATA TTTTCAAGCC AGAAAACATG	300
CTAAGYYCTC ACGCTTTCAA AAAGCATAAA GAC	333

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

ATGTTGCGTT TATTAGCCCA AAAAAGCGCT ATTAACTCA TTCTTATCCC CCCAAGCGCG	60
AACGCTTTAG GCATCGCTTC TATTTGCGAA TTGAGCGAAG AAGTTTTTGA ACATGAAAAA	120
ATCGTAGGCA TTCGCGCTCA AGGGGATTTT ACTATCAATA GCGACGATAG GGGTTTTTGG	180
GAAAGACGCT GTCAG	195

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 804 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ATGAAAAAAC TTCTTTTACT CTTAGAGCAT AAGATCGTAA AAATTGGCTT AATTATTGTG	60
ATTGTGTTAG TGGGTTTTTT TCTTTTTTAT GAACAAGAAA TCAAAGAAAA AGCTGTTAAT	120
GTTTCTCAAG GTAAATTCCC CACTTCATCT TATTTGTTTC AAGCTTACGA AGGCATTAAG	180
AATAAATAG ATACTATCAA TCAAGTGAAG CCAAACGATG AAATAAAAG CGTTAATGAG	240
AATATAGAAA AAACACAAAA AGATTTAGAT GATTTTAATG CGCTAGTGCA AAAGTTACCA	300
AATTTGCCTA AGGACTTTAA TAAAACACTT ATTAAACCAC AAAGTCCATT TTTCAACTAC	360
AATACCGCTA ACGAAGATGA AAAAAACCGC CTGGTGATTT TAGCGTCTCG TATTAGCAGC	420
CAAAAAGAAA CGCAACCTCC CATTTCTATA AAAAATAGCG TTTCTCACAT AAAATCCAAA	480
GAAAAACGAG AACTTGAAAA AGAATGGGCA AAACCTAGTG TTTCTTTTGG TTCTTTTTCC	540
TTGCTTTCCA GTTCTTCTTC TTTTCTTCT TTTGAAGTTT CTTTTTTATC AAGGGGAATA	600
GGATTGGATT GTGAGAAGCT CAAATCCTTT TTAAAAGCTT TTTCAAGTTC GCTATTTTCC	660
TTATTATCTT CATTGTTTTG CCATCCACTT TCTCTTTTTT GCTCTCTAAT AGGATTAATC	720
TTTTGTTTTT CTAAGTTTTT TAGAGAGCTA GTGAATGCGT CTAACAATTC GCTTGAGTTT	780
TCATCATTGT CAAGGCTAGG ATCA	804

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...300
(D) OTHER INFORMATION: /note= " UDP-N-ACETYLMURAMYL-TRIPETIDE
SYNTHETASE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

```
ATGGGAGCGA TAGCGAGTTG TTACGCGCAT CAAATCATCT TAACTTCAGA CAATCCTAGA      60
AGCGAAAACG AAGAAGACAT CATTAAGGAT ATTTTAAAAG GCATCAATAA TTCTTCTAAA      120
GTCATTGTAG AAAAAGACCG AAAAAAGGCC ATTTTAAACG CTTTAGAAAA TTTAAAAGAC      180
GATGAGGTGT TGTGTATTTT AGGCAAGGGC GATGAAAACA TTCAAATCTT TAAAGACAAA      240
ACGATTTTTT TTAGCGACCA GGAAGTCGTT AAAGATTATT ATCTCAATTT AAAACAAGGA      300
```

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...240
(D) OTHER INFORMATION: /note= "FLAGELLAR MOTOR SWITCH PROTEIN F"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```
GTGATGGACA AACTCACTAA AAGCTTGCAA ACGCAAAAAA ACTTCGCTTA TTTAGGCAAA      60
ATCAAGCCCC AACAACTCGC TGATTTCATC ATTAACGAAC ACCCTCAAAC CATCGCCTTG      120
ATTTTGGCCC ACATGGAARC CCCTAATGCG GCTGAAACTT TGAGCTATTT CCCTGATGAA      180
ATGAAAGCCG AGATTTCCAT TAGAATGGCG AATTTTAGGC GAAATATCGC CCCAAGTGGT      240
```

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

ATGCGGTATT TTAGAAGCGC TTTTATTATTA TTTTTCATGA CGCTTTTTTTT TGTTTCTTGC	60
TCTAAGCACC CTTTTTCTAA GCAAACCCCT AAGACTAAGG AGCGGATCCG ACAAGAAGAA	120
GCCAATAAAA AAAGAGAAGA GACTTTGAAT GCCTTGCGCC AATTCAGACT CATTTACATT	180
AACACGCCGG TTTTTCGCTT TTATGATTAC GGCACGATCA AAACCGATAA AGACCACAAT	240
ACTGAAGTAA CCCTTTATAA GCTCAGCCAA AAAGTGGGCG ATATTTACAT GACTAAACGG	300
AGCATTTGTT TTAGCCAAAA ATGTCGGCC AAATGGATTG CTGCAAGGGA TTTGTTTGGC	360
AAGGTGAGCT ATGGGGATTT GTTTGATGAT ATTGTTTTAG GGAGGGATAT TTTTAAAGGT	420
TTAGGGAAAC GCCACCTAAC CCCTGAATAT GTGATCCAAA GGTTTCAAAA AAGCGGGGAA	480
ATTATCCTTT ATGAAAGAAA AAATGGCCTG ATTTCTTTCC AAAACTTGAC TCAAAAAAATT	540
GCTATTAGGA TTGAACCCTA TGAGCCTTCT TTGCAAGATT TAGAAGACAA TGAAAACGCT	600
GATAGCGAGC TTCAA	615

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...372

(D) OTHER INFORMATION: /note= "flagellar hook polypeptide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

```
ATGCGCATTG AAGAAAATGG CGTGATTCT CTAGCCTTTA GTAACGGGGT GGTAGAGCCG      60
GTCGCTCGCA TCGGTATTTW AGCTTTCCT AACGATCAAG GCTTAAGGAA AATCGGCGGT      120
AACCTCTATG AAATGCAAGA AGGCACCATT AATGGCGAAA ACAGACCCCT AAGSGGTAAC      180
CCCATTTTAG GGTGGGACGA AGAGGGCAAG CTCAAGTTTG GGAAAATCAG GCACAAATAT      240
TTAGAAACGA GCAACGTGAA TGCCGGGAAC GCCCTAACCA ATCTCATTTT AATGCAAAGA      300
GGCTATTCTA TGAACGCTAG AGCCTTTGGC GCGGGCGATG ACATGATCAA AGAAGCCATT      360
AGCTTGAAAA AA                                     372
```

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...279

(D) OTHER INFORMATION: /note= "vacuolating cytotoxin - *Helicobacter pylori*"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

```
GTGGAAGCGC GTTATTATTA TGGGGACACT TCATACTTTT ATTTGCATGT GGGAGTTTTA      60
CAAGAGTTCG CTCACTTTGG ATCGAATGAT GTGGCGTCTT TAAACACCTT TAAAATCAAT      120
GCCGCTCGCA GTCCTTTAAG CACCTATGCA AGAGCGATGA TGGGTGGGGA ATTGCAATTG      180
GCTAAAGAAG TGTTTTTGAA TTTGGGCGTG GTTTATTTGC ACAATTTGAT TTCCAACGCA      240
AGCCATTTCT CTTCCAATTT AGGAATGAGG TATAGTTTC                                     279
```

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 642 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GTGGAGGAGC TAGCTAAATT GATCAACAAT AATAATAACA ATAAAAAACT GAGAGGCTTT	60
TTTTTGAAAG TTCTCTTAAG TCTCGTTGTT TTCAGTTCGT ATGGGTCAGC AAATGACGAT	120
AAAGAAGCCA AAAAAGAAGC GCTAGAAAAA GAAAAAAACA CTCCCAATGG GCTTGTTTAT	180
ACGAATTTAG ATTTTGATAG TTTTAAAGCG ACTATCAAAA ATTTGAAAGA CAAGAAAGTA	240
ACTTTCAAAG AAGTCAATCC CGATATTATC AAAGATGAAG TTTTGTACTT CGTGATTGTC	300
AATAGAGTCC TTAAAAAAT AAAGGATTTG AAGCATTACG ATCCAGTTAT TGAAAAAATC	360
TTTGATGAAA AGGGTAAAGA AATGGGATTG AATGTAGAAT TACAGATCAA TCCTGAAGTG	420
AAAGACTTTT TTACTTTCAA AAGCATCAGC ACGACCAACA AACAACGCTG CTTTCTATCA	480
TTGCACGGAG AAACAAGAGA AATTTTATGC GATGATAAGC TATATAATGT TTTATTGGCC	540
GTATTCAATT CTTATGATCC TAATGATCTT TTGAAACACA TTAGCACCAT AGAGTCTCTC	600
AAAAAATCT TTTATACGAT TACATGTGAA GCGGTATATC TA	642

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GTGGGGGGCA TTGTGGCAAA CATGAACGAT CTTTCAACTT ACATGGTTGA GAATTTACTC	60
ATGGGTTTGT ATCTTTTTTC TAGCGCTTTA GATTGGGGCG TGAAAAAAGC CATTAATCTA	120
GCGAGCTCTT GCGCTTATCC TAAATACGCC CCTAACCTT TAAAAGAGAG CGATTATTTG	180
AACGGCTCTT TAGAACCAAC GAATGAAGGC TACGCTTTGC CAAACTCTCT GTRR	234

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ATGAAGAAAA GAAAACATGT ATCCAAGAAA GTGTTTAATG TCATTATCTT GTTTGTGGCA	60
GTATTCACTC TTTTAGTCGT CATTACAAAA ACCCTTTCAA ACGGCATTCA CATACAAAAT	120
TTAAAAATTG GAAAACCTGG CATTCTTGAA TTATACTTAA AACTCAATAA CAAGCTTTCT	180
TTGGAAGTTG AGCGGGTTGA TCTCTCTTCT TTCTTCCATC AAAAACCAC TAAAAAGCGT	240
TTAGAAGTTT CTGATTTGAT TAAAAATATC CGTTATGGCA TTTGGGCGGT GTCTTATTTT	300
GAAAACTTA AAGTCAAAGA AATCATTTTA GACGATAAAA ATAAAGCCAA TATCTTTTTT	360
GATGGGAATA AATACGAGTT WAGAATTTCC AGGAATCAAA GGGGAATTTT CCCTAGAAGA	420
CGATTAAAAA TATCAAGCTT AAAATCATCA ATTTGCTTTT TAAAGATGTT AAAGTCCAAG	480
TGGATGGCAA CGCCCACTAT TCRCCCAAAG CCAGGAAAAT GCGTTCAAT T	531

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GTGTCATGTT GGGGAGCGTC AAAAAAGCGG TTTTtagGGT TTTGTGTTTG GGGGCGTTGT	60
GTTTATGCGG GGGGGTTAAT GGCAGAGCAA GATCCTAAAG AGCTTATATT TTCAGGTATA	120
ACTATTTACA CGGATAAAAA TTTCactAGA GCTAAGAAAT ATTTTGAAAA AGCTTGCAAA	180
TCAAACGATG CTGATGGCTG TGCAATCTTA AGAGAGGTTT ATTCTAGTGG TAAAGCCATA	240
GCGAGAGAAA ACGCAAGAGA GAGCATTGAA AAAGCTCTTG AACACACCGC TACTGCTAAA	300
GTTTGTAAT TAAACGATGC TGAAAAATGC AAGGACTTAG CAGAGTTTTA TTTTAATGTA	360
AACGATCTTA AAAATGCTTT AGAATATTAC TCTAAATCTT GTAAGTTAAA TAATGTTGAA	420
GGGTGTATGC TGTCAGCAAC TTTTtataAC GATATGATAA AGGGTTTGAA AAAAGATAAA	480
AAAGATCTAG AATATTATTC TAAAGCTTGC GAGTTAAATA ACGGTGGAGG GTGTTCTAAA	540
TTAGGAGGGG ATTATTTTTT TGGTGAAGGC GTAACAAAAG ATTTCAAAAA AGCTTTTGAA	600
TATTCTGCCA AAGCTTGTGA GTTGAACGAT GCTAAAGGGT GTTACGCTCT AGCAGCGTTT	660
TATAATGAGG GTAAAGGCGT GGCAAAGGAT GAAAAGCAAA CGACAGAAAA CCTTGAAAAG	720
AGTTGCAAGC TAGGATTAAA AGAAGCATGC GATATTCTCA AAGAACAAAA ACAA	774

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

GTGGCTCTCA CTTTGGGGGC TAGAGGGGGG GTGTATTTGT GTGGGGGGAT TATCCCACGA	60
TTCATTGATT ATTTTAAAAC TTCGCCCTTT AGAGCGCGTT TTGAAACGAA AGGGCGCATG	120

GGAGCGTTTC TCGCTTCCAT CCCTGTGCAT GTCGTGATGA AAAAACTCC CGGACTTGAT	180
GGGGCGGGCA TTGCGTTAGA AAATTATTTA CTGCATGATA GAATA	225

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:SEQ ID NO:224:

ATGAAAGGTT TAACAATGAA AAAATTAGTT TTTAGCATGC TTTTATGTTG TAAAAGCGTG	60
TTTGCAGAGG GGGAAACTCC TTTGATTGTC AATGACCCAG AAACCCATGT AAGTCAAGCC	120
ACTATCATAG GCAAAATGGT AGATAGTATC AAAAGATACG AAGAGATTAT TTCTAAGGCT	180
CAAGCTCAAG TCAATCAGTT ACAAAAAAGTC AATAACATGA TAAATACGAC TAATTCTTTG	240
ATTAGTAGTA GTGCTATCAC TTTAGCCAAT CCTATGCAAG TTTTACAAAA CGCTCAGTAT	300
CAAATAGAGA GCATTAGATA CAACTATGAG AATTTAAAGC AAAGCATAGA AAATTGGAAC	360
GCACAAAATT TGTTAAGAAA CAAATACTTA CAGCAACAAT GCCCTTGGCT TAATGTCAAT	420
GCTCTTACTA ACAATAAGAT TGTCAATCTT AAAGATCTCA ATAACCTAAT CACCAAAAAAT	480
GGCGAACAAA CCCAAACCGC AAGAGATGTG CAAAATCTCA TTCAGTCCAT TAGTGGCAGT	540
GGCTATGGAA ACATGCAATC ACTTGCTGGG GAATTGAGTG GTAGAGCGTG GGGGGAAATG	600
TTGTGTAAAA TGGTAAACGA TAGTAATTAT GAAAGCGAGC AAGCTCTTTT AGCAACAGGC	660
AATAACCCAG AAGAGCAAAA ACGAAGATTT TTGCTTAGAG TAAAGAAAAA GGTTAATGAT	720
AATAAGCAGT TAAAAGATAA ACTTGACCCA TTTCTAAAAA GACTTGATGT CCTACAAACT	780
GAGTTTGGTG TAACTGACCC TACAGCTAAC CATAATAAGC AAGGGATACA TTATTGCACA	840
GAAAATAAAG AGACAGGTAA ATGCGACCCCT ATTAAAAATG TATTTAGGAC AACTCGCTTA	900
GATAACGAAT TAGAACAAGA AATCCAAACG CTCACACTTG ATTTAATCAA AGCCTCCAAT	960
AAAGACGCTC AAAGCCAAGC CTACGCAAAT TTCAATCAAA GGATTAAATT ACTTACTCTA	1020

AAATATTTAA AAGAAATTAC CAATCAAATG CTCTTTTAA ATCAAACAAT GGCAATGCAA	1080
AGCGAGATTA TGACAGATGA TTATTTTAGG CAAAATAATG ATGGCTTTGG GGAAAAAGAA	1140
AACCATATAG ACGAACAATT AACGCAAAAA AGAATAAACG AAAGAGAAAG AGCTAGAATA	1200
TACTTTCAAA ACCCTAATGT TAAATTTGAC CAATTTGGCT TTCCCATTTT TAGTATATGG	1260
GAT	1263

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

ATGAGCGTGA ATTTATTGGA ATTGTTAAAA CTCGCTGTGC CTTTAGCGGT TATTTTGAGC	60
GTTCAAGTGG CGGTTATGAT CCTTTATGTG GTGCTTGTA CTTTAGGGT ATGCGGGAAG	120
GATTATGATG CGGCGGTGTT GTGCGCGGG CATTCGCGTT TTGGGCTTGG AGCGACCCCA	180
ACGGCTATGG TGAATATGCA AACCATCACC AACCACTATG GGCCATCGCA TGTGGCGTTT	240
ATCGTCGTGC CTTTAGTGGG AGCGTTTTTT GTTGATATTA TTAACGCTTT AGCGATTAAA	300
GGCTTTTTGC TTTTGCCTTT TTTCCCTAGT	330

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

ATGCAACTAA GCCCCTTACA AAGCGCGCTG TTATATTTCC GTTACTTTAT TTATCCGGAA	60
AAAAAAACAA GGAGCTTTGA TTTAAGCGAT TTAATTTTAA TTGTCATGGT TTTTTTAGTC	120
CTAGCTTTGG GGCTGTTGAT GAGCGAAGAA ATTTCTATCA GCTACAATGA AGCGAAAGAC	180
TTTTTTTATA GCGATGCGTG GTTTGTCAAA ATCGCTCAAA AAAGCGTAGC CATTTTAAGG	240
CCTAAACGAT TTGGCTTTAA GATTGCCTTT TTTGATCGCT CACGTCATCA ACATGTTTTT	300
ATTCTACCTC ATAGGGCGAA AGATTTTAAA AAAGCC	336

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GTGTATGCGC TCATGGTGGC GTTTTTTGCT TACATGAGTT ATTGCTTGGG GTATCAATTC	60
TCCAAATTCTG TTTCTAAAAA CAACATTTCA TCGCTCTCAT CGCTTTTATC AAGCTGTGTG	120
CGCGTGGTCT CTGTGCTAAT CTTGTCGCTC AGTAGCCTAG AGTTGCGTTA CTTCTCACCC	180
CTAACTATCA TAACCATGCA TTTTGCCCTA ACGCTTATCA TCCTCTTTTT CTTTTTGTAT	240
AAGGCTAAGC CGTTTGATGA G	261

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

ATGAGGTCTT GGATGAAGAA AAAATACTTC ACGCTTTTAT TGCAAAGTAG TGTGGTATTA	60
GCGGTTTTTA TAGGGTGTTC TTCTACCAGG AATCATACTT TTTCAGCCCT TAGTAATCAA	120
GAAAATACAG ACGATAAGCT CCCAGTGGTC CATTCCATTA AAACGATTAA CGATGTGAGT	180
TCAGTGGGCT TTGAATGGTC TAAAGTCGCT GACACTTATG ACATTGACGG GTTTGTTTTG	240
TATCGTTTGA AAAAAGACTC CAAGCTTAAA AGAATCGCCA CCATTAAAAA CCCTTATGCG	300
ACCCACTATT ATGATGAGGG GTTAGAAACA GAGAGTTCCT ACACTTACCA ATTAGCCACC	360
TACAAGGGCG ATAAAATTTT CAAACTTTCA GAACCCATTT TAGTAAAAAC CTCCTTTATC	420
AATCCTGTAG AAAGCGTGTG TGCAAGCCTT GAATACCCTA AAAGCGTGAA AGTCTTTTGG	480
AGCCCGCACC CAAATCCCAG CGTTTCTAAA TACATCATTC AAAGGCAGAA TAAAGACGGC	540
AAATTTTTAA ATGTGGGGGC TGTA AAAAAC CGCTTATTCG TGGAGTTTTT TGATAAAGAT	600
TTAGAAGATG GGCAAAAATA CCGCTACCAA ATCATCGCCG AAAATTTTCAT GGGGGATAAA	660
TCCAGGCCTA GCGTGATAGT GGAGGGGAAA ACCAAAGACT TGCCCAAAGA AATCGCTAAT	720
GTTAGAGTGA GTCAAAACCT CACACGACAA ATTGAATTGA GTTGGGATAA ATCCCCAGAA	780
GAAGATGTGA TAGCTTATCG CATTTACGCT TCCAATAACC GCAACGATAA ATACAAATTC	840
ATCGCTCAAA CCACCAACAC TTCCTATGTG GATAAGATAG AAAAAGACAA TCTCACTCGT	900
TATTATAAAG TCGTCGCCGT AGATAAAACG CATCTTGAAG GGGCGTTACC CAAAGAGCCT	960
GCCATGGGTG AGACCTCTGA TAGGCCTGAA GCCCCTATCA TCACTAAAGG GACTATTCAA	1020
GACTCTTCGG CCTTGATCCA ATGGGAAAAC AACCCAAGCC CTAAAATAGC CACTTATGCG	1080
GTGTATCGTT TTGAAGCCAA CTCCAAAACC CCTTTGCGTT TTGGGAATAT CACACAAAAC	1140
CAGTTCGTGG ATAAGGACAT GAAAGTGGGC GTGGCTTATC GCTATCAGGT GGTGAGCGTG	1200
GATAAAGATG GTTTAGAGTC GCACCCAAGC AAAGAAGTGC GTTTGTTTTT AGAGCGC	1257

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

ATGCTTCCTA CTAAACACG CATTAGAGAT CCGAACAAGC AAGAACTTAC ACAACCAAAA	60
ATAAAAGGAT TGAGTATGGG AAAAATTTTA GCTTCTTTGT TGGGTGGCGG AACAAATCTT	120
TTTACAGGTT TATCCAGTGA TTTGTTTTCT ATGATATTAA ATTTTTTGTT CTTCTGATG	180
TTAATGATGG GACTTAATGA AGCATTAGGG AAAAATTTA ACTTGCCTAT GGACAATATC	240
AAGAATTTTA TGGCAGAAGT GCTGAAGAAT GGATTCGATA GTATCAAAAA CATGGGATCT	300
GCTTTGGTTG GTAATGGTTT TGGTAGCAGC AAATCAGACA AAACCACTAA TAAAATGAGT	360
GTCCCACAAG TAAGACTC	378

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...216
 - (D) OTHER INFORMATION: /note= "OXYGEN-INSENSITIVE NAD(P)H NITROREDUCTASE"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

ATGGCGAACA TGATGATGGC AGCGGCCATG TTAGGGATTG ATTCTTGCCC GATTGAAGGG	60
TATGATCAAG AAAAAGTGGG GGCTTATTTA GAGGAAAAAG GCTATCTAAA CACGGCAGAA	120
TTTGGCGTGT CGGTAATGGC CAGTTTTGGT TATCGTAACC AAGAGATTAC CCCTAAAACC	180

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

ATGGCCGGGC TTGTTTTGAT GGTGCTGCTC GCCAGTTATG AAAGCTTTGT TTCTAAATTA	60
GACAAGGTGG ATGCTAGCGA AATCACTTGG CTAAAACACA CAGATTTTAA CGCTTTAAAA	120
TTAAAGGTTT CCCTCTCCAT TGTAGCCATT TCGGCGATTT TCTTGCTCAA ACGCTACATG	180
AGTTTAGAAG ACGTTTTATC CAGTATTCCT AAAGACACGC CCCTATCGCA TAACCCTATT	240
TTTTGGCAAG TGGTGATCCA TTTGGTGTTT GTGTGTTT CAG CGCTGTTAAC CGCTGTTACC	300
AATAACATCG CTTTTTCGCA GAAAGAAAGG CAT	333

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

ATGATTACGA TCGTTATTGC AAAAGCGGGG AATATAGTCA AAGYCGATAT TTTTACGCAC	60
ATTAGCGATA TTAAATGGG GCTTATTAAA GGAGGTCAAT GGGGGGTTAT TGGTTTAGGC	120

AATATCGGTA AAAGAGTCGC CAAGCTCGCT CAAGCTTTCG GGGCAAAGGT GGTGTATTTT	180
TCCCCTAAAG ATAAAAAAGA AGAATACGAG CGCTTGAGTT TAGAGGAATT GCTTAAACA	240
AGCGGTATTA TCAGCATTCA TGCCCCCTTA AATGAAAGCA CGCGCGATTT AATCGCTCTG	300
AAAGAATTGC AAAGCTTAAA AGATGGGGCG ATTTTAATCA ATGTGGGGCG TGGGGGCATT	360
GTGAATGAAA AGGRTTTGGC TTTRRTTTTA GAAACCACAG ATTTGTATTA CGCGAGCGAT	420
GTGTTT	426

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...189
 - (D) OTHER INFORMATION: /note= "vacuolating cytotoxin of Hpylori"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

GTGAATTTCA ACGCTAAAAA TATTTCAATT GATAATTTGG TAGAAATCAA TAATCGTGTG	60
GGTTCTGGAG CCGGGAGAAA AGCCAGCTCT ACGGTTTTGA CTTTGCAAGC TTCAGAAGGG	120
ATCACTAGYA GTAAAAATGC GGAAATTTCT CTTTATGATG GCGCCACGYC AATTGGCTT	180
CAAACAGMG	189

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 930 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

ATGCGAACGC TCATTCTGTC GCTTCTAAAA CATGCGATTT TAATGGGCAT GCTTTTAAAA	60
GAATGCCAAG AAAAGTTAAA GCGTTCTTTA AATTTGAGTG CTAATCATTG CGTCTTGAGC	120
GCGGGGTATG GGGCGAGTTC AGCGATTAAG AAATTTCAAG AAATTTTAGG GGTGTGTATC	180
CCTTCAAAAA CGAAGAAAAA TTTAGAGCCG TATTTGAAAG ATATGGCTTT AAAGCGTGTG	240
ATTGTAGGGC CTTATGAGCA TCATTCTAAT GAAGTTAGCT GGCGTGAAGG CTTGTGTGAA	300
GTGGTGCGTA TCCCTTTAAA TGAACATGGT TTATTGGATT TAGAAATTTT AGAGCAAACCT	360
TTAAAAA AAA CCCCTAACAG CTTGGTTTCT GTGAGCGCGG CTTCTAATGT AACGGGAATT	420
CTTACGCCTT TAAAAGAAGT TTCATCATTG TGTAAGGAAT ATAGGGCTAT TTTAGCTTTG	480
GATTTAGCGA ATTTTAGCGC GCATGCTAAC CCTAAAGATT GCGAATACCA AACCGGTTTT	540
TATGCGCCTC ATAAGCTTTT AGGGGGCGTT GGAGGGTGCG GTCTTTTAGG CATTTCTAAA	600
GATTTGATTG ACACGCAAAT YCCTYCGAGT TTTAGCGCAG GGGGCGTGAT TAAATACGCT	660
AATCGCACAC GGCATGAATT TATTGATGAA TTGCCTTTAA GAGAAGAATT TGGCACGCCA	720
GGATTGTTGC AATTTTACAG GAGCGCTCTA GCGTATCAAT TAAGAGATGA ATGCGGTTTG	780
GATTTTATCC ATAAGAAAGA AAACAACCTT TTAAGGGTGC TTGTGTATGG CTAAAAAGAC	840
TTGCCCGCTA TTAATATTTA TGGGAATTTA ACGGCGAGTC GTGTGGGGGT AGTGRCTTTT	900
AATATTGGAG GGATTTTCRCC CTATGATTTA	930

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 564 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GTGGCATGCA ACACCGCGAG CGCTCTGGCT TTAGAAGAGA TGCAAAAGTA TTCTAAAATC	60
CCTATTGTGG GCGTGATTGA GCCAAGCATT TTAGCGATCA AGCGGCAAGT GGAAGATAAA	120
AACGCCCCTA TTTTAGTGCT AGGGACAAAA GCGACGATTC AATCCAACGC CTATGACAAC	180
GCCCTGAAAC AACAAGGCTA TTTGAACATT TCGCATTTAG CTACTTCTCT TTTTGTGCCT	240
TTGATTGAAG AAAGTATTTT AGAGGGCGAA TTGTTAGAAA CTTGCATGCA TTATTATTTT	300
ACTCCCTTAG AGATTTTACC CGAAGTGATC ATTTTAGGTT GCACGCATTT TCCCTTAATC	360
GCTCAAAAAA TTGAGGGCTA TTTCATGGGG CATTTTGCcc TtCCAACGCC CCCCCTACTC	420
ATCCATTGGG GCGATGCTAT TGTAAGATAT TTGCAACAAA AATACGCCCT TAAAAACAAT	480
GCATGCACAT TCCCTAAAGT GGAATTTTCAT GCGAGCGGCG ATGTGATCTG GCTAGAAAAGA	540
CAAGCTAAAG AATGGCTCAA ATTG	564

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

GTGTTGTGGG TGCTATATTT TTTAACCAGT TTATTTATTT GCTCTTTGAT TGTTTTGTGG	60
TCTAAAAAAT CCATGCTCTT TGTGGATAAC GCTAATAAAA TCCAAGGCTT CCATCATGCA	120
AGAACCCAC GAGCCGGGGG GCTTGGGATC TTTCTTTCTT TTGCGTTGGC TTGTTATCTT	180
GAACCTTTTG AGATGCCTTT TAAGGGGCCT TTTGTTTTCT TAGGGCTATC GCTAGTGTTT	240
TTGAGCGGTT TTTTAGAAGA CATTAACCTT TCATTAAGCC CAAAATACG CCTTATTTTG	300
CAAGCTGTAG GGGTCGTTTG CATCATTTCA TCAACGCCTT TAGTGGTGAG CGATTTTTCG	360
CCCCTTTTTA GCTTGCCTTA TTTCATCGCT TTTTATTTCG CTATTTTSTA TGCTGGTGGG	420
TATCAG	426

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

ATGGCGTGTA AATTTTGCCC TAAGATCAGA AAAACAGATT GGATTTTAT TTTAATCGCC	60
GCTTTAGGCT TTTATTCAGT TAATAAGCTA GGGTATGCGC CCAAATTCAA TACCCCACT	120
CCAAAATCTT CACGCCCTCT TTCACGCCCT ATTGAAAAGC CTAACAATAT GACTGAAGAA	180
GAAAGGAAAA AGCGTTTTAT AGAGTTGCAA AAAGCATGCT TACTTCATAA AGACAAAAAG	240
GCATGCGAAG AGGTTTTT	258

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...363
 - (D) OTHER INFORMATION: /note= "PREPROTEIN TRANSLOCASE
SECA SUBUNIT"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GTGGATTCCA TTTTAATTGA TGAAGCGAGA SCTCCTTTAA TCATTTTCAGG GCCTGTGGAT	60
--	----

AGGCGCATGG AAAATTACAA CAAGGCTGAT GAAGTCGCTA AAAGCATGCA AGTGGAAGTG	120
GATTTACCA TAGACGAAAA AAACCGCGCG ATTTTAATCA CTGAAGAGGG GATTAAAAAA	180
GCCGAAAATC TCTTTGGCGT GGATAATTTA TACAAAATTG AAAACGCCGC CCTATCGCAC	240
CATTTAGACC AAGCCTTGAA AGCGAATTAC CTCTTTTTTA TTGRTAAAGA TTATATTGTA	300
GCCAATAATG AAGTGGTGAT TGTAGATRRA TTTACCGRCC GTTTGYYTGA AGGGGAGGCG	360
CTT	363

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

ATGACGATCA CCACCCTATC TTTTATTATC ACAACGCCAG AAGTGTTTGT CAATCAGGAT	60
TTCCCATGGC TTTCTGGGGC TGGAAGGCTA GTGGTTAAAG ACTTGCGGTT ATTTGCTGGA	120
GGCTTGTTTG TGGCCGGATT TGATCGAAAC GCTATTTGGA GGGTAAAGGG TTTTGCT	177

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

GTGTTTTCTG GCAATAAAG GGCTATAAAT TATCGCACGA TTGTCAGCGC CTTTGTGATT	60
CAAGTGGCTT TAGGGGCGTT GGCTTTATAT GTGCCTTTGG GCAGAGAAAT ACTGCAGGGT	120
TTAGCTAGCG GCATACAAAG CGTGATTGGT TACGGCTATG AGGGGGTACG CTTTTTATTT	180
GGCAATCTCG CTCCAAACGC TAAGGGCGAT CAAGGGATAG GAGGCTTTAT CTTTGCGATC	240
AACGTTTTAG CGATCATTAT CTTTTTTGCT AGCTTGATTT CACTTCTATA TTATTTAAAA	300
ATCATGCCTT TAGTAATCAA CCTCATCGGS GGGGCGTTGC AAAAATGCTT AGGCACTTCT	360
AAAGCAGAAA GCATGAGCGC AGCGGCTAAT AYTYYTGTGG CGCACACCGA AGACRCCCTT	420
AGTCAT	426

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

ATGCTGGTGG GTATCAGTAA CGCTATTAAT ATCATTGACG GGTTTAACGG GCTTGCATCT	60
GGGATTTGCG CGATCGCGCT TTTAGTCATT CATTATATAG ACCSTAGCAG TTTGTCTTGT	120
TTGCTCGCTT ACATGGTGCT TGGGGTTTAT GGTGTAAAW TTCCCTTCAG GAAAGATTTT	180
TTAGGWCAT CGGGGGGCG TATTTTTTGG GTTGGTGWR CGGRATTCT CTCTTGCAAT	240

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...225
(D) OTHER INFORMATION: /note= "invasion protein A"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

ATGCTACATA AAAAATATCG TCCTAATGTT GCGGCCATTA TCATGTCGCC AGACTACCCT	60
AACACATGCG AAGTTTTTAT CGCTGAGCGC ATAGACATTG AAGGGGCGTG GCAGTTCCCC	120
CAAGGAGGCA TTGATGAGGG AGAGACCCCT TTAGAAGCAC TCTATAGAGA ATTACTAGAA	180
GAAATTGGCA CGAATGAAAT AGAGATTTTG GCGCAATACC CTAGA	225

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GTGATGCTAA TGGCAATTTT TACCCCTTAT ATTCTTATTT TGAAAATGAT GAAAAAGTCT	60
ATGAGTTTAT TCGCCAATAT GGGGTTGGAG CAAATTTTTT GCAACAGAGA CATTAAAGAT	120
TTAAATGATT TTGTTTTTGG TATAGAAGTG GGGCTTGATA GCAATGCGAG AAAAAATCGT	180
AGCAGAAAGG CTATGGAAAA TCATCTTATC GGTCTTTTTG TCCAAGCTCA ATTAAATTTT	240
AAAGAACAAG TAGATATTAG AGAATTTGAG GATTTACGCC AGGCTTTTGG AAATGATACT	300
AAAAAATTTG ATTTTGTTAT TTTTAGCAAA GAGAAACTT ATTTTCATAG AAGC	354

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 627 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

ATGATCCGTC TAGCCGCGTT TTTTITAGCT CTCGCTTGCG CGATTACGCC AAAAAGCCGC	60
CTTCTTTTAA AAAATGTCTT GCTCAACCCC ACTCGCATAG AAGCTTTTGA GGTTTTGAAA	120
AAAATGGGCG CTCATATAGA ATATGTTATC CAATCCAAAG ATTTAGAAAGT TATTGGCGAT	180
ATTTACATAG AGCATGCCCC TTAAAAGCG ATCAGTATTG ATCAGAATAT CGCCAGCCTT	240
ATTGATGAAA TCCCCGCTTT AAGCATCGCT ATGCTTTTTG CAAAAGGCAA AAGCATGGTG	300
AGAAACGCTA AAGATTTACG AGCCAAAGAA AGCGATAGGA TTAAAGCGGT TGTTTCTAAT	360
TTCAAAGCTT TAGGGATTGA GTGCGAAGAA TTTGAAGACG GGTTTTATAT AGAGGGATTA	420
GGAGATGCGA GTCAATTAAA GCAGCATTTT TCTAAGATTA AACCCCCTAT TATCAAGAGT	480
TTCAATGATC ACAGGATTGC GATGAGTTTC GCTGTTTTAA CTTTAGCGTT GCCTTTAGAA	540
ATTGATAATT TAGAATGCGC GAACATTTCT TTCCCAACCT TTCAGCTTTG GCTCAATCTA	600
TTCAAAAAAA GGAGTCTCAA TGGAAAT	627

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...225

(D) OTHER INFORMATION: /note= "PROBABLE COPPER-TRANSPORTING ATPASE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GTGGGGAGTT TGAAATTTTT AAACGCTATG GGGGTTGATT TAAAGGTAA AGAGAGCGCT	60
AATATCATGG TAGGCTTTGC GAAAAATAAG ACCTTATGCG CGTTATTCAT TTTAGAAGAG	120
CGTTTGAAAG CTAACGCTAA AGAAGTCATT CAGGCTTTAC AAAATCAAGG CTTGGAATTA	180
GAAATTTTAA GCGGGGATAA TGAAAGCTCG GTTAAGGAGT GCGCG	225

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

ATGGAGGCTT TAAACGCTTT GAACGCGCAA AGTGATGAGC AAATTTTATG CGAGGGTTAT	60
TTTGTGTTGT TGCAAATCTT AGAGCCTATG ATCCCGCACA CGGCATGGGA ATTGAGCGAG	120
AGGCTTTTTTA AAAGAGAGAA TTTCAAGCCT ATAGAAGTAG ATGAAAGCGC TTTGATAGAA	180
GACTTTATGA CTTTAGGGCT TACCATTAAT GGCAAAGGC GCGCGGAATT GAAAGTCAAT	240
ATTAACGCTA GCAAAGAAGA GATTATTATT TTGGCTAAAA AAGAATTAGA GAAATATTTA	300
GAAAACGCGA GCGTTAAAAA AGAAATTTAT GTGCCTAATA AACTTGTTAA TTTTGTACC	360
GCA	363

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

```
ATGAAAGAAA GTATTAAATA CTTGCTAGAA AGCGTGGGGC TAGTGCTTTT AATGAGCGTG      60
AATCCGGGCT TTGGCGGGCA GAAGTTTTTA GATCTAGTGC TAGAAAAGTG CTTGAAAGTT      120
AAAGAACTGA TCAAACGCTA CAACCCTAGC TGTCTTTTAG AAGTGGATGG GGGCGTGAAT      180
GATAAAAATA TCTTTGAACT CCAACAAGCG GCGTGATG TGGTGGTTTC AGGGAGTTAT      240
ATTTTTGAAT CCAAAGATYG TAAGCTGGCT ATTGAAGGCT TACAGAATGT CAGACAACCT      300
CTTGCA                                     306
```

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

```
GTGCATGACG GCGTGCTTGG GTGGGTAGGC TTCACTTTGA TTGCGAGCAT GTATCACATG      60
ACCCCTAGGC TTTTCAAAG AGAGATCTAT TCAGGAAGAC TTGTGGATTT CCAATTTTGG      120
ATCATGACTT TAGGGATTGT GCTTTACTTT TCGTCCATGT GGATTGCAGG GATCACGCAA      180
GGGATGATGT GGAGGGATGT GGATCAATAC GGAATCTCA CTTACCAATT CATTGACACG      240
GTTAAGGCGC TAATCCCTTA TTACAATATT AGAGGCGTTG GGGGTCTTAT GTATTTTATT      300
GGATTTATTA TTTTGTCTTA CAATATCTTT ATGACAATCA CGGCAGGCAA AAAATTAGAG      360
CGTGAGCCCA ATTACGCCAC SCCTATGGCA RRA                                     393
```

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

ATGATAACGC TCTTTAGTTT TGGAGCGTTC GCTTACTATT TCGTGTCTTC TCAAATCAGT	60
CACGAAAAC TATCAAAACGA AATGCGCCAT TACCAGTTTG TTACCACTAT CAATGAAATT	120
TTAAATAACT ACTCTGATTA TAGAGCCATA GAAGATTACC TCTATAAAAT TGGCTTTAGA	180
GAAACCACAA TAGAAAATTT AGAAAAGGTT TTAGCCAAAA GACGCCACCA GTTGCACCAC	240
AGAAATATTT GGTATGCTGA AGTGTTTAAA TTCAGCGATA TGGTTTTTAT CCTTTTAAAA	300
AAGGATGAGC ATTTTGTGCT TTATAAAGAT TTGCATTCGG TTTCTTATAG GAATTATTTT	360
TTAGCCATTA CGGTGGGTTT ATTATTGATT TTATTCCTCT TTTTATTTGT TTTGCAGAGT	420
TTATTGCCTT TAAGAGAGTT AAGATCTCAA GTGAAACGCT TCGCTCAAGG GGATAAAAGC	480
GTGAGTTGTA AAAGCAAGCA AAAAGATGAA ATAGGGGATT TGGCTAACGA ATTTGACAAT	540
TGCATCCAAA AAATCAATGC GATGAATGAA TCTCGGGTTT TATTTTTGCG CTCTATCATG	600
CATGAATTAC GCACCCCTAT CACTAAGGGC AAGATACTAA GCTCTATGCT CAAAGAAGAG	660
CTGTCTTGCA AACGCTTTTC ATCTATATTT GATCACTTGA ACATGTTGAT TGAGCAATTT	720
GCCCGCATTG AGCAGCTCGC TTCCAAAAAT TATGGGAGCA ATAAAGAAAA ATTTTTAATG	780
AGCGATTTGA TAGATAAGAT TGAAAAAATG CTTTTAATTG ATGAAGATAA AAAAAGCCCT	840
ATCCATGTAT CCTCTTCAA TTACATCATT GAAGCGGATT TTGAATTGTT TGCTATAGCG	900
TTAAAAACA TGATAGACAA TGCGATCAAA TACAGCGATG ACAAACAGGT GTTTTTGGAT	960
TTCATAGGGA ATAATTTAGT GGTGTCCAAT AAAAGCAAAC CTTTAAAAGA AGATTTTGAA	1020
AAGTATTTGC AACCCCTACTT TAAATCTTCT AACCCAGCC AAGCCCATGG GTTTGGGTTA	1080
GGCATGTATA TCATTAAAA CGCTTTAGAG GCTATGGGAT TGAATTTGAG CTATCATTAT	1140
AGCAATGGAA GAATCTGTTT CACTATCCAT GATTGCGTTT TTAATAGTTT TTACGATTTA	1200
GAAGCGGATA ATGAAGAGCT ACCCCCCCCC GAAAATTTGA GAGAGGTGAA GGAATGAAG	1260
GGAACAGAAA AAGCCAATTG TGGGGTTAAA GAAAAACAAA AAGAGAGAAC ATGTTCAAAC	1320

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

GTGCTTCTCC TTTCTCGTAT GGGTATCGCT TTTGCCCACT CTATTTTTTG GTCCATCACG	60
GCTTCTTTAG TCATTTCGTGT CGCGCCAAGA AACAAAAAAC AACAGGCCTT AGGGCTGTTA	120
CGGTTAGGGA GTTCGTTAGC GATGATTTTA GGGTTGCCGC TTGGGAGGAT CATGGGGCAA	180
ATTTTGGATT GGCGATCCAC TTTTGCGGTG ATTGGGGGCG TTGCGACTCT TATAATGCTG	240
CTTATGTGGA AATTGCTCCC GCATCTACCG AGTAGAAACG CCGGCACGCT CGCAAGTGTT	300
CCTATATTAA TGAAACGCCC GCTTTTAGTG GGGATTTATT TGCYTGTGAA TCATGGTTAT	360
TTCTGGGCAT TTCACCACTT A	381

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

ATGCGCATT A TCATAAGGTT ACTTTCATTT AAAATGAACG CTTTTTTAAA ACTCGCGCTC	60
--	----

GCTTCTTTGA TGGGGGGGCT TTGGTATGCT TTCAATGGCG AAGGCTCTGA GATTGTCGCT	120
ATAGGGATTT TTGTGTTGAT CTTGTTTGT TTTTTTATCC GCCCTGTGAG TTTCCAAGAC	180
CCAGAAAAAC GAGAAGAATA CATAGAACGG CTTAAAAAAA ACCATGAGAG GAAAATGATC	240
TTACAAGACA AGCAAAAAGA AGAGCAAATG CGCCTCTATC AAGCCAAAAA AGAGCGAGAG	300
AGCAGGCAAA AACAAGACCT TAAAGAACAA ATGAAAAAAT ACTCA	345

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

GTGCGATCTT GCAAACAGAT TTTTGATAAG GGTTTAAAGC CCTATTATAA ACATTCTGTT	60
TGCTTAAAGC CTTTTTTTAG GTTTTGTTTT CTCAAATTC ATGCTTATCA ACAGCGTTAT	120
AGAGCGTTTG CTCTAACGCT CTTTCTTGT AAGTTTTTTA ACGCTTGTA GATTTTATT	180
CCCATAATTG ATTTTAAAT CGTTTTTATC CCTATTCTAA AACACCAAGC CAAGCTAAAA	240
AGAGTCTCTA ATGCCTAT	258

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

ATGTGTGGAA TGGGGTTTAT TGGCTTCAAA ACAAACCTTA CTCAAACAAA GGCATTTATT	60
ATATTGATCC CAATCTTTCA GGACAGAGCG GTCAAAGCGG CAACACGCTC AGCACCTATA	120
CAGCTAATTT GT	132

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

ATGGGGAATT TTAATAGCTA TGGCGATTTG GTGTTTAACC TCAGTCATTC AGTTAGTCAT	60
GCTATTATCA ATACTCAAGG CACAGCGACG ATCATGGCCA ATAATAACCC TTTGATCCAA	120
TTCAACGCTT CTTCAAAAAGA AGTGGGTACT TACACGCTGA TTGATAGCGC TAAAGCCATT	180
TATTACGGGT ATAACAACCA AATCACAGGA GGCAGTAGCC TGGATAATTA CCTTAAGCTT	240
TATGCGCTCA TTGATATTAA TGGCAAGCAC ATGGTGATGA CTGACAACGG CTTAACCTAT	300
AACGGGCAAG CCGTGAGCGT TAAAGATGGC GGTTTAGTTG TAGGCTTTAA GGA CTCTCAA	360
AATCAATACA TTTACACTTC CATTCCTTTAT AATAAAGTGA AAATCGCTGT TTCTAATGAT	420
CCTATCAATA ACCCACAAGC CCCCACTTTA AAACAATATA TCGCTCAAAT TCAGGGCGTT	480
CAAAGCGTGG ATAGCATCRA TCAAGCTGGG GGAAATCAAG CGATTAATTG GCTCAATAAA	540
ATCTTTGAAA CTAAAGGAAG CCCTTTATTC GCTCCCTATT ATCTAGAGAG CCACTCCACA	600
AAAGATTTAA CCACGATCGC TGGAGATATT GCTAACACTT TAGAAGTCAT CGCTAACCCCT	660
AATTTTAAAA ATGACGCCAC TAATATTTTA CAGATCAACA CCTACACGCA GCAAATGAGT	720
CGTTTAGCCA AGCTCTCTGA CACTTCAACT TTCGCCGTT CTGATTTCTT AGAACGCTTA	780
GAAGCCCTTA AAAACAAGCG ATTCGCTGAT GCGATCCCTA ACGCTATGGA TGTGATTTTA	840
AAATACTCTC AAAGGAATAG AGTTAAAAAT AATGTGTGGG CGACAGGAGT TGGAGGGGCT	900

AGTTTCATTA GTGGAGGTAC TGRAACTTTA TATGGTATCA ATGWAGGGTA TGATAGGTTT	960
ATTAAGGGCG TGATTGTGGG AGGTTATGCC GCTTATGGGT ATAGCGGGTT CCATGCAAAC	1020
ATCACTCAAT CAGGCTCTAG CAATGTCAAT GTGGGCGTTT ATAGCCGAGC GTTTATCAAA	1080
AGAAGCGAGC TAACCATGAG CTTGAATGAG ACTTGGGGAT ACAATAAAAC TTTCATCAAC	1140
TCCTATGACC CCCTACTCTC AATCATCAAT CAGTCTTACA GATACGACAC TTGGACGACT	1200
GACGCTAAAA TCAATTATGG CTATGATTTT ATGTTTAAAG ATAAAAGCGT TATTTTAAAA	1260
CCCCAAGTAG GCTTAAGCTA TTATTACATT GGTTTGTCTG GTTTAAGGGG CATTATGGAT	1320
GATCCTATTT ACAACCAATT CAGAGCCAAT GCTGACCCTA ATAAAAATC CGTTCTAACG	1380
ATCAATTTTG CCCTAGAAAG TCGGCATTAT TTCAATAAAA ACTCTTATTA TTTTGTGATT	1440
GCGGATGTGG GCAGAGACTT ATTCATTAAT TCTATGGGGG ATAAAATGGT GCGTTTCATC	1500
GGTAATAACA CCCTAAGCTA TAGAGATGGT GGCAGATACA ACACTTTTGC TAGCATTATC	1560
ACAGGCGGGG AGATAAGATT GTTCAAAACC TTTTATGTGA ATGCGGGCAT AGGGGCTAGG	1620
TTTGGGCTTG ATTATAAAGA TATTAATATT ACCGGAAATA TTGGTATGCW SYATRCTTTT	1680

(2) INFORMATION FOR SEQ ID NO:255:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 423 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

ATGGAGTCGA ATCAWTCCT CCCCATGGCA TTAATATCAT GCTCACCTAA CGCTAAAGGG	60
GCGGACATTA AAGGCTATAA CGGCTTAGTG GGGGAATTGA TTGAAAGGAA TTTCCAACGC	120
TATGGCGTGC CGTTACTGCT TTCTACGCTC ACTAACGGCC TATTGATTGG GATCACTTCG	180
GCTTTAAACA ACAGAGGCAA TAAAGAAGAG GTGACTAATT TCTTTGGGGA TTATCTTTTA	240
TTGCAATTGA TGAGGCAAAG CGGCATGGGG ATCAATCAAG TGGTCAATCA AATTTTAAGA	300
GACAAGAGCA AGATCGCCCC CATTGTGGTG ATTAGAGAGG GGAGTAGGGT CTTCATTTTCG	360

CCCAATACTG ACATCTTCTT CCCTATACCC AGAGAGAATG AAGTCATCGC TGAGTTTTTG 420
AAG 423

(2) INFORMATION FOR SEQ ID NO:256:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...153
 - (D) OTHER INFORMATION: /note= "PHOSPHATIDYLSERINE DECARBOXYLASE"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

GTGAATTTTT ACCTTTCGCC CAAAGATTAC CACCACTACC ACGCCCCTTG CGATTTAGAA 60
ATTTTAGAGG CTCGTTATTT TGCGGGGAAA TTACTACCAG TCAATAAGCC CTCATTACAC 120
AAAAAACAAA ATCTGTTTGT GGGCAATGAA AGG 153

(2) INFORMATION FOR SEQ ID NO:257:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 699 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...699
 - (D) OTHER INFORMATION: /note= "PROBABLE ABC TRANSPORTER"

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:257:

```
ATGGATATTT TAAAAGCAGA GCATTTAAAC AAACAGATTA AAAAAACCAA AATCGTTTCA      60
GATGTTTCTT TAGAAGTGAA AAGCGGCGAA GTGGTGGGGC TTTTAGGGCC TAATGGGGCG      120
GGTAAAACCA CCACCTTTTA CATGATATGC GGGCTTTTAG AGCCTAGTGG GGGGAGCGTT      180
TATTTAAACG ATGTGGATTT AGCTAAATAC CCCTTACACA AGCGTTCTAA CTTGGGCATA      240
GGCTACTTGC CCCAAGAATC CAGTATTTTT AAAGAATTGA GCGTGGAAGA GAATTTGGCC      300
CTAGCAGGGG AGAGCACTTT TAAAACTCT AAAGAGAGCG AAGAAAAAAT GGAAAGCTTG      360
CTTGATGCTT TTAATATCCA AGCCATAAGA GAGCGCAAGG GCATGAGCTT GAGTGGGGGA      420
GAAAGAAGGC GCGTAGAAAT CGCTAGGGCT TTAATGAAAA ACCCTAAATT CGTGCTGTTA      480
GATGAGCCTT TTGCGGGCGT GGATCCGATT GCGGTGATTG ACATTCAAAG AATCATTGAA      540
AGCTTGATTG GATTAAACAT TGGCGTGTG ATTACTGATC ACAATGTGCG AGAGACCTTG      600
AGCGTGTGCC ATAGGGCGTA TGTGATCAAA AGCGGCACGC TTTTAGCGGC GGGAACGCTA      660
ATGAAATTTA TGAAAACGCT TTGGTGCGTA AGTATTATT      699
```

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...474
- (D) OTHER INFORMATION: /note= "HYPOTHETICAL ABC TRANSPORTER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

```
ATGAAAGAAA TCGTTACAAT AGAGAATGTG TCTTTTAACT ACCACAATCG CGCTATTTTT      60
AAGGATTTTA ATTTAAGCAT TCAAGAAGGG GATTTTTTAT GCGTTTTAGG GGAGAGCGGG      120
AGCGGTAAAA GCACGCTTTT AGGCTTGATT TTAGGGCTTT TAAAACCCAG TCTGGGGAGC      180
GTAAATCT TTAATGAGAC CCTTCAAAC AACGCTTTTT TACGCCAAAA AATAGGCTAT      240
```


ATCGCTCAGG GCAATTCCTT ATTCCCTCAT TTAAACGCCT TACAAAACAT GACTTTTTTGC	300
CTTAATTTTAC AAGGCATAAA CAAACAAGCC GCTCAAAAAG AAGCCAAAGC CTTAGCGTTA	360
AAAATGGGGT TAGACGAGAG CCTTATGGAT AAATTCCTTA ATGAATTGAG TGGGGGGCAA	420
GCCAAAGAGT GGGCATTATT AGGGGGATTA TCCACAGGCC AGAACTCATT TTAT	474

(2) INFORMATION FOR SEQ ID NO:259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 573 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

ATGATTTTCC CCGAGCGCTT TCAAAACGCC TTTTATAGGT TAAGCGAATT GTTTTACTAC	60
GCTTCCAGCT TGAGTTTTTA TACGATTTTG TCTTTATCGC CTATTTTGTT GTTCGTGTTC	120
AGTCTTTTTG TGTCTCATTA CTTGCAAGCG CACAGCGGTG AAATGGAAGC CTTGATTTTC	180
CCTAACGCTC CTAAACTCAT TGGCGCGATT AAGGATTTTT TAGAAAATTT TAAAAAACA	240
GACATGACCT TAGGCACGCT TGAAGAGGTG TCTATTGTGG TGGCGTTGGT GCTTTTTTGT	300
GAAAACTACC GCTCCATCGC GTCAAAAATT TTTGACGCAA AGCCCAGAGA TTATGCGCAT	360
TTTAAGGGTA AAGAAATCTT TTTATTTTGG GGGTTTGGCA CGACTTTAGT GTTTTTATTC	420
GCTTTGCCTT TGGTGGTGTT TTTGATATT AAGATCCAAG TGTTTTTTGA AGATAAAGAT	480
TCAAGCTTGT TGCATGTTTT AAGATGGATA GGCACCTACG CGTTTTTTTT GATCCTTTTT	540
ACCATTCCCA CGAATAAGGT GTTTAAACTA YYA	573

(2) INFORMATION FOR SEQ ID NO:260:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 729 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

ATGGTTTTGA TGATTTTCAC AAGCATCTTG AAGATAGCGT TAAAAGTTTT ATCAGAGCGA	60
AAAAAAATC GTTATGGTTT TCCTAGAATC TTTGATGTTG CAGACATAGA ACAAGAAGAG	120
AGGGAAGTCA TTGAATGGCG AGAAAAAAG AAAGCGTCAA AACAAAGCTA TAAACAAAAC	180
CTTCAAATCA ATAAATCGC TAACGATTTA AAGCGTGATA AGATAGTGGA TAAAAGAACG	240
ATTTTAAGCG TGATAGACGC TGATATAGAG CGTGGTTTTA TCCCGCCTAA AGATTGTGTTA	300
AAACAATTAG AAAAAATTAG CGCTTCTCTT TCTAAAGACA TCGTAATAAC GATAAAGCAA	360
GTAGAAAAAT TAGAGCTTAA CTATGCGCTA ATAGACAATA TCCAACATAA CACGCTTGAT	420
GACACGCTTG ATTTTACCTT TATTGTTGGG GATTCTTTGA GCGTTCAGTC GCTTTATGTT	480
ACCTTTAATC TTGTGATTGA TATTGATAGA CCCATGAGCG AGCAGTTTCT CAACCWTATT	540
GGGAAATTGG GGAGTTTTGA ATCTAGAGAG CAAGCGTTAG AGTGGGTGCG ATTATCGCAA	600
ACTAACTGA TCATTGAAAC GCCTAAAGAA GCGTTAAAAA ATGCGGAATT ATCACAAATT	660
GAAGAAATAT TGACCGGCTG TATTTTAAAT GGCGCTTACC GCCTTCAAAA CGATCTTAAG	720
AAAGGGCGA	729

(2) INFORMATION FOR SEQ ID NO:261:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 708 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GTGAGTGAGG TCGCGAGCGT GGGGGGCTTT GTGAAGGATT ATGAAGTAAC GCTTCAAAAC	60
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GATTCTTTGA TCCGTTATAA CTTGAGTTTA GAACAAGTCG CTAACGCGAT TAAAAATTCC	120
AATAACGATA CCGGTGGGGG CGTTATTTTA GAAAACGGGT TTGAAAAAAT TATAAGATCG	180
CATGGCTATA TCCAATCTTT AAACGATTTA GAAGAAATTG TGGTTAAAAA AGAAGGGGCT	240
ATCCCTTTAA AAATCAAAGA TATAGCGAGC GTTAGGCTAG CGCCCAAACC GCGCAGAGGG	300
GCGGCTAATC TCAACGGCGA TAAGGAAGTG GTGGGCGGGA TTGTTATGGT GCGCTATCAC	360
GCTGACACTT ATAAGGTGCT TAAAGCCATT AAAGAAAAAA TCGCCACCTT ACAAGCGAGT	420
AACCCTGATG TGAAAATCAC CAGCGTGTAT GACAGGAGCG AATTGATTGA AAAAGGCATT	480
GACAATTTGA TTCACACGCT CATAGAAGAA AGCGTCATTG TGCTAGTCAT TATTGCGATT	540
TTCTTACTGC ATTTCAGGAG CGCTTTAGTG GTGATTATCA CTCTGCCTTT AAGYGTGTGC	600
ATCAGTTTCT TGCTCATGSG TTATTTCRAT ATTGAAGCGA GCATCATGAG TTTGGGGGGC	660
ATTGCAATCG CTATAGGGGC GATGGTGAAT GCGGCGATTG TGATGGTG	708

(2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...525
 - (D) OTHER INFORMATION: /note= "KERATIN- TYPE II CYTOSKELETAL-intermediate filament"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

GTGGAAACTT TTCTTAGAAT TTTTGAAAAA GATATTTTTA ACACGCCCTA TAAATTAGAA	60
GTCATTAACG CTACTGAGGG GGGGGCTAGG ATTAAAGGGA CTAAAGAAAT GCCCTTTAAA	120
GAAGTGTGCG AAAAAWTAGA CAAATCCAAG CCAAAGCCTC CTATCAATCT TATTTATCCC	180
ACCCAATCAG AACAGGCTAA AAATTTAAAG ATCGCCAAGA AAAAATGCGA AGAGATCATC	240
AAATACGCCA ATGAGAAAAA AACGCAAGTT GAAGAAGCGT TTTTAAAGGT GGCAGAGTTT	300

TTAGAAAAAG TGGAAAAGCT TCATGAAAAA AACAAATTAG AAGAGTTGGA TTTTGAAGAA	360
TTAGAAAATT TGAGCGCTGA AATTGATAAC GTTAAAGAGC TTTTGTATGA CAAACGATTC	420
AATTCGTATT TTATGGATGC GATACAATCT TACATTTTCC ACCAGGAATT GCATATCGCT	480
GAAATCGTGT GTAAAAAAAC GAGTAATGAA GACGGGATTA AGGGC	525

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

ATGAAAACGC CTTGCAACGC CTATTTTCTC AAAACGCCAC CCAAAAACAA AAAAGAAGA	60
GTTTATGTTA ATTTAGCGGT GTTCTTTTTT TTATTGCTAG CGAGCGCTTT ATGGCTCATT	120
CCTAGAAGTG CCATAGAAGR AAAGCCCTTA GTCGTGGCGA CAAAACCTAG CAGCGAGCAG	180
TATATTTTGG GCGAAATTTT AAGCCTTTTG TTAGAAAAAC ACCATATCCC TATCAAGCGA	240
GCGTTTGGCA TTGGTGGGGG GACGATGAAT ATCCATCCGG CATTGATTAG GGGCGATTTT	300
GATTTGTATG TGGAATATAC CGGCACCGCT TGGGTGAACA CGCTCAAAAA CCCTTTGACT	360
CAAAAAGTGG ATTTTGAAAC GATTAAAAAG CGTTATGAGA AGGAATTTAA TCTTTTGTGG	420
GTGGGACTTT TGGGCTTTAA TAACACCTAT TCTTTAGCGA TTTCTAAAGA AGACGCTCAA	480
AAATACGCAA TTGAAACTTT CAGCGATTTA GCCTTTCATA GCCCGAATTT TGATTTTGGA	540
GCGGAGYTTG ATTTTGTGGA AAGAGAGGAC GCTTTTAAGG GCTTAATCAA AGCTTATCGC	600
TTTCATTTTA GAAGTTTGCA TGAAATGGAY ATTAATTTGC GTTATAAAAG TTTTGAATCC	660
CTCATAAGAT YAACGCTT	678

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

GTGATGGTTT ATAAACTCCC CAAACACCAG CAAAATAAGG TCATGATTTT AGGCTTGGGC	60
TTAGCGATGA TCACTCGTAT AGGGCTTTTA GGGAGCTTGT TTTTCATCAG CCATTTGCAA	120
AAGCCTTTAT TCGCTATAGC GGGCATGAGC TTTTCATGGC GTGATGTGGT GCTGCTTTTA	180
GGGGGGGCGT TTTTGGCTTT TAAGGCGTTA GTGGAATTAA AAAGAGCAGA TCTATCC	237

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 630 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

ATGTTTGTGG TTTTATAGA AGGTTTGGT TTAGCGATTT CTTTGTGCGC GCGGTGGGG	60
GCGCAATCCT TGTTTATTGT GGAAAGGGGG ATGGCTAGGA ATTATGTGTT TTTGATTGTC	120
GCCTTGTGTT TTATGTGCGA TATTGTCTTA ATGAGCATGG GCGTGTTTGG CGTGGGGGCT	180
TATTTGCTA AAAACCTTTA TTTGAGCTTG TTTTGAATT TATTTGGGGC AGTTTTTACC	240
GGATTTTACG CTTTTTTGGC TTAAAAACC CTTTTTCAA CCTTTAAAA AAAGCAAGTC	300
CAAACCCCTA AAAAATTATC CTTAAAAAAG ACCTTATTAT TCACTTTAGG CGTTACCTTA	360
CTCAATCCTC AAGTGTATTT GGAAATGGTG TTTTAAATTG GCGCGAGCGC TATGTCTTTT	420
AACCTAGTGC AAAAATTCGT CTTTCTAGCT GGCACCTTAT CGGCTGCCTT TTCTTGGCTT	480

TTATTGTTAT GCACCATGTC CTTACGCTAT GGCTCTAAAC TTTTGAACAA CCAAAAAATC	540
TTTATGGGCG TGAATCTCTT TGTAACCGCT ATCATGGGAA CGCTCAGCGT TACTTTATTC	600
AGGGATTTTT TAGCGTTATT GAGCAAAACC	630

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GTGAAGCCAA AGAGCATGAA AGAGAAGCTA AGAGGCGCTA TGGTGAATAT CTTAAGGATA	60
AAAATGATTG AAATAAGCGA ATGGTTGCAA AAAC TAGACG ATGCCTTAGA TAAAGTTGTT	120
GCTAAAAAAG AGCCAGAGAG TTTTCTCAAG CCGATCATT CACCAATAGA GGACTACCAA	180
AAGAGTGTC A GGCAAATTCA AGCGCAATTC ACAGACGCGC CGAAGTTCAA TGAAGAGGGT	240
GCTTACCCTC AATTTTTTAAG CTGTGGTTTA TTGCAAGTTA GGGGCAAAAA TGGTGCTAAC	300
ATGGAATTTT TATTGCCTAA AGTTTATCCT TTCCCCCTA AAAGCTTGTA TATAGAGCAT	360
GAAAAAGACG GGCAGTTTTT GAGAGAAATG CTCATGCGCT TACTCTCCAG CGCGCCTTTA	420
GTGCAATTGG AAGTGATCTT AATTGATGCG TTGAGCTTGG GGGGCATTTT CAATCTGGCC	480
AGAAGGCTTT TAGATAAAAA CAATGACTTT ATTTACCAGC AAAGGATTTT GACCGAAAGC	540
AAGGAAATAG AAGAAGCCCT AAAGCATTTG CATGAATATT TAAAGGTAA TTTGCAAGAA	600
AAATTAGCCG GTTTTAGAGA TTTTGTGCAT TATAATGAAA ACGCCAAAGA CTCCTTGCCT	660
TTAAAAGCGC TTTTTTTAAG CGGGGTGGAT GCTTTGAGTA AAGACGCGCT TTATTATCTA	720
GAAAAGATCA TCGTTTTTGG CTCTAAAAAT GGGGTTTTGA GCTTTGTCAA TTTGGAGAGC	780
GAAAAAACA ATCAATCCGC AGAAGATTTG AAACGCTATG CGGAGTTTTT TAAAGACAGG	840
ACAAGTTTTG AGTGSTTAAA ATACCTTAAT GTAGAAATCA TCAGCGAT	888

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

GTGCTTATAA GCGTGATGAT AGGCCAAAAT CAAGTCTTAG GCTTTATAGG GACTAATTTTC	60
AAGCAAGAAT TAGTCGTGGA TTTCATTGTC CCAAGCGCTG AAATCAACAT AGGCRRTCAA	120
GTGYTAACGA GCGGGCTAGA TGGGATTTTT GGAGCGGGGG TGTGTGTGGG TGAAGTTTCA	180
AGCGTTGAAG ATCATTACAC TTATAAAAGC GCGGTGTTGA AAAACGCTTT TTAAAGCGAA	240
GCCAAACTTT TAAGGCATGT GTTTTAAAGC GGTGTGAAAA AC	282

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

ATGGAAGCGC AATTACGATT TACGGGTGTT GGAGGGCAAG GCGTGTTGTT AGCGGGAGAG	60
ATTTTAGCTG AGGCTAAGAT CGTGAGCGGG GGCTATGGCA CTAAGACTTC CACCTACACT	120
TCGCAAGTGC GTGGAGGTCC CACTAAAGTG GATATTTTGT TAGATAAAGA TGAAATTATT	180
TTCCCTTATG CTAAAGAGGG CGAGATTGAT TTCATGCTTT CAGTCGCTCA AATCAGCTAC	240
AACCAGTTT	249

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

ATGCAAGCTT GGGTGGATAA GCCGGTATTG TTAGAGCCAG ATAGTAACGC CCAATACGCC	60
GCTGTCATTG AAATTGATGT GGCAGAAATC ACGGAGCCTA TTTTGGCATG CCCTAATGAC	120
CCTGATGACG TCGCTACTTT GAGCGAAGTT TTAGCGGATA CGACCGGCAA AAGACCCCAC	180
GCTATTGATG AAGTGTTTAT TGGCTCTTGC ATGACGAATA TTGGGCATTT CAGAGCCTTT	240
GGTGAAATCG TTAAAAACGC CCCTCCCACT CAAGCACGCC TTTGGGTAGT GCCACCCAGT	300
AAAATGGACG AACAAGAGCT TATTAATGAG GGCTATTATG CGATTTTTTG GGCTGCCGGG	360
GCAAGGACTG AAGTACCAGG CTGTAGCTTG TGCATGGGCA ATCAAGCGAG GGTTAGGGAT	420
AATGCGGTCTG TTTTTTCTAC TTCCACACGG AATTTTGATA ATCGTATGGG TAGAGGGGCT	480
AAAGTGTATT TGGGCAGTGC GGAGCTTGGG GCGGCGTGCG CTTTACTAGG GAGGATCCCC	540
ACTAAGAAG AATACATGAA TTAGTGAGT GAAAAGCTAG AGAGCCAAAA AGACAAGATC	600
TATCGCTMC	609

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GTGGGCAATG CCGGGGTGGC TTTAGCGGGT TTGATGAGCG ATGAAATTTA TTTGTGCGCT	60
TTAGATTGCG CTTATATCAA AGGGTTTAAA AAGCACGCTC AAAATTCCTA TTATGGAGAT	120
GAAAAAGAGA TTGACACCTC ATCTTTAATC AGCGTAGAGG GTAATGTTGA AGGTTATGAA	180
ACTTTTAGCG ACTCGCTTTT TTTGCTCTCT AAAGAAAGGA TTGAAGAAGC CCTTCATTAT	240
TACCAGCCTA AAAAAGTCTA TAATTTAAGC TATGGGGCGA AAATCAAGCA CGCCGTTAGC	300
CTCAATCACT CTCAAGTGAA ATTGAAACAA ATCAACAAAC AAGACGCTAT CGTTCGCATT	360
AAAAGCATGT TTAGCCCTAG AAGTAATCAT GCTAAGGATT TAAAAAATTT ACAAAAAAAT	420
CTGATTCGTT TTAAAGAGGA TTTTTCACG CATTTAAACA CGCCTTGTA Aaccaagcaa	480
GAAGCATTTG AATGGGTGGA TAGCTTGAGT GGATTTTGCC AAACAGCCAG CGCTAAAACC	540
CCCACTATAG GCATTTTATT TGAAGGGAGT GTCGCCATA TCTTACAAAG CGTTCTAATC	600
GTTTCATTGC ATCTTAAAGA AAATGAGCTG ACGCTTTTAT CAAATTCTCT CAAAACGCCT	660

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

ATGCAAAAAA GTATATTCAA AATAACTCTG TTGTTGGTTT TCCTCTTTT AAGGAATGCT	60
GTTGGTTTAG ACGATAAAAA AGCAGCTCCT AAAAGCGTTC AAAATACCCC TAAAAATTTA	120
CCCCCTATCC AGTTAAGGCT CGATCAAGCC TATGAAGACC TTATCAAAAT GTTAGACAAT	180
ATGGGAAAAA GCACGCAGTA TGAGTTCCCT AAAATTAAAG AAATCCTAGA ACAAAGCGAA	240
GAGGAATGGC TAGGAGTCGC CCATGAAGAA TGTGTGGCGT TAGTCATGTT AATAAGCCCT	300
AAGGCTTCTA TTGAAAACAG CCCGATTTAT AAGAATTGCT ATGAAGCTTA TGTGAAACAA	360

AGAATCCATG ATTTATATGA TTTTATATA GAGGGCAAAA AAGTGAAAAG AAAAATCAAG	420
AAAGCCCATG AGCATGAAAT GGCCCTCAAC AAATCCCAAC CCTTAAAAAA GGAACCGCCT	480
AAAAGCGAGA ATAAAAAGGG CTTAACAAAA CCTAGCTTGA AAGACGCAAA GATCCCTAAA	540
GGGTATTACT TGCAAATTGG GGCTTTTTTA AATTCGCCCA GTAAGGATTT TTTGCAAACG	600
CTCAAAACTT TCCCTCACCA AATGGAGGAA AAAGACTCCC TCACGCATTA TTTGATTGGC	660
CCTTATAAAA CCAAAGAAGA AGCCCTAAAA CAGCTTGAAA ATGCGGCTAA AAGCTTTAAA	720
AATAAGCCTG CGTTGGTAGA GAAG	744

(2) INFORMATION FOR SEQ ID NO:272:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

ATGCAAGAAA TCTTAATCCC TTAAAAAGAA AAAAGCTATA AAGTGTTTTT GGGGGAAGT	60
CCTGAAATAA AATTGAAACA AAAAGCGCTC ATCATTAGCG ATAGCATCGT GGCCGGGTTG	120
CATTGCCCCT ATTTGTTAGA GCGCTTGAAC GCCTTAGAAG TCAGAGTGTG CGTGATAGAG	180
TCCGGGGAAA AATACAAAAA TTTTCATTCA TTAGAGCGGA TTTTAAACAA CGCCTTTGAA	240
ATGCAATTAA ACCGCCATTC TTTAATGATA GCCCTTGGTG GGGGAGTGAT AAGCGATATG	300
GTGGGGTTTG CGAGCAGTAT TTATTTTCAGG GGGATTGATT TTATTAATAT TCCCTACGAC	360
TTTACTCGCT CAAGTGGATG CGAGCGTGGG GGGGAAAACA GGGATCAACA CGCCTTATGG	420
CAAGAACCTA ATCGGATCGT TCCACCAGCC	450

(2) INFORMATION FOR SEQ ID NO:273:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 561 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...561
 (D) OTHER INFORMATION: /note= "UDP-N-ACETYLMURAMYL-TRIPETIDE SYNTHETASE"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

ATGCGAATAC TTCATTATGG AGGTGAGCTC CCATGCGATT GTCCAAAACG CATCGCTGGG	60
CTTGATTTTCG CTCTTAAAAT TCTCACCAAT ATCACAAGCG ATCATTTAGA TTTCCATCAA	120
AATATAGAAA ATTACAGGGA CGCTAAAAAC AGCTTTTTTTA AAGATGAGGG CTAAAAAGTC	180
ATCAACAGAG ATGAAACAAA CGCCCTTTTTT AACCCCATTA ACGCGCGCAC TTACGCACTG	240
GATAAAAAAG CGCATTTGAA TGTTCAAGCC TTTTCGCTCA ACCCTTCCAT TAGCGCGTCT	300
TTATGCTACC AACACGATTT AAGAGATCCC AATCTTAAAG AAACCGCCCT GATCCATTCC	360
CCCCTTTTAG GCGGTTACAA CCTTTATAAT ATTTTAGCGG GCGTTTTAGG GGTAAATTG	420
CTCACTCAAT TGCCTTTAGA AACGATCGCA CCGTTATTGG AAAACTTTTA TGGGGTTAAG	480
GGGCGTTTGG AAATTGTACA TTCTAAACCT TTAGTGGTCG TGGATTTTGC CCACACAACA	540
GACGGCATGC AACAAGTTTT T	561

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 594 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1...594
(D) OTHER INFORMATION: /note= "PREPROTEIN TRANSLOCASE SECA SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

GTGAGCATT AAGAAGAGAG CCAAACCTTA GCCGATATTA CTTTCCAAAA TTATTTTCAGG	60
ATGTTTTCTA AACTTTTCAGG CATGACAGGC ACGGCTCAAA CCGAAGCCAC AGAATTTTTA	120
GAAATCTACA ATTTAGAAGT GGTGTCCATC CCTACTAATC TAGCGATCAA GCGAAAAGAT	180
TTGAACGATC TGATCTATAA GAGTGAAAAA GAAAAATTTG ACGCTGTGAT CCTTAAAATT	240
AAAGAATTAC ACGATAAGGG TCAGCCCGTT TTAGTCGGCA CGGCTAGCAT TGAAAAGAGT	300
GAAACCTTGC ACGCTTTACT CAAAAAAGAG CGCATCCCTC ACACCGTTTT AAACGCCAAG	360
CAACACACTA AAGAAGCTGA AATCATCAAA GACGCCGGGC TTAAAGGGGC GGTACGATT	420
GCGACCAACA TGGCAGGCAG GGGCGTTGAT ATTAAGCTCA CTGATGAAGT TAAAGAACTT	480
GGGGGGCTGT ATATCATTGG CACTGAAAGG CATGAGAGCC GTAGGATTGA CAATCAATTA	540
AGGGGGCGAA GCGGGCGTCA AGGCGATCCG GGAGTGAGTC AGTTTTATTT GAGC	594

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 624 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1...624
(D) OTHER INFORMATION: /note= "putative chemoreceptor"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GTGGTGGCTG ATGAGGTGAG AAAGCTCGCT GAAAAAACCC AAAAAGCCAC TAAAGAAATC	60
GCTGTCGTGG TTAAAGCAT GCAACAAGAA GCGAACGATA TTCAAACCAA CACCCACGAT	120
ATTAATTCTA TTGTAGGCTC TATTAAGGGT GATGTGGAAG AGCTTAAATC CACCGTAAAA	180
AATAACATGA TTGTCGCGCA AGCCGCAAAA TACACCATCT ACAATATCAA TAACCGGGTG	240

TTTTGCGGTY TGGCTAAACT CGATCATGTG GTCTTTAAAA ACAATCTTTA TGGCATGGTG	300
CSTTTGGTCT CAATTCCTTT GACATTACCA GCCCATAAGA GTTSCCGTTT AGGCAAATGG	360
TATTATGAGG GTGCGGGTAA AGAAAACTTT GCTAACACTT CAGGCTATAG AGCTTTAGAA	420
AGCCACCATG CGAGCGTGCA TGCTGAAGCT AATGATTTGG TTAAAGCCGT TCAAGAAGAT	480
CACGTCACCG ATTCAAAATA CCTAGAACAT AAAGTGCATT TAATGGAAGA TAGCGCTAAG	540
CATGTCAAAG AAAATATTGA TAAGATGTTT TATGAAAAAC AAGATGAACT CAATAAAATC	600
ATTGAAAAAA TTCAAAAAGG CGAA	624

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 603 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

ATGAATACAT CAAAAAATT AGGTAACCCC TTGCTTTTTT TGCATGATAA TAAATTTTG	60
TTGTTTGTCTG TAGGGGTGAG CATGGGCGGG TGGGCCACTT CTAAATCTA TCAATTTGAA	120
AGCGCTTTAG AGCCGATTCA TTTTAAGTTT GCGCGAAAAC TCTCTTTAAG CCCTTTTTTA	180
AATTTGAGCC ATTTAGTAAG GAATAAGCCT TTAAACACCA CTGATGGCGG GTTTATGCTA	240
CCACTCTATC ACGAATTAGC CACCCAATAC CCCTTGTTGT TGAAATTTGA CCAACAAAAT	300
AACCCAAGAG AGCTTTTAAG GCCTAATACC TTAAACCACC AGCTCCAACC AAGCTTAACC	360
CCCTTTAAAG ACTGCGCTGT CATGGCGTTT AGAAACCATT CTTTAAAGA TAGCCTCATG	420
CTAGAAACCT GTAAAACCCC CACTGATTGG CAAAAACCCA TTTCTACAAA TCTTAAAAAC	480
TTAGATGATT CTTTAAATTT ACTCAATTTA AATGGAATAT TGTATTTGAT CCACAACCCCT	540
AGCGATTTAT CACTGCGTCG TAAAGAACTT TGGCTTTCTA AATTAGAAAA CCYYCAACTC	600
RTT	603

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT TTGCCTTCCT	60
GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA	120
CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC	180
GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC	240
CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG	300
GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA	360
YGCWGGTGGT GCCATAACCA T	381

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

GTGAACGTGG GCGTGCCTTT TAGCTATCAA GTGAGCGCGA CCTTTCAAAA CTCACGCCTT	60
TCTAGTTTGC TAGAACTTT AAAAAAGAGT TTTTtagaaa AGCCCTTAAT TGAGAGCAGC	120
GCGAATAAAA TCGCGGATAT TTTTtctaaa GCGGTGTTGT TTTTAGCCTT TGTGAGCTTT	180

TTATTGTGGC AATTTGGTTT GGGGGGTAAT TTTGAAAAAS GCTTTAATGG TGTGTAT

237

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...147
- (D) OTHER INFORMATION: /note= "antigen [*Entamoeba histolytica*]"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

ATGCTAATGG TTAATGGCTA TCAAATCACG ATGCATAAGG GTTATAAGGT AGGGTTTTTTT	60
ACAAGCGGTT ACAACCCTGA TTTCGCTCAA ACCATTCAAA ATAGAAGCTA TTTGATGAGC	120
TCTTATGAGT TATCGTTTTT AAGAAAT	147

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

ATGGTGCAAT TTCAAAACAC GCTTATAAAA TTCCATGCCC TATCCTTTAA AAACGCAAAT	60
TTAATTTATA ATGCAAAATT AAACAAAACA TGCTATAAAG AAAATTCAAA TACTATCATT	120

TTAAGGATTA AAATGCTCAC CCAAGAAGAT GTCTTAAACG CGTTAAAAAC GATCATCTAC	180
CCTAATTTTG AAAAGGATAT TGTCAGCTTT GGTTTTGTTA AAAACATCAC CTTGCATGAC	240
AACCAATTAG GGCTTTTAAT AGAAATCCCC TCAAGCTCTG AGGAAACGAG TGCGATTTTA	300
AGGGAAAATA TCTCCAAAGC GATGCAAGAA AAAGGCGTGA AAGCTTTGAA TTTGGATATT	360
AAAACCCCGC CTAAACCGCA AGCTCCAAAG CCCACCACTA AAAATCTGGC TAAAAACATC	420
AAGCATGTGG TCATGATAAG CTCAGGCAAG GGCGGTGTGG GTAAAAGCAC CACCAGCGTG	480
AATTTAAGCA TCGCTTTAGC GAATTTAAAC CAAAAAGTGG GGCTACTAGA CGCTGATGTG	540
TATGGCCCTA ATATCCCTAG AATGATGGGC TTGCAAAACG CTGATGTGAT CATGGATCCT	600
AGCGGTAAAA AACTCATTCC TTTAAAAGCT TTTGGCGTTT CTGTGATGAG CATGGGGCTT	660
TTGTATGATG AGGGGCAGAG TCTCATTTGG AGAGGACCCA TGCTCATGCG AGCGATTGAG	720
CAGATGCTAA GCGATATTAT TTGGGGGGAT TTAGACGTGC TGGTGGTGGA TATGCCCCCA	780
AGGAACAGGC GATGCGCAGC TCACGCAGCC CAAGCCGTGC CACTCAGCGC AGGAATCACC	840
GTTACTACGC CTCAAATCGT GAGTTTAGAT GACGCTAAAC GGAGTTTGGA CATGTTTAAG	900
AAACTACACA TTCCTATTGC GGGCATTGTA GAAAATATGG GGAGTTTTGT GTGCGAGCAT	960
TGCAAGAAAG AGAGCGAGAT TTTTGGCTCA AATTCCATGA GTGGATTATT AGAGGCTTAT	1020
AACACGCAGA TTTTAGCCAA GCTCCCTTTA GAGCCTAAAG TCGTCTAGG GGGGGATAAG	1080
GGTGAACCGA TTGTGATTTT TCATCCCACT AGCGTGAGTG CTAAAATTTT TGAAAAAATG	1140
GCAAAGGATT TGAGTGCTTT TTTAGACAAG GTGGAAAGGG AAAAACTAGC CGATAATAAG	1200
GACATCCAGC CCACACAAAC GCATGCTTAT TCGCAT	1236

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

ATGGGTGTGG TGATTGGCGA GACCACAGAG ATTGGAGATG ATGTTACCAT TTATCATGGC	60
GTAACCTCTGG GGGGTACGGG CAAGTTTAAAG GGCAAACGCC ACCCTACTTT AGGCAACCGA	120
GTGGTAGTTG GGGCAGGGGC TAAGGTCTTG GGC GCGATTT GCGTGGGCGA TGATGTGAGG	180
ATTGGGGCTA ATGCGGTGGT GCTTTCAGAT TTACCCACGG GTTCTACGGC TGTAGGTGCT	240
AAAGCCAAAA CCATCACAAA GGATCGT	267

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

ATGCTATCTT TTATAAGCGC GTTTGATAAA AGGGGCGTTT CAATACGCCT TCTAACAGCC	60
TTGTTACTGC TTTTGTAGTTT GGGTTTGGCT AAAGATTTAG AAATCCAAAC TTTTGTGGCT	120
AAATACCTTT CTAAAAATCA AAAAATACAA GCCCTACAGG AGCAAATTGA CGCTTTAGAT	180
TCTCAAGAAA AAGTCGTTAG CAAATGGGAT AACCTATTT TGTATTTAGG CTATAACAAC	240
GCTAACGTGA GCGATTTTTT CAGGCTGGAT AGCACCTTAA TGCAAAACAT GAGCTTGGGT	300
TTGTCTCAAA AAGTGGATTT AAATGGTAAA AAATCTACGC AGTCTAAAAT GATCAATTTA	360
GAAAAACAAA AAAAAATATT AGAGCTTAAA AAAACCAAGC AGCAATTGGT GATTAATTTA	420
ATGATAAACG GCATTGAAAA CTATAAAAAC CAACAAGAAA TAGAGCTTTT AAACACAGCG	480
ATTAAAAATT TAGAAAACAC CCTCTATCAA GCCAACCATT CCAGTTCGCC CGATTTAATA	540
GYGATYGYCA AGTTRGAAAW TTTAAAAATC GCCAWT	576

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

GTGCCGGCTG TTGGGGGGGC TTTGATTGG ATYCYTATAG YGATTTATGA GCTTTATCAT	60
GGGYATGTGA ATGAGGYTAT TTTTAYYGT TTGTATTCCA TTTTGTTAAT TGGTGTGTTG	120
ATTGATAGCG TGATCAAGCC AATTTTAATC GTTTTTATCA AAAAAAGAAT CTTTAAACC	180
ACCCTTAAAA TCAATGAAAT ATTGATTTTC TTTTCTATGA TTGCTGGGAT TTCTCAATTT	240
GGTTTTTGGG GGATTATCGT AGGCCTACC ATCACGGCGT TTTTATCGC GTTACTGCGA	300
TTGTATGAAA ATTACTTTAT TCAAAAGGAG CAAAAACAT GCGAATGT	348

(2) INFORMATION FOR SEQ ID NO:284:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

GTGGTTGTCA TTATTTTAGT GGTCGTTATC ATTCAAAACA GCTCTTCTTT AAAAGAAGAG	60
AGAGAGCAAG AACGCGCTAT TAAGCCCGAC ACCAAAAATA ATTCTTTCAA TGAAACTAAT	120
CCTACAGAAG AAAAAAGTT AGAGCCAACG CCTAAATTAG AAGAAAAACA CAAAGAACAA	180
GACAAGCAAG GCAAAGAAGC GATCAAAGAA AATCCTAATA CCATTTACAT TATCCCTAAA	240
CGAGATATTT GGGTAGAAGT GATTGATTTA GATGAGAAAA AAAACTCTTT TCAAAAGGTT	300
TTTAAAAAAA GTTATCCTTT AGAGGCTAAA AACCACCGCT TGTTGTTACG CTTTGGGCAT	360
GGGCATCTTA TTCTTAAAA CAACCATCAA GAACAAGATT ATAACGACAG CAAAACTAGG	420

CGGTTTTTAT ACGAGCCAAA TAAAGGTTTA ACGCTCATCA ATGAGGCCCA ATACAAAGCG 480
CTCCAGCAA 489

(2) INFORMATION FOR SEQ ID NO:285:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...120
 - (D) OTHER INFORMATION: /note= "HAEMOLYSIN SECRETION ATP-BINDING PROTEIN"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

ATGGATGAAA TCTATCAAAT CGCTAAAAAT AAAACCCTAA TCGTTATCGC CCACCGCTTA 60
AGCACGATTG AACGCTGTGA AGTCATCATT GACATGAGCC AACACAAAGA CAATCTCGGC 120

(2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

GTGGCGGGCA GCTTTATTAT TGCTCTTTTT AGCGTTTTAG CGGATCAATT TGTGAGCGTG 60
TTTCAGCATG AAAACGCCTT GCAACGCCTA TTTTCTCAAA ACGCCACCCA AAAACAAAAA 120

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

ATGGTAGCTT TAAGCAACGC TCTTTCAAGG GTTTTTGGTT CTGTGGCTGG CTATAAATTC	60
CCTTCTTTTA TCCAAAAAAG CATCAACGCT CTTTATGTTA AGATCTTTAA AATTGATTTG	120
AGCGAGTTTG AGCCTTTAGA AAATTATAAG AGTTTGAACG CTCTTTTCAT GCGCTCTTTA	180
AAAAAAGAAC GCCCCTTTGA CAAAGCCCCT ATATTTGCAT TGCGCCTTGC GATGGCTTTA	240
ATCACTGAAT GCGCTTTTTT AGACAACGAT AGCGCTTTAC AAATTAAAGG CATGCCCTAT	300
AAAGCGCATG AATTAGTGGG CGAAATCAAC CCCTTAAGCC CTCTTTTTTC TATG	354

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

ATGGCAGTGT TAAAAAAGAT GATAGGTTTG GTGGCGGTTT TAAGCGTTTT ATTAGCCAGA	60
GACAACCCTT TTGAGCCTGA AATCAATTCC AAGAATTTGC AAGGGGGCTT TAGCGGGATC	120

TATGATGACT ACCTCAAAGA AATCCATGTG GATTTGCCCA CGAGCGCTAG GATCTTAAAA	180
AAAATCACGC TCACTTACCA AGATATTGAT GGCTCTATCC ATTCTAAAGT CGTGGGTATT	240
GATAAAAGCA TTGATTGGCA CTACCCCTTA AAACCTTTCCC AACACACCCT TAATCAAGAC	300
GCCTTTGAAA AACGCTACCA GATCCAAGAT TTTGATTTTT TAATGGCAAA CAACACGATG	360
ATTTTGCGTT CCCCTTATAA AATTTTGCGC TCTTTTGTGT TAGTCAATCC TTATAGAATC	420
GTGTTAGACA CGCAAAAAGG CCCTTTGGAT ATTTATCAAA ACATGGATTT AAACCAGAAG	480
TTTTTTTCTC ACATTAAAGT CGGCACGCAC AAAGATTATT ACCGCATCAC GCTCATTTTA	540
GACGGGAAAT ACCGCTATCT TTTGGAAGAA AAAAACGGGG CGTATGAATT AAAACTGAAA	600

(2) INFORMATION FOR SEQ ID NO:289:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

ATGGGCGGAT TCACAAGCAT ATGGCATTGG GTCATTGTTT TATTAGTGAT TGTGTTGTTA	60
TTTGGGGCTA AAAAGATCCC AGAATTGGCT AAAGGTTTAG GCAGTGGGAT TAAGAATTTT	120
AAAAAAGCCG TGAAAGACGA TGAAGAAGAG GCTAAAAACG AGCTAAAAAC CCTAGACGCT	180
CAAGCAACAC AAACCAAAGT GCATGAAACT AGCGAAATTA AAAGCAAACA AGAAAGT	237

(2) INFORMATION FOR SEQ ID NO:290:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 618 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

GTGCGTTTGA ATGCGGCGGT TGTGGTGGAT GGCAAGTATA AAATCGCGCT CGAAGACGGG	60
GCAAACGCTT TAGAATACGA GCCTTTAAGC GATGAATSGS TTAAAAAAT CAACGYCCTA	120
GTCAAACAAG CCATTGGTGA TAACCAAAAT AGAGGCGATG ACGTGGCGGT GAGTAATTTT	180
GAGTTTAACC CTATGGTGCC TATGATTGAC AACGCCACCT TGAGTGAAAA AATCATCTAT	240
AAAACCCAAA AAATTTTAGG TTTATTTATG TTTTTAATCA AGGTATATTT GGTGTTTATA	300
GTGTTATTCA TTTTCTATAA AAAAGTGATC GTGCCTTTCA GCGAACGCAT GCTGGAAGTG	360
GTGCCTGATG AAGATAAGGA AGTGAAATCC ATGTTTGAAG AAATGAACGA AGAAGAAGAT	420
GAGTTGAACA AACTCGGCGA TTTGAGGAAA AAAGTAGAAG ATCAATTAGG GCTTAATGCA	480
AGCTTTAGCG AAGAAGAAGT AAGATATGAA ATTATTTTAG AAAAGATTAG AGGAACCCTT	540
AAAGAGCGTC CTGATGAAAT CGCCACGCTC TTAAACTCT TAATCAAAGA TGAAATCTCT	600
TCAGACAGCG CGAAAGGT	618

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

GTGTGTTTTA TATTGCCTTT TTGTTTAGGG GTTTTAGGCA CGCAAATCTT TAAACAAGAG	60
ACCCCAAGAC AGCTCCCTAT CGTGGTGGTG GATTTGGATA AGACCACTAC AAGCCATCAA	120
GTGGCGTTTG AATTAGGCGC AACGAGTGCG GTTGAAATCA AATACCAAGT GACTAGCCTT	180
TCAGAAGCTA AACGCTTTTT AACTCCGCT GAAGTGTATG GGGCGTTAAT TTTGCCTAAG	240
GATTTGGAGA GAAAAATCAA AATGGGGCGA AAAGTGSAT TTGCCCTTTT ATTA	294

(2) INFORMATION FOR SEQ ID NO:292:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 591 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

ATGAAAGGCT TATGGCTTGT AATCTCTTTA GTTTTTGTTG GTTTTTTGTG GGCTAATGAA	60
TCTTATGTTT TTAACAATTC TAAGGGGCGT TTAACAGAAA AAAGCGTTGC GTTTATAGAG	120
GGCGTTTCTA AAGAGCTTTA TCTTAAACC GGC GTGCGTT TTGCGATTGA TATGACGGAT	180
TTTGAAAAAA ATCCTATCGC TCTAGCGAAT AAAAAAGAGC GCCAAAGCTA TCAAGAGGGC	240
TTTTTAAAGC AGCTCAAACC CCCTTTTGTG GTATTCTTTT TCTACCATGA CGCTCAAAAA	300
ATAGAATTAG TGGCTAACCC TAAAGATTTG CTAGACACTG ATAAAATCTT TTTTGAAAAA	360
ATCGCTCCCT TACTCCCCAC AAACGCTAAA GAATACACGC CCCAAAGAAT TTCAGCCATG	420
CTCATTAACG GCTATTCGGT CGCAGTAGAT GCTTTAGCGG AAAAATATCA TGTGAATATC	480
ACGCAAAATT TTAGCGCTCC TAAGGGAGTA ACTTTTGTA AGGTGGTTAT TTATATTTTG	540
TTATTGACGC TTTTGGGCGC GTTTTTGGGG CTTTATTTTT TTAAAAAATC T	591

(2) INFORMATION FOR SEQ ID NO:293:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

ATGTGTTCTA AAAAAATAAG AAATCTCATT TTATGCTTTG GTTTATTTT AAGCTTGTGC	60
GCTGAAGAAA ATATCACCAA AGAAAACATG ACTGAAACGA ACACGACTGA AGAAAACACC	120
CCTAAAGACG CTCCCATTCT TTTGGAAGAA AAACGCGCCC AAACCTCTAGA GCTTAAAGAA	180
GAAAATGAAG TGGCAAAAAA GATT	204

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

GTGCTAAAGA CATTATCCAT ACGATTAGTC ATACTTTTAA ATTGCTCCCT AGCGACAAAC	60
GCTTGCAAGTG GGGTGCAAAA ATTGCGCGAT GAAAGCCACC GGTATGCGAT AAACCTCCAT	120
AGATCCACTA AACTTAAAAA CATGAAACAA ATCGCTCTTT TAAAAGAAAA GGGCATAGGA	180
GAAGCCAGCG TGAAAAAATT GTTGGATTAT TTTGGGAGTT TTGAAGCGAT AGAAAAAGCG	240
AGCGATCAGG AAAAAAACGC CGTTTTAAAA AAACGAAAA	279

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...219
- (D) OTHER INFORMATION: /note= "SULFATE TRANSPORT ATP-BINDING"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GTGGGCATTA TTAGGGGGAT TATCCACAGG CCAGAACTCA TTTTATTAGA TGAGCCTTTT	60
AGCGCTTTAG ATAGTTTGAA TCGTAAGAAT TTACAGGATC TCATCAAAGA AATACACCAA	120
AATTCTTGCG CTACTTTCAT TATGGTAACG CATGATGAAA ACGAGGCGCA AAAGTTAGCC	180
ACAAAAACCC TAGAAATCAA AGCCCTTAAA CAAGAGCAG	219

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

GTGATTTTTTA TCGCTACCGC TAATAATATT GACAGGATCC CAGCTCCTTT AAGAGACAGA	60
ATGGAATTTTA TCAGCGTGTC CAGCTACACG CCTAGCGAAA AAGAAGAGAT CGCTAAAAAC	120
TACCTCATCC CCAAGAATT AGAAAAGCAC GCCTTAAAGC CTAGCGAAGT GGATATTAGC	180
CATGAATGTT TGAAACTCAT TATTGAAAAA TACACCAGAG AAGCGGGCGT TAGGGATTTA	240
CGAAGACAGA TCGCAACGAT TATGCGTAAA GCGGCTTTAA AATACCTAGA AGATAACCCG	300
CACAAAAAAG GCGGACCAA AAAAAGCGAA GACAAAGATA AAAAAGGCGG AAATGAAGAA	360
AACGAAAAAA GAGGTGAGAG TAAAGATTTT TGCGTCTCTA TCACGCCTGA TAACCTTAAA	420
GAGTATTTAG AACGCATGGT GTTTGAAATT GRCCCCATAG ATGAAGAAAA TAAAATCGGT	480
ATCGTCAATG GCTTGGCATG GACTCCAGTG GGCGGTGATG TGCTTAAAAT TGAAGCGGTT	540
AAGATTAGAG GCAAGGGGGA ATTGAAACTC ACCGGGAGTT TGGGCGACGT GATGAAAGAA	600
TCCGCCATTA TTGCCTTTTC TGTTGTCAAA GTCTTGTTGG ATAACGAAAC CTTAAAAGTG	660
CCTAAAATCC CTAGCGAGAC CGATGCAGAG AATWAGAAAA AGAAAAAAGT GCTGAAAGTT	720

TWWAACGCTT ACGATTGCA CTTGCATGTC CCTAAGGGGC TACGCCTAAA GACGGCCCCGA	780
GCGCTGGGAT CGCTATGGCG AGCG	804

(2) INFORMATION FOR SEQ ID NO:297:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

ATGGGGTGTT CGTTTATCTT TAAAAAAGTT AGGGTTTATT CTAAATGTT GGTGCTTTG	60
GGGCTTTCAA GCGTGTGAT CGGTTGCGCG ATGAATCCAA GCGCTGAGAC AAAAAACCA	120
AATGACGCCA AAAACCAACA ACCAGTTCAA ACTCATGAAA GAATGACAAC AAGTTCTGAA	180
CATGTTACGC CACTAGATTT TAATTACCCG GTGCATATTG TTCAAGCCCC ACAAACCAT	240
CATGTTGTAG GTATTTTAAT GCCACGCATT CAAGTGAGCG ATAATCTAAA ACCCTATATT	300
GATAAGTTTC AAGACGCTTT AATTAATCAA ATCCAACTA TTTTGAAAA AAGAGGCTAT	360
CAAGTGTTGC GTTTTCAAGA TGAAAAAGCT TTGAATGTGC AAGATAAGAA AAAGATTTTTT	420
TCCGTTTTGG ATTTGAAAGG GTGGGTAGGA ATCTTAGAAG ATTTGAAAAT GAATTTAAAA	480
GATTCCCATATA GTCCCAT	498

(2) INFORMATION FOR SEQ ID NO:298:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

ATGGATAGAA AACTCTTAAG ATTATACCAG CCCTTAAACG CTTATTCTTA CAATAGCGAT	60
TCGCTTTTTT TATACGATTT TTCACGCCCT TTTATCAAAA ATAGCGGCGC GATTTTAGAC	120
ATAGGCTCAG GGTGTGGGGT TCTAGGCTTG CTCTGCGCTA GAGACAACCC GCTAGCGAGC	180
GTTCAATTTAG TGGAAAAGGA TAGCAAAATG GCGTTTTGCT CCCAAAAAAA CGCCCTTAAA	240
TTCCCTAACG CTCAAGTGTT TGAGAGCGAT TTTTATAGATT TTAACCCTCC GATTTTGTAT	300
GATGCGATTG TGTGCAACCC TCCTTTTTAT GCTTTAGGAT CTATTAAATC TCAAATTAAA	360
GGGCATGCGA GGCACCAGAG CGAATTAGAC TTCGCTTCTT TGGTGGCTAA AGTGAAAAAA	420
TGCCTGAAAC CC	432

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

ATGTTGAGTG CGTTGGTGAT GCTGCCTTTT ATGGAGGTTT TTTATTATTT CAATTTTCCG	60
TTGTGGCTCA ATCTTTTCTT AGGGCAAACC ATTGGAGCGG TGATTTTTTTT CAAGTTGGAT	120
AAGTTGATTT TTTCTAAAAA A	141

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

ATGAATACTA TTATAAGATA TGCGAGTTTA TGGGGCTTGT GTATTACTCT AACTCTAGCG	60
CAAACCCCCT CTAAACCCCC TGATGAAATC AAGCAAATCC TTAACAATTA TAGCCATAAG	120
AATTTAAAGC TCATTGATYC GCCGACAAGT TCTTTARRAG CGACACCGGG TTTTWWCCC	180
TCGCCTAAAG AAACAGCGAC CACGATCAAT CAAGAGATCG CTAAATACCA TGAAAAAAGC	240
GATAAAGCCG CTTTGGGGCT TTATGAATTG CTAAAGGGGG CTACCACCAA TCTCAGTTTG	300
CAAGCGCAAG AACTCAGTGT CAAGCAAGCG ATGGAAGAAC CACACCATCG CCAAAGCGAT	360
GTTTTTGCCT ACTTTGAACG CGAGTTA	387

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

ATGGTTTTGT TTCTATCCAT TTTTAAAAA AGCTTTAATG ATTTTTTAAG CGCTAGAATG	60
CTTTTAATCA ATCTTGGCCC TATCCTTTTG AGTTTGGCGT TTTTGGGAGC TATCTTTTAT	120
TACAATGGCG GGAGTATTGT GAATTATTGC CAACTTTAT TACCGCAATC TTTGAATGAT	180
TACGCTCATT CTCAAGGCTT TTTGCCGGT GTGTTCGCAT GGGTTTTTAA AGCGTTAGTG	240
TATTTTCTTA TTTTGGGAT CGTAATTCTT TTGAGTTTAG TCATCAATAT TTTGCGTCT	300
ATTTTTTACA CCCCTTTAGT GGTCTCTTAT TTGCACCAA AATATTATCC CCATGTCGTT	360
TTAGAAGAAT TTGGCTCTAT CCTTTTTTCT ATTAAATATT TTTTAAATC GCTCACTTTT	420
ATGCTTTTAT TCTTAGCGGT TTTAACGCC CTTTATTTC TCCCTTTAT AGGGGTCTTT	480

GGGGTCTTTT TTTCTATAGT CCCGCATTTC CYCTTTTTC AAAAAACACCAT GAGTTTGGAT	540
ATAGCCAGCA TGATTTTCAA CCATCAAAGC TATCAAAATT TACTCAAACA GCACCGATTG	600
AAGCATTATC GTTTTTCGTT TTTTGTCTAT CTTTTTTCCT TGATTCCTTT TTTTAATTTT	660
TTTGCCACCT TGTGCAAAC CCTAAYGCTA ACGCACTACY TTTTATCTT TAAAGAGAAA	720
GAATGC	726

(2) INFORMATION FOR SEQ ID NO:302:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...378
 - (D) OTHER INFORMATION: /note= "flagellar protein flis"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

ATGCAATACG CTAACGCTTA TCAAGCCTAC CAGCATAACC GAGTGAGTGT GGAATCCCCG	60
GCAAAACTCA TTGAAATGCT TTATGAAGGG ATTTTAAGAT TTTCTTCGCA AGCCAAACGC	120
TGTATTGAGA ATGAAGACAT TGAAAAGAAG ATCTATTATA TTAATAGGGT TACGGATATT	180
TTCACGGAGT TGTGGAATAT TTTAGACTAT GAAAAAGGGG GGRAAGTGGC GGTGTATCTT	240
ACAGGCTTAT ACACCCATCA AATCAAAGTT TTAACGCAAG CCAATGTGGA AAATGACGCG	300
AGTAAGATTG ATTTGGTGTT GAATGTGGCT AGGGGGTTGT TAGAGGCATG GAGGGAAATC	360
CATTCAGATG AACTCGCC	378

(2) INFORMATION FOR SEQ ID NO:303:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 429 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

ATGATGTTTG ATAACACGCT TATCAATTTA TTTGAGACAG CGCCTCTTTT AACYTCGCTT	60
TTAGCTGGGA TTTTAACTTT TTTAAGCCCT TGC GTGTTGC CTTTGATCCC GCGTATATG	120
TCTTATATTT CGCAAATTC TTTAGAGGAT ATTAAAGATG GTAAGGCTAA AAGGGTTTCG	180
GTTTTTTTAA AATCCTTGAT GTTTGTGGTG GGGTTTTTCGC TCGTGT TTTT GGGCGTGGGC	240
ATGTCTATGG CCAAGCTTAT CCATAGCTTT TCGTTTTCTT GGGTGAATTA TATCGCTGGG	300
GGGATTGTGA TCCTTTTTTG TTTGCATTTT TTAGGCGTGT TTCGTTTTGC ATTTTGTAT	360
AAAACCCAAA GCGTTGGTTT AGCGAGCAAA TCTAACAGCA TGCAGCGCTT TACCCCTTTC	420
TTTTTGGCA	429

(2) INFORMATION FOR SEQ ID NO:304:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...252
 - (D) OTHER INFORMATION: /note= "Plasmodium falciparum gametocyte specific antigen"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

GTGCTGGTGG TGGGCAAACC CAACGAAAGC TATGCAGATA CCCACGCCCG CATTGAGCAT	60
TTTATCAAGC TTGTAGATTT TAAGGGCGAA ATCGTTTTTA TCAATGAAGA TAATTCTAGC	120

GTAGAAGCTT ATGAAAATTT AGAGCATTTG GGTAAGAAAA ATAAGCGGAT CGCTACCAAA	180
GATGGCCGGT TAGACTCTTT GAGCGCTTGT AGGATTTTAG AGCGCTATTG CCAGCAGGTT	240
TTAAAAAAGG GC	252

(2) INFORMATION FOR SEQ ID NO:305:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 465 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

ATGCGGATAT TAATTCTCAA AAACAAGCCA CCAACGCTAC GATCAAAGGC TTTGACGCGC	60
TCTTGGGGTA TCAATTTTTC TTTGAAAAAC ACTTTGGCTT ACGCCTTTAT GGGGTTTTTT	120
GACTACGCTC ATGCCAATTC TATTAAGCTT AAAAACCTA ACTATAATAG CGAAGCGGCG	180
CAAGTGGCTA GTCAAATTCT TGGGAAACAA GAAATCAATC GTTTAACAAA CATTGCCGAT	240
CCCAGAACTT TTGAGCCGAA CATGCTCACT TATGGGGGGG CTATGGACGT GATGGTTAAT	300
GTCATCAATA ACGGCATCAT GAGTTTGGGG GCTTTTGGCG GGATACAATT GGCCGGCAAT	360
TCATGGCTTA TGGCGASACC GAGCTTTGAG GGCATTTTAG GGGAACAAGC CCTTGTGAGC	420
AGAAAGCCAC TTCTTTCCAA TTTTATTCA ATGTGGGGGC TCGCM	465

(2) INFORMATION FOR SEQ ID NO:306:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

ATGAATGTCA	AAAAAAGGA	AAAGCCACAA	AGTGGAAAGA	TTGATAGGGT	GGATTGTTTG	60
GAGAAACTTG	GGAAAGAAAA	CACTACTTTT	TTAAGCAGTA	TAGCTATGGG	GAGCATTGGT	120
CAATTAGCGA	TCCCCATTCC	TGGAGTTGGA	GTGCTCATTG	GGGGCTTTGT	GGGTGGGGTG	180
ATGAGTAAAA	CTTTTTATGA	TGTCTCGCTA	ACGATTTTCA	AAGAGGCTAA	ATTAGCGCGT	240
CAAAGGCGTA	TTGAGATTGA	AAAAGAATGC	CGTGAGAGTA	TCAGACAGTT	AGAGATGTAT	300
CAAAATCAAT	TTAATGAAGT	GTTTGAGCGG	TATTTTCATG	GGACTATAAA	ATTCTTTAAT	360
GAAAGTTTTG	ATGAGCTGGR	GAGGGCGCTT	TGTGCGGGCG	ATGCGGATTT	GGCTATAGCA	420
GTCAATAACA	AGATCCAAGA	GGGGATGGGT	CAAGAGTTGC	TGTTTGACAA	TAAGCAAGAG	480
TGCTGGGAAT	TTATCACTAG	CCGTAAAGAG	GGT			513

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

ATGTGGCCGT	RAAGCTTTT	TCTAAAACCC	CTAAAAGAAA	CGAGCCTTGC	CCTTGTGGGA	60
GTGGCAAAAA	ATATAAAGAT	TGTTGCGCTA	AAAGCGGGCC	TAAAAGGGC	TTATTGCCA	120
AATAGATCCT	TAATCTTTT	CCTTATCAAG	CGTTATTTGC	GTTTTGATAA	AAGCCAGCCT	180
TTCATTAGTA	TCACTGCTTT	GTTAGCCTTT	TTTGGCGTGG	CGGTTGGCGT	GATGGTTTTA	240
ATTGTGGCTA	TGGCGATCAT	GAACGGCATG	AGTAAGGAAT	TTGAAAAAAA	GCTTTTTGTG	300
ATGAACTACC	CCTTAACGCT	CTATACCACA	AGCCCTTATG	GGATCAGCGA	AGAAGTGTTT	360
CAAGCTTTAG	AAAAAAGTT	CCCTAATTTG	CCTTTTTCAG	YCCCTATTTG	CAAACCCAAA	420
GCC						423

(2) INFORMATION FOR SEQ ID NO:308:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

ATGGTATCGT TGCTTGGCGC GCTTAAACGC ACCCCTTGCA CTAATCGCTT TTATCTTAAA	60
GCACTACTAT TTGCTATATT CTATCATGCA GTAAATAATT TTCTAACGCA ATGCCCCGCC	120
CATCAAGTCC GGGAGTTTTT TTCATCACGA CATGCACAGG GATGGAAGCG AGAAACGCTC	180
CCATGCGCCC TTTCGTTTCA AAACGCGCTC	210

(2) INFORMATION FOR SEQ ID NO:309:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

GTGCATCATT TGAAACGGCT TTTAGACTCA GGCTCTGAAA GGTGTATAGG CTGTGGGCTG	60
TGCGAAAAGA TTTGCACGAG CAACTGCATA AGGATCATCA CGCATAAGGG CGAAGACAAC	120
CGCAAAAAGA TCGATTCTTA CACGATCAAT TTGGGGCGTT GCATTTATTG CGGGTTGTGT	180
GCGGAAGTTT GCCCAGAATT GGCGATCGTT ATGGGGAATC GGT'TTGAAAA CGCCAGCACC	240
CAACGCTCCC AATACGGCTC TAAAAGCGAG TTTCTAACGA GCGAACAAGA CGCTAAAAAC	300

TGCTCGCATG CCGAATTTTT AGGCTTTGGT GCGGTAAGCC CTAATTATAA CGAACGCATG	360
CAAGCCACCC CTTTAGATTA TGTCCAAGAA CCTTCAAAAG AAGAATCCAA AGAAGAGTTT	420
YCCACAAGCC CAGAAAGCCA TAAGGGAGAT GAAAATGTT	459

(2) INFORMATION FOR SEQ ID NO:310:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 549 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

ATGGCTATTT GGGGGTGGTG TTTTATTTT TTATCGTCCT TGATGTGGGG TTCAAGCATG	60
CATGAGTTGG TTTTAAGATC CCAAGCTTTA GGGTTTGAAA CGCGCTTAGT CCAGTGCGAT	120
TTATCGTTTT CTTATGAAAG GTTTATTTCT AAAACCAAAC GCTCTTTAGC GGTGTTAGAA	180
GAATTTGATT GGTAAATTC TGGCTTTGAT TTTTCACGCT TGAACGTTGA AAATGACACT	240
CTGGAATTAC TCAAAGCGCT GTATTTTAAA TTAGAAAAAT TAGAGAGCCT GCTTTTAAAA	300
GAAAATTTAC TTGAATTGGA GCAAAGGAT CGCATCATCG CTTTAGGGCA TGGGCTAGTT	360
TGCCTAAAAA AACAAAGCCT GATAGCGCCT CAACTTACT ATGGGCGTTG CGTGTTAGAG	420
GGGAAAATCC TAGCCTTTTT TGGCGTGGCA AGGGATAAAG ATTTTTTTAGA AATCACTCGC	480
ATGCACGCCT TAGACATTAA GCGTTATGAT TCCTTCATTG TTGATAGCGA AAGAAAAGGC	540
TTGAAATTA	549

(2) INFORMATION FOR SEQ ID NO:311:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

ATGCCGAAA ATTCTAAACT ACAACCTGCT AAGTTAGGGA AAAATTTTGA CCCTGTGGAT	60
CATTCTAACA GGAATTTTTT CTTTCTCTC ATTCTGTCTG TATTGTTACA CTGGTTGATT	120
TATTTTTTAT TTGAACACAG AGAAGATTTT TTCCTTCAA AACCCAAGCT CGTTAAATTA	180
AATCCTGAAA ATTTATTGGT Y	201

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 519 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

GTGTTTTTAG TTCAATCGTG GGCTTTGAGC TTGAAAATAG ACAGCCTGTT TTCTCTTTTT	60
AGCGTGGGTA AAATCCCTAG CGGATCTAAA GATCCCTTTG CGTTAAGGCG TTTGAGTTTT	120
GGGCTATTGA AAATCATCGC GCATTACGGG TTAGAATTG ATTTGAAAGC GGATTTAAAA	180
AACCTCTTTG AAAAAGTGGG CGTTTATCAA AGCTTTGATT TAGAGGTTTT AGAAAAGTTT	240
TTACTGGAGC GCTTTCATAA TTTAATAGAT TGTAACCTCT CTATTATAAG AAGTGTGTTA	300
AACACCAACG AGCGAGACAT TGTTAAAAATC ATTCAAAAAG TCAAAGCCTT AAAACGCTTT	360
TTAGACAATC CTAAGAACGC TCAAAAAAAAA GAGTTGCTTT TTAGCGCTTT CAAACGATTA	420
GCTAATATCA ATAAAGACAG AAACCCTAAC GAATCAAGCG GGTTTTCTAC GAGTCTTTTC	480
AAAGAATTAC AAGAGCATGC CCTTTTTGAA GCGTTCAAC	519

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

ATGAGTCTTG CTCCAAGCGT TATGGCGGGC TTCTTGTTTT GTGCCGGCTC TTGCTCGCTT	60
CGCTTCCCTA ATTATTCTAA AATCATTTCC ATAGATGTGG ATACGGTGTT TTTAGGCGAT	120
GTTGCAAGCG CTTATTTTGC GCTGGATAAT GAACCCACTA AATTGCTTGG CATGGTGAGA	180
GACACTTTTT CCCACCTTCC TTTTGAAGCC TTTTGTGATT TTTGCGAACG CACATGCAAG	240
AATTTTAAAA TTGATCTTTT GCGCTTTAGC CAAAACGAAT TAAAACGCAT CCATCAGGGC	300
TTTAACATGG GCTTTTTTGGT GCGGAATTTA GATTTATGGC GCGAAAATGG GTTTGAAAAA	360
ATCGCTTTAG AGTTTTTGAA AACTAGGGGA AAGGATCTTT TCTACCCTGA GCAGTGTTTA	420
ATCAATATGG TGTTTTTAGA GCGTATTTTA GAATTGCCTA TTCATTATAA TTGCTATTCT	480
GATTTTTTCA AAGAGCACTA CCCTAAAAGT ATCATCATGC TCCATTTTCAT CAAATACAAG	540
CCGTGGCGTT CTGTCAGTTC TTTGAACGGG CGTTTGATTT GCTATGAAGC TGAAGCGAGT	600
TTTTGGCTCG CCAACCTTTT TTGCACCCCT TTTAAAAACG ATTTTTTTAA AGAACGCCTT	660
GAAATGGCTA AAGACCAACA AATGCAATCT TTTAAAACCC ACATCCGATC AAAAACGATT	720
AGGGATTATT TTTATTTTAG GATAAAAAAT ATTTTGAAAA AAGTTTTCGA ACTCTCT	777

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

GTGATTGTTT GCAGCGCGGC GGGGTTGAGC CATTTTTTTTG GGTTTTCTAT GTCTTTGGGG	60
GCGTTCATTG TGGGCATGGC GATTTCTAAA TCGCGCTATA AAATCAATGT CCAAGAAGAA	120
TTCGCGCAAT TAAAAAACCT CTTTTTGGCC CTTTTTTTCA TTACGATAGG GATGCAGATT	180
AATGTGAGTT TCTTCATGGA GAAATTCTTT GTCGTCATCT TTTTACTCAT TTTAGTGATG	240
AGTTTTAAGA CTTTTATCAT TTATGCGCTA TTGCGTTTTT TTAGAGACGC TAAAACCGCC	300
ATCAAAACCG CTCTTTCTTT GCGCAAATT GGGGAGTTTT CTTTCGTGAT CTTTTTAAAT	360
TCAGGCTCGC ACCAGCTCTT TAATTGCAA GAAAAAAG GGATTCTTGG TTTTTTACAC	420
CAAAAAATA TCTTAAATAT TGCTCAAAT GACATCCACC AGCTCCTTAT TCTCATGGTG	480
GTCTTTTCTA TGTTAGCAAC CCCTTTTATT TTAAAATACC TAGAATCTAT CGCTCAATTT	540
ATTTTGCACC AAAAGAGCCA AGAAAACGAG CCGGCTAAAA AA	582

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

ATGTTCTATC TTATCAATAC AGGAGTGCCT CATTTAGTGG GATTTGTGAA AAATAAAGGG	60
TTATTAAATT CTCTTAACAC ACTGGAATTA AGGGCTTTAA GGCATGAATT TAACGCTAAT	120
ATTAACATCG CTTTTATAGA AAATAAAGAG ACGATTTTTT TACAACTTA TGAGAGAGGG	180
GTTGAAGATT TCACGCTAGC TTGCGGGACA GGCATGGCAG CGGTTTTTAT CGCCGCGCGC	240
CTTTTTCATA ACACCCCTAA AAAAGCCACT CTCATCCCTA AAAGCAACGA ATTTTTAGAG	300
CTTCTTTTAA AAAATGATGG AATTTTTTAT AAAGGAGTCG CGCGTTATAT CGGCATGAGC	360
GTTTTAGGCA TGGGTGTTTT TAAAAATGGG TGTTTT	396

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...639
- (D) OTHER INFORMATION: /note= "hypothetical abc transporter
n tesA region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

ATGATTAAAG CGATTGATAT TTCTCATGST TTTGAAAARC CTCTTTRTRA TGGCGTGAAT	60
TTGCGCATT AACCCTAAAGA AAGCYTGGYG ATTTTAGGCG TGAGCGGGAG CGGTAAAAGC	120
ACGCTTYTAA GCCATTTGGC CACCATGCTA AAACCGGATA GCGGAACAGT CAGTTTGTTA	180
GAACACCAAG ATATTTATGC CCTAAATTCC AAAAAGCTTT TGGAATTGCG GCGCTTAAAA	240
GTGGGCATCG TTTTCAATC GCATTACCTT TTTAAGGGTT TTAGCGCTTT AGAAAACTTG	300
CAAGTCGCTT CAATCCTAGC CAAGCAAGAA ATAAATCATT CCCTTTTAGA ACAATTAGGC	360
ATAGCCCACA CCCTAAAACA AGGCGTGGGC GAATTGAGCG GCGGCCAGCA ACAACGCTTA	420
AGCATCGCCA GAGTGCTTTC TAAAAAACC CAAATCATT TCGCTGATGA ACCCACC GGG	480
AATTTAGACA CCACTAGCGC TAATCAAGTC ATCAGCATGC TGCAAAATTA CATTACAGAA	540
AACGAAGGGG CGTTAGTCTT AGCCACGCAT GATGAGCATT TAGCCTTCAC TTGCTCTCAA	600
GTCTATCGCC TAGAAAAAGA ATCTTTGATT AAGGAAAAA	639

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

ATGCTTGATA AACGCATTAA AACGCTTTTA CTTTTTTTTG GTCTTAATAT GGTGTGTTTG	60
AGCGTGAGTT TTACCAATAA GCCTCATTG TGTTTTTGGT TTTTAGTGTT AGGTTGTTAT	120
TTAGTTTATG AGTGGCAAAA GAAACAAAAA AAAGATTTTC AAAGCGCTAA AAGTTTGAAA	180
TTTGACAGCG TTAGCGAATT AGAAAAGGAT TTTGAACATG GAAGTAAC	228

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

ATGAAAACAA TTAAAAATGG TATTATGATC GGCACACTCG GTGCGTTGTT ATTGAGCGGT	60
TGTTCTAGCT TTGATGCTCA GCGTTTCGCT TGTCTCCCTA AAGACCATTTC TTCAAAAAGAC	120
GCTTCTACCA AAAAAGAAGC GCAATACATT CCTAAGGGCT TTTTGTACCC TTATTCTTCT	180
AACTTAAACC ATTGGGATTC TACATTC	207

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 570 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

ATGGAGCTTA TTTTAGGCTC TCAATCCAGC GCTAGGGCGA ATCTTTTAAA AGAGCATGGG	60
ATTAAGTTTG AACAAAAAGC GCTCTATTTT GATGAAGAAA GCCTAAAAAC CACAGACCCT	120
AGGGAGTTTG TCTATTTGGC GTGCAAGGGG AAATTAGAAA AAGCTAAAGA GTTACTTGCG	180
AATAATTGCG CTATCGTGGT GGCTGATAGC GTGGTGAGCG TGGGTAATCG CATGCAACGA	240
AAAGCTAAAA ACAAGCGAGA AGCCCTTGAA TTTTAAAC GCCAAAATGG CAATGAAATA	300
GAGGTTTTAA CTTGCTCTGC ATTGATTTCT CCTGTGTTGG AATGGCTGGA TCTATCGGTT	360
TTTAGAGCGC GTTTAAAGGC GTTTGATTGC AGCGAAATAG AAAAATATTT AGAGAGCGGT	420
TTATGGCAAG GAAGTGCGGG CTGTGTGCGT TTAGAGGACT TTCATAAGCC TTATATTAAA	480
AGCTCAAGCA AGAATTTAAG CGTGGGGTTG GGGCTGAATG TGAAGGCTT GTTAGGGGCA	540
CTAAAATTAG GGGTTAAACT TTCATTATTA	570

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

ATGCTTATTT TAGGACACCC TTTAATCCCT AGCGCTCGTT TTGTTTTTCAT TAAAAACACC	60
GATGCTATTC ATTCCAGCGC CAATAACGAT ATAGTGTGTT TTGAAGCAAA CCCAAAAAAT	120
TTGGAATTAG CCAATATTG CTGTGAAAAT GGCCTCCATT TTAGCGTGAT CTTTTTATCG	180
CACAAGATAG AGACGGACAC CTTTTTTTTT TTCAACGCTT TCAAACCGCT CTATTGTATT	240
TTTAAGGATA TTAAGCAAGC CATACTCGCC CAACAACACG CCACTAATTA CTTGTTAGAT	300

AGCAAAATCT TGTTTTCTAT GGATTTTAAC GATACAGAGT CATGGGAGAT TTGCGCTAAA	360
AATCAAATAG ATGGTGTCAT TTCTAAAGAT TCACTCCTTT TGAAA	405

(2) INFORMATION FOR SEQ ID NO:321:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 765 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

ATGAAAAAAA GATTGAATAT AGGGCTTGTG GGTTTAGGGT GCGTGGGGAG CACGGTCGCT	60
AAAATCTTAC AAGAAAATCA AGAAATCATT AAAGACAGAG CCGGCGTGGA AATTAAAATT	120
AAAAAAGCGG TGGTGCGAGA CGTGAAAAAA CACAAGGGCT ATGCTTTTGA AATCAGTGAT	180
GATTTAGAAA GCGTGATAGA AGATAAAGGG ATTGATATTG TCGTGAGCT TATGGGTGGG	240
GTGGAAGCGC CTTATCTTTT AGCTAAAAAA ACTTTAGCCA AACAAAARGC CTTTCGTTACA	300
GCCAATAAAG CCATGTTAGC GTACCACCGC TATGAATTAG AACAAATCGC TAAAAACACC	360
CCCATAGGCT TTGAAGCGAG CGTGTGTGGG GGTATCCCCA TTATCAAGGC TTAAAAGAC	420
GGCTTGAGCG CTAATCACAT CCTTTCTTTT AAAGGGATTT TAAACGGCAC GAGCAATTAC	480
ATTTTAAGCC AGATGTTTAA AAATCAAGCG AGCTTTAAGG ACGCTTTGAA AGACGCGCAG	540
CATTTAGGCT ATGCGGAATT GAACCCTGAA TTTGACATTA AGGGCATTGA TGCGGCGCAC	600
AAATTATTGA TTTTAGCGTC TTTAGCGTAT GGCATTGATG CGAAATTAGA AGAAATCTTG	660
ATTGAAGGCA TTGAAAAGAT AGAGCCAGAT GACATGGAAT TTGCAAAGA GTTTGGTTAT	720
AGCATCAAAC TTTTAGGCAT CGCTAAAAAA CACCAGGGAT TGCAT	765

(2) INFORMATION FOR SEQ ID NO:322:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 729 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

ATGCAAGAAA AACGACTTAA AGCCATTCAA AACAAAATCG CTTCTTGGAT CAAGGAAATT	60
GAAAGCGGCT TTATAGATGC ATTGTTTTCT AAGATTGGCC CTTCAAAGAT GCTGCGCTCC	120
AAACTCATGC TCGCTTTGTT AGACGAAAAA ACAGACGCTA TTTTATTAGA TAAAGCGCTC	180
AATTTGTGTG CGATTGTGGA AATGATACAG ACCGCTTCTT TATTGCATGA TGATGTGATT	240
GACAAGGCGA CCATGCGCCG AAAGCTCCCT AGCATTAAACG CTCTTTTTTG GAATTTTAAC	300
GCCGTGATGC TTGGGGATGT GTTTTATTCT AAAGCCTTTT TTGAGTTGTC TAAAATGGGC	360
GAATCCATCG CTCAAGCCCT CTCTAATGCG GTTTTAAGGC TCTCTAGGGG CGAGATTGAA	420
GACGTGTTTG TGGGGGAATG TTTTAATAGC GACAAACAAA AATACTGGCG TATTTTAGAA	480
GACAAGACCG CCCATTTTCAT AGAAGCGAGC TAAAAAGCA TGGCGATTCT TTTAAATAAA	540
GACGCCAAAA TGTATGCGGA TTTTGGGTTG CATTTTGGCA TGGCGTTTCA AATCATTGAT	600
GATTTGTTAG ACATCACTCA AGACGCCAAC ACTCTAGGTA AGCCCAATTT TAGCGATTTT	660
AAAGAGGGCA AGACCACTCT ACCCTACTTG CTTTTATATG AAAAATTGAA TCAGCATGAA	720
CAGGGCTTT	729

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 756 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

ATGTTAGGGA	AAAAAACGA	AGAAGTCTTG	ATTGATGAAA	ATTTGGTTGG	GGGTGTGATA	60
GCCCTTGATA	GATTGGCAAA	ACTCAATAAG	GCCAATAGGA	CTTTCAAAAG	GGCTTTTTTAT	120
CTCTCTATGG	TGCTCAATGT	CGCCGCTGTA	ACGAGTATTG	TGATGATGAT	GCCTTTGAAG	180
AAAACAGATA	TATTTGTTTA	TGGCATTGAT	CGATACACAG	GAGAATTTAA	AATCGTCAAA	240
CGCTCCGATG	CTAGGCAAAT	CGTCAATTCT	GAAGCCGTTG	TGGATAGTGC	AACTTCAAAA	300
TTTGTCTCAT	TGCTGTTTGG	TTATAGCAAA	AATTCTTTGA	GGGATCGCAA	GGATCAACTA	360
ATGCAGTATT	GCGATGTGAG	TTTCCAAACC	CAAGCAATGA	GAATGTTCAA	TGAAAATATC	420
AGACAATTCTG	TAGATAAAGT	CCGAGCAGAA	GCTATCATTA	GCTCCAACAT	ACAAAGAGAA	480
AAAGTCAAAA	ATAGTCCCTT	AACGAGATTA	ACATTTTTTCA	TTACCATCAA	AATCACGCCT	540
GATACAATGG	AAAATTATGA	ATATATCACT	AAAAACAAG	TAATATTTA	TTATGATTTT	600
GCTAGAGGTA	ACTCTTCTCA	AGAAAATCTT	ATCATCAACC	CTTTTGGCTT	CAAAGTGTTT	660
GACATTCAAA	TCACGGATTT	ACAAAACGAA	CAGACAGTAA	GCGAAATTTT	GAGAAAGATT	720
AAAGAAGTGG	AATCAAAAAA	TAAGGCATTA	AATAAA			756

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

ATGAGAGCGA	TCGCTATTGT	TTAGCCAGA	AGTTCCAGTA	AAAGGATTAA	GAATAAAAAT	60
ATGATTGATT	TTTTCAATAA	ACCCATGCTC	GCTTACCCTA	TTGAAACAGC	ACTAAATTCC	120
AAGCTCTTTG	AAAAAGTGTT	TATCTCTAGC	GATAGCATGG	AGTATGTCAA	TTAGCCAAA	180
AATTATGGGG	CGAGTTTTTT	GAATTTACGC	CCTAAAAATT	TAGCAGACGA	CAGGGCCACG	240
ACTTTAGAAG	TGATGGCCTA	TCACATGAAA	GAATTAGAAT	TAAAAGATGA	AGACATTGCG	300
TGTTGTTTGT	ATGGCGTTTC	AGTATTTTTA	CAAGAAAAGC	ATTTACAAAA	CGCTTTTGAA	360

ACTTTAAAAC AAAATCAAAA TACGGATTAT GTTTTCACAT GCTCTCCCTT TAGCGCTTCG	420
CCTATCGTTC TTTTAGCCTT GAAAACGGCG TTCAAATGGC TTTTAAAGAG CATTCAAACA	480
CGCGCACGCA AGATC	495

(2) INFORMATION FOR SEQ ID NO:325:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 513 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...513
 - (D) OTHER INFORMATION: /note= "Cell division inhibitor"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

ATGAGTAATC AAGCGAGCCA TTTGGATAAT TTTATGAACG CTAAAAATCC CAAAAGTTTT	60
TTTGATAATA AGGGGAATAC CAAATTCATC GCTATCACAA GCGGTAAGGG GGGCGTGGGG	120
AAATCCAACA TTAGCGCTAA TTTAGCTTAC TCTTTATACA AGAAAGGTTA TAAGGTAGGG	180
GTATTTGATG CGRATATTGG TTTAGCGAAT TTAGATGTCA TTTTGGGGT GAAAACCCAY	240
AAAAATATCT TGCATGYCTT AAAAGGCGAA GYCAAATTGY AAGAAATCAT TTGCGAGATT	300
GAACCCGGGC TTTGCTTAAT CCCTGGGGAT AGCGGCGAAG AAATTTTAAA ATACATCAGC	360
GSSGCGGAAG YTTTCGATTC ATTCTTAGAT GAAGAGGGGG TTCTAAGCGC TTTAATTTAT	420
ATTTTAATTA ATACATTTTC TAAAAATTTG GGTCCACTAT CTCAAACCTT TCTTAATTTT	480
CAGTCATTTT TTTTATTTT TATTCAATCT CCC	513

(2) INFORMATION FOR SEQ ID NO:326:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

ATGCAGCATT TAGTCTTAAT CGGTTTTATG GGGAGCGGTA AAAGCTCTCT AGCACAAGAA	60
TTGGGGCTGG CTTTGAAATT AGAAGTGCTG GATACGGATA TGATCATTAG CGAGAGGGTG	120
GGCTTGAGCG TGAGAGGGAT TTTTGAAGAG CTTGGCGAAG ACAATTTTCAG GATGTTTGAA	180
AAAATT	186

(2) INFORMATION FOR SEQ ID NO:327:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 654 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

ATGAGCATTAG AGGAAAATTT AGAGCAAGTT AGAAACGAAT TTAAAAGCGA TGAAAAGCTT	60
TTAGAAGGAG CGTTTAGATT AGAAAAGTTT TTCAAACGCT ACAAGTGGGT GTTGTGTTT	120
ATCGTGGTGG CTTTTATCGC TTATTTAGGG GATACAAAAT TACAAGATTA TAAGCATGAG	180
CAAACGAGAG AGCGGATCAC TCAAATTTAT AATGAAGTGC TAGAGAGTCC TAATAATATA	240
GCCTTGCAAA AAAGATTGAA AGAAGTCGCC CCAGAGTTGT ATGACTTGTA TCAGTTCGCC	300
AGAGCGAGTG AGAGGAACGA TGCAAACGAG TTAAAAGGC TTTGCAATC TTCTAATGAA	360
ATCGTTAAAG CGTTCGCCAA ATATTCTTAC GCATCGCTCT CTAGAGATAA AAACCTGCTT	420
GAAAAAAGCC CCATTCTTAA AGAAATGAGC GCTTTACAAG AAGTGAACCT GTTGTATGAA	480
GAAAATTCTA AAGACGCAAT CAAAAAAGCG CATCAAAGTT TATCAACTAT CCCTCTAAGT	540
TCTTCACTCT ATGCTATAAT CTCTGTTTAA AACATTATG GAATGTTAGA AGATATTCAG	600

(2) INFORMATION FOR SEQ ID NO:328:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

GTGCATTTCA ATCAGGTTGT TCTCCCAAAA GCGGTGGGCG CGATTTTAGT CGCACCAAAA	60
GGGCCCCGGGA GCGCTTTAAG AGAAGAATAC CTAAAAATA GGGGTTTATA CCATCTAATC	120
GCCATAGAGC AAGAAAGCTC AATTCATAAC GCTAAAGCGG TGGCTTTAAG CTATGCTAAA	180
GCGATGGGTG GGGGGAGAAT GGGGGTTTTA GAAACGAGTT TTAAAGAAGA ATGCGAGAGC	240
GATTTATTCG GCGAGCAAGC GGTCTTGTGC GGGGGGTTAG AAGTCGATCG TAAGAATGGG	300
GTT	303

(2) INFORMATION FOR SEQ ID NO:329:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

ATGAAAAAAT TTTTTTCTCA ATCTTTGTTA GCTCTTATTA TCTCTATGAA TGCGGTATCT	60
GGCATGGATG GTAATGGCGT TTTTTTAGGG GCGGGTTATT TGCAAGGACA GGCGCAAATG	120

CATGCGGATA TTAATTCTCA AAAACAAGCC ACCAACGCTA CGATCAAAGG CTTTGACGCG	180
CTCTTGGGGT ATCAATTTTT CTTTGAAAAA CACTTTGGCT TACGCCTTTA TGGGGTTTTT	240

(2) INFORMATION FOR SEQ ID NO:330:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

ATGCTAAAAA AGATTTTTTA TGGTTTTATC GTTTTATTTT TGATTATCGT AGGGTTGTTG	60
GCCGTTCTTG TCGCTCAAGT TTGGGTAAGT ACGGATAAGG ATATTGCTAA AATTAAAGAT	120
TATCGCCCCA GTGTCGCTTC ACAGATTTTA GACAGAAAAG GCGGTTTGAT CGCTAATATT	180
TATGATAAGG AATTTGTTTT TTATGCGCGT TTTGAAGAAA TCCCCCACG ATTTGTTGAA	240
AGCCTTCTAG CGGTAGAAGA CACCCTCTTT TTTGAGCATG GGGGGATCAA TTTAGACGCT	300
GTCATGCGCG CTATGATTAA AAACGCTAAA AGTGGTCGTT AACTGAAGG GGGTAGCACT	360
CTAACCCAAC AACTCGTTAA AAACATGGTG CTCACACGGG AAAAAACCCT AACCAGAAAA	420
CTCAAAGAAG CTATCATCTC CATACGCATT GAAAAAGTCT TAAGCAAAGA AGAAATTTTA	480
GAGCGTTATT TGAACCAAAC TTTTTTTGGG CATGGGTATT ATGGCGTGAA AACCGCAAGT	540
TTAGGGTATT TTAAAAAACC CCTTGACAAA CTCACGCTTA AAGAAATCAC CATGTTAGTC	600
GCCTTACCTA GGGCTCCAAG TTTTATGAC CCTACCAAAA ATTTAGAATT TTCACTCTCT	660
AGGGCTAATG ATATTTTAAG GCGGTTGTAT TCTTTAGGCY GGATTTCTTC TAACGAGCTC	720
AAATCCGCTC TCAATGAAGT GCCAATCGTC TATAACCAA CTTCCACGCA AAATATCGCT	780
CCCTATGTCG TGGATGAAGT GTTGAAGCAA TTGGATCAAT TAGACGGGTT AAAAACTCAA	840
GGCTATACCA TAAAACTCAC GATAGATTTG GATTACCAAC GCTTAGCGTT GGAGTCTTTG	900
CGTTTTGGGC ATCAAAAAAT CTTAGAAAAA ATCGCTAAAG AGAAGCCAAA AACTAACGCT	960
TCTAATGATA AAGATGAAGA CAACTTAAAC GCCAGCATGA TAGTTACAGA AACGAGCACC	1020

GGTAAGATTT TAGCCTTAGT GGGGGGGATT GATTATAAAA AAAGCGCTTT CAATCGCGCC	1080
ACGCAAGCCA AACGGCAGTT TGGGAGCGCR ATCAAGCCTT TTGTGTATCA AATCGCTTTT	1140
GATAATGGCT ATTCCACCAC TTCCAAATC CCTGATACCG CGCGAAATTT TGAAATGGC	1200
AATTATAGTA AAAACAGCGT GCAAAACCAC GCATGGCACC CTAGCAATTA TRCTCGCAA	1260
TTTTTAGGGC TTGTAACCTT GCAAGAAGCC TTGAGCCATT CGTTAAATCT GGCTACGATT	1320
AATTTAGCGA TCGCTTGGCT A	1341

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

ATGAACGATA CAACAGAGCA CCATGGATCC AATCCGCTAA ACGCCCCACC ACCTAGCAAC	60
TCACAGAGCA ACGATCTCTT AAATTGCTA GACTCGTTAT ATCCTAAAGG GAGTTTAGGG	120
GAACAAAGAT TTCACGAAGC TTAAAGAAT CAAGAAGAGT TGAAAAATAT CCTAATAGAA	180
ATAGAAAAGC TACCGCAAGA AAAAAGGTAT GAACTTCTGA TGCAGATAGG ACAAGCCAAA	240
CAGAGAATAA TGGAAGCATA CGCTCATTCA TTCTTAGGAT ATATAGGGGG ACTAGAGCAT	300
CTGTTAGGAT TGTGTATGGG TGGGATATTT GTTTTGTTTG CAATCTATTT TGTATTTT	360
AGAACTAGCA AAAACACAGA GCTAGTGGA AGTCTAAAA CAAAATTAAA ACTTCAGTAT	420
TTTTACTATG CCTTTGGTGT GGGTGCGGT TTGTTTTTTG GATTAGAAAC AATTAGATCG	480
ATTTATGAAC TATATATCTT AGGAATTGGT AGCACTAACG ACAAGGTGCT CTTTGTTTTG	540
AAAAACATTT GCTTCATAGG TATGGGCTAT TTGATTTATA AAGTTATTAA AGTTATTGGT	600
ATAAAAAATT TTATCAATGG TCTTTTCGCT TCAAAGAAAC AAGGCGGTGC AGAA	654

(2) INFORMATION FOR SEQ ID NO:332:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

ATGATGGATA AGGTGGGTTT TAAATCTCAA GGCATCTTTG TGATGGACGC TAGCAAGAGG	60
GATGGGCGTT TGAACGCGTA TTTTGGAGGC TTGGGTAAAA ACAAGCGGGT GGTGTTGTTT	120
GACACTTTGA TCTCTAAAGT TGGGACAGAA SGGCTTTTAG CCATTTTAGG GCATGAGTTA	180
GGGCATTTTA AAAATAAGGA TTTGTTGAAA AATTTAGGGA TTATGGGAGG CTTGCTCGCT	240
CTTGTTTTTG CTTTGATCGC TCATTTGCCG CCGTTGGTTT TTGAAGGCTT TAATGTCTCG	300
CAAACGCCAG CGAGTTTGAT CACGATTCTA CTCTTGTTTT TGCCGGTGTT TTCCTTTTAC	360
GCCATGCCTT TGATTGGGTT TTTTAGCCGC AAGAACGAAT ACAATGCGGA CAAGTTTGGG	420
GCGAGTTTAA GCTCTAAAGA GACTTTAGCC AAAGCGTTAG TGTCCATTGT GAATGAAAAT	480
AAAGCGTTCC CCTATTCGCA CCCTTTTAT GTTTTCTTGC ATTTACGCA CCCGCCGCTA	540
TTAGAACGCC TAAAAGCTTT GGATTATGAA ATTGAA	576

(2) INFORMATION FOR SEQ ID NO:333:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 603 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

ATGAATATTT ATCAAAAAAA CTTGCAAGCT CTTTTCAAAA AAGACCCTCT TTTGTTGCA	60
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AAGCTCAAAG CCATTAAAGA AAACAAAAAA TACGAAGTGT TTTTAGGGAA TGATAGCGCG	120
AATTTCAACC TCTTAGATAA AGAAACAAAC ACGCCCTTAT TTGAAAAAAG CCCGCTAGAT	180
TCAAGCTTAG AGCTATATAA AAATAGCGAA ATTCACATGC TCTATCCTTA TTTGTATTAT	240
TTTGGCTTGG GTAATGGGGT GTTTTATCGC TTGCTTTTAG GCAATGAAAA TTTAAAACGC	300
TTGGTGGTCA TTGAGCCTGA AATAGAGGTG ATTTTCATTG TGCTGAATCT TTTGGATTTT	360
TCCACTGAGA TTTTAGAAAA TCGTTTGATT TTATTGCATG CAAGTTTTTG CAATTACAAC	420
ATGATTGCTT CATTATTTGA TATGGATAAA AAGTCTCGTT TATACGCAAG AATGTATGAT	480
TTAAAACTTT TTAACGCTTA TTATGAACGA TACTCTCATC AAATGATAGA AATCAACCAG	540
CATTTACGC GCGCTTTAGA GCATGGCGCT ATTAGCGTAG GCAATGACGC TAAAGCGCAC	600
TCA	603

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

ATGAAAAAGA TTATTCTTGC ATGCCTTGTG GCTTTTGTGG GTGCCAATTT AAGCGCAGAG	60
CCTAAGTGGT ATAGCAAGGC CTATAACAAA ACAAACGCCC AAAAAGGCTA TCTTTATGGG	120
AGTGGTTCAG CCACTTCTAA AGAGGCTTCT AAACAAAAAG CGTTAGCGGA TTTAGTGGCG	180
TCTATTAGCG TGGTGGTCAA TTCACAAATC CACATTCAAA AAAGTCGTGT GGATAATAAG	240
TTAAAATCCA GCGATTCAAC AACGATCAAC TTAAAACCG ATGACTTGGA ATTGAATAAT	300
GTAGAAATTG TCAATCAAGA AGCGCAAAAA GGGATCTACT ACACCAGAGT GAGGAATCAA	360
TCAAACTTG TTTTTCAGG GTTTAAGGGA	390

(2) INFORMATION FOR SEQ ID NO:335:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

ATGAAAATCC AAACAATTTC AACACTTGTC CTTACAATAA TAATGGTAAT ACAAAAAATG	60
ATTGTTGGCA AAATTTTACC CCACAAAACC GCAGAAGAAT TCACYAATTT AATGTTGAAC	120
ATGATCGCTG TTTTAGACTC CCAATCTTGG GGCGATGCGA TCTTAAACGC TCCTTTTGAG	180
TTCATAACA GCCCAACAGA TTGCGATAAT GATCCTTCAA AATGCGTAAA TCCTGGGACA	240
AACGGGCTTG TCAATTCTAA AGTCGATCAA AAATATGTGT TAAACAAACA AGACATTGTC	300
AATAAATTTA AAAACAAAGC RGATCTTGAT GTAATTGTTT TAAAGGATTC AGGGGTTGTA	360
GGGTTRGSCA ATGGATATGG CAATGATGGT GAATATGGCA CATTAGGGGT AGWAGCCTAT	420
GCTTTAGGAT CC	432

(2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 927 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

GTGGTAATAA GGTTAGTCCT AAACATGCTA ACATGTCAAA TTAGCTATAT AAGGATAAGT	60
TATCTTGTCT CTGTTAGCGA TTTTGTGATT TGCAAGGAAA GATTTATGGA TGAAATTAAA	120
ACGCTGTTAG TGGATTTTTT CCCGCAGGCA AAGCATTTTG GGATAATCTT AATCAAGGCT	180

ATTGTTGTCT TTTGTATAGG TTTTATTTT TCGTTTTTCT TACGGAACAA AACCATGAAA	240
CTCTTATCCA AAAAGGATGA GATTTTGGCG AATTTTGTCTG CGCAGGTTAC TTTTATCTTA	300
ATCCTTATCA TTAATAAAT CATCGCGCTC AGCACGCTAG GCGTCCAAAC CACCTCTATT	360
ATCACTGTTT TAGGAACGGT GGGGATTGCG GTGGCGTTGG CTTTAAAAGA TTATCTTTCA	420
AGCATTGCTG GAGGGATAAT CCTTATTATT TTACACCCTT TCAAAAAAGG AGACATCATT	480
GAAATCTCTG GCCTAGAGGG CAAAGTAGAA GCGCTTAATT TTTTAAATAC TTCTTTACGC	540
TTGCATGACG GGCGCTTGGC GGTTTTGCCT AATAGAAGTG TCGCTAATTC TAATATTATC	600
AATAGCAATA AACTGCGTG TCGGCGCATT GAATGGGTCT GTGGGGTAGG GTATGGGAGC	660
GATATTGAAC TGGTGCATAA GACTATAAAA GATGTTATTG ACGGGATGGA AAAAATTGAT	720
AAAAACATGC CCACTTTCAT TGAATCACG GATTTTGGAC AAAGTTCGCT GAACTTCACC	780
ATTAGGGTTT GGGCAAAGAT TGAAGACGGG ATCTTTAATG TGAGGAGCGA ACTCATTGAA	840
CGCATCAAAA ACGCCCTGGA CGCTAATCGT ATTGAAATCC CTTTCAACAA GCTAGATATT	900
TCTATCAACA AACAAGACTC TTCTAAG	927

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

ATGAAAACT TTTCCCCACT CTATTGTCTT AAAARGCTCA AAAAACGCCA TTTAATCGCT	60
CTGAGTCTGC CCTTGCTTTC TTATGCGAAT GGCTTTAAAA TCCAAGAGCA AAGCTTGAAT	120
GGCACGGCTT TAGGCTCGGC GTATGTCGCT GGGGCTAGGG GTGCTGACGC TTCTTTTAC	180
AACCCGGCTA ACATGGGCTT TACTAACGAT TGGGGCGAAA ACAGAAGCGA ATTTGAAATG	240
ACCACCACCG TGATCAATAT CCCGACCTTT AGCTTTAAAG TCCCTACGAC CAATCAAGRC	300
TTATATTCGG TAACAAGTTT AGAAATTGAT AAAAGCCAAC AAAATATTTT AGGCATCATC	360

AACACTATAG GGTTAGGCAA TATCCTTAAA GCGCTTGGCA ATACGGCCGC TACCAATGGC	420
TTATCACAAG CTATCAATCG TGTTCAGGG CTTATGAACT TAACCAATCA AAAAGTCGTA	480
ACCCTCGCTT C	491

(2) INFORMATION FOR SEQ ID NO:338:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

ATGTGTTTAG CGATCCCCTC TAAAGTCATA GCCATTAACG ATAATGTGGC ACTCTTAGAG	60
ACTTTGGGCG TTCAAAGAGA AGCGAGCTTG GATTTAATGG GCGAGTCCGT TAAAGTGGGC	120
GATTATGTGC TACTACACAT CGGCTATGTG ATGAGTAAAG AT	162

(2) INFORMATION FOR SEQ ID NO:339:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 606 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

ATGAAATATT TATGGCTTTT TTTAATATAC GCTATAGGGC TTTTGTCAAC AGATAAAACG	60
CTAGATATTA TTAAAACCAT TCAAAAACCTT CCTAAGATTG AAGTGCGCTA CTCCATAGAT	120
AACGATGCCA ATTACGCTTT AAAATTGCAT GAAGTCTTAG CGAACGATTT AAAGACTAGC	180

CAGCATTTTG	ATGTTTCTCA	AAACAAAGAG	CAAGGTGCTA	TCAATTACGC	AGAACTCAAG	240
GATAAAAAAG	TCCATCTTGT	AGCGCTTGTG	AGCGTGGCGG	TAGAAAACGG	CAATAAAATT	300
TCACGATTAA	AACTTTATGA	TGTGGATACA	GGAACGCTCA	AAAAGACTTT	TGACTACCCC	360
ATTGTAAGTT	TAGATCTATA	CCCTTTTGCA	GCGCACAACA	TGGCCATTGT	GGTGAATGAT	420
TATTTAAAAG	CCCCTTCTAT	CGCTTGGATG	AAGCGCCTGA	TTGTTTTTTC	TAAATACATT	480
GGACCAGGAA	TCACAAACAT	CGCACTAGCG	AATTATACGA	TGCGTTATCA	AAAAGAAATC	540
ATCAAAAACA	ACCGACTCAA	TATTTTCCCC	AAATGGGCGA	ACGCTGAGCA	AACGGAGTTT	600
TATTAC						606

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(A) ORGANISM: *Helicobacter pylori*

GTGGTGAGCG	GGGTGGTGAT	CATTATTGTG	TTTTTTGTGC	CGATTCTAAC	CTTACAGGGG	60
TTAGAGGGCA	AGATGTTTAG	GCCTTTAGCG	CAAAGCATTG	TGTATGCGCT	TTTAGGCACT	120
TTAGTTCTAT	CCATCACTAT	CATTCCTGTA	GTGAGCTCTC	TTGTCTTAAA	AGCCACGCCC	180
CATAGCGAAA	CCTTTTTTAA	GAGGTTTTTA	AACAGAATCT	ACGCCCTTTT	ATTGGAATTT	240
TTTGTGCATA	ACCCTAAAAA	AGTGATTTTA	GGAGCGTTTG	TTTTTTTTAAT	CGCAAGCCTT	300
TCTTTATTCC	CTTTTGTGGG	GAAGAATTTT	ATGCCTGCCT	TAGATGAGGG	CGATGTGGTT	360
TTGAGCGTGG	AAACCACCCC	CTCTATTTCC	TTAGATCAAT	CTAAAGATCT	CATGTTAAAC	420
ATTGAAAGCG	CGATTAAAAA	GCATGTCAAA	GAAGTTAAAA	GCATTGTCGC	GCGCACAGGG	480
AGCGATGAAT	TGGGGCTGGA	TTTAGGGGGT	TTGAATCAAA	CCGATACTTT	TATTTCTTTC	540
ATCCCTAAAA	AAGAATGGAG	CGTTAAAACC	AAAGATGAAT	TGGTTAGAAA	AAATCATGGA	600
TTCTTTAAAA	GACTT					615

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

GTGGGATATA TCCCTARGGA AAAGATTGTA GGCATTAGCG CGATCGCTAA ACTCATTGAA	60
ATTTATAGCA AACGCCTGCA AATCCAAGAA AGGCTGACCA CTCAAATTGC AGAAACTTTT	120
GATGAAATCA TAGAGCCAAG GGGCGTGATC GTGGTTTGTG AAGCCAAGCC ACTTGTGCAT	180
GAGCATGCAA GGGGTGCAAA AGCAAAATGC GATCAT	216

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

GTGGCTCTTG TGTTTGATAG TTTGATAGAG AACAAGAAG	39
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(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

ATGAAAAAAA TTGGTTTGAG CTTGTGTTTG GTTTTGAGTT TGGGTTTTTT AAAAGCCCAT	60
GAAGTGAGCG CTGAAGAGAT TGC GGATATT TTCTACAAAC TCAACGCCAA AGAGCCTAAA	120
ATGAAAATCA ACCACACGAA GGGGTTTTGC GCTAAAGGCG TGTTCCTCCC TAACCCGCAA	180
GCAAGAGAGG ATTTAGAGGT GCCACTACTC AATGAAAAAG AAATCCCTGC GTCTGTAAGG	240
TATTCTTTAG GGGGCGTGGT CGATTGGACG ATAAAAGCAA GGTTAGGGGA ATGGCGT	297

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

GTGATCAAAC CTCATAGCGT GGGATTGGTA AGGATTGGGA TTTGTTTGTC TTTAGAAGTG	60
GGGTATGAAC TGCAGGTACG CACCCGTAGC GGCTTGGCTT TGAATCATCA GGTGATGGTG	120
TTAAATTYCC CTGGCACGGT GGATAATGAT TATAGGGGCG AAATTAAGGT CATTTTAGCG	180
AATTTGAGCG ATAAAGATTT TAAAGTTCAA GTAGGGGATA GGATCGCTCA AGGGGTGGTT	240
CAAAAACTT ATAAAGCCGA ATTTATAGAA TGCGAACAAT TAGATGAAAC CTTCAAGGGG	300

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 765 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

ATGGAATCA TTTTATTAAT TGTTCGGCG GTTGTGTTGT TTTATTTTCA CAACACCCTC	60
AAAGAATATT TGAAAAACCC CCTAACCCCT AAAACCAAAA CCGAAGAATA CGACTTGAAA	120
AATGACCCCT ATTTGCTGGT GCAATCTAGC CCCCTAGACA AATTCAAGCA AACCCAAATA	180
GGCGCGTATA TCGTCTTTT AAAATTTTCA GACATTCAAA AAAACGCCTT GGATAACGCT	240
TTAAGAACGC TTTTATATCA TGAATTGGAG CAGCCCTTAA ACAGCGAACA GCAAAATTTA	300
GCCAAAGAGC TTCTCAATGA GCCSGTGGAT AAAAAAGAAA ATTTTGAATC CTTATGCCAA	360
GAAATCGCCG ACCACACGCA TGGAGAATAC ACCAAACGCC TGAAATTAGT GGAATTTCTT	420
ATGCTATTAG CCTATGCTGA TGGGATTTTG GACAGCAAAG AAAAAGAATT GTTTTATAGT	480
GTGGGGGCGT TTTTGCAGAT AGACAATCAA GATTTTAAAC AGCTTTATGA CAATTTTGAA	540
CACTTCAATT CAATAGAAAT CCCTATGTCT TTAGAAGAAG CAAAAAATCT TTTTGAAATC	600
CAAACCCACA CCACCATGCA AGATTTAGAA AAAAAAGCTT TGGATTTAAG CGCCCCCTAT	660
TACCATAAAA TGAATGACAA CAAACGCTAC AGCGAACAAG ATTTTATCTC TTTGAAAAAA	720
ATCGCCCTCG CTTCCCAACT TTTAGAAAAT GATTTAAAAG ACTCA	765

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

ATGGAAGTAG AGCATGGCAA GATTGAAACC ACTTTAAGCT TGGGGGCGTC TCATTGGA	60
GTCATTAAAA TGATGCTTTT AGAGAGCCTG CCTTCTTTAG TGAATAATAT CACCATCACT	120
TTAATTTCTC TAATAGGCTA TTCGGCTAWG GCYGGAGCGT TAGGGGCTGG GGGATTGGGG	180
GATTTAGCCA TTAGGATTGG CTATCAAAGT TATAGGGGCG ATGTGCTTTT TTATGCGGTG	240
GTCGTGATCA TCGTTTTAGT GCAAATCATT CAAAGCGCGG GGGATTATGT GGTGAAACGC	300
TTGAGAAAGA ATAAGTAT	318

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

ATGAACGAAA TTGACAAATC CGTTGATATC GGATTCTTAC GGATTCTGGA TGTTATTAAA	60
AAAGTTAAAA CCCCAAAGGG TGGTATTGAG GTTTTAAGGA CTTTAATTGA TTTCACGCCC	120
AAAATTGAAA ACGCCCTAAA TTTAGCGACC AAAAGCCATA AGGGGCAATA CAGAAAGAGC	180
GGTGAGCCTT ATATTGTCCA TCCTATTTGC GTGGCGAGCG TGGTGGCGTT TTGTGGGGGC	240
GATGAGGCGA TGGTGTGCGC CGCGCTTTTG CATGATGTGG TAGAAGACAC GCCTTGTGAG	300
ATTGAAACGA TTGAGCGAGA ATTTGGGCAA GATGTGGCTA ATTTAGTGGA TGCGCTCACC	360
AAAATCACTG AAATCAGGAA AGAAGAGTTA GCGGTGAGTT CTCAAGATCC CAGAATGGTG	420
GTTCAGCCC TCACTTTTAG AAAGATCCTT ATTAGCGCGA TACAAGATCC AAGAGCCTTA	480
GTGGTAAAGA TTAGCGACAG GTTGCAAC ATGCTCACCT TAGACGCCTT GCCTCATGAC	540
AAGCAGGTGC GTATTTCTAA AGAACTCTA GCGGTGTATG CCCCATAGC GAGTCGATTG	600
GGCATGTCTT CAATCAAAA CGAATTAGAA GACAAGAGCT TTTATTATAT TTATCCAGAA	660
GAGTATAAAA ATATTAAGGA GTATTTGCAC AAAACAAAC AGTCTTTACT CTTAAAACTC	720

AACGCTTTTG CGAGCAAGTT AGAAAAAAG CTTTTTGACA GCGGGTTTAG CCATTCGGAT	780
TTTAAACTCG TTACAAGGGT GAAACGCCCT TATTCTATTT ATCTTAAGAT GCAACGAAAA	840
GGGGCGGTTA ATATTGATGA AATTTTGGAC TTGTTAGCCA TTAGGATTTT ATTGAAAAAC	900
CCGATTGATT GCTACAAGGT TTTAGGGATT ATTCATTTGA ATTTCAAACC CATTGTTTCT	960
CGTTTTAAAG ATTACATCGC TTTGCCCAAA GAAAATGGCT ATAAGACAAT ACACACGACG	1020
ATTTTTGATG AATCTTCTGT TTATGAAGTG CAGATCCGCA CTTTTGATAT GCACATGGGG	1080
GCGGAGTATG GTAATTCAGC CCATTGGAAG TATAAAGCCG GGGGCGTGGA TCATGAAGAA	1140
CATCATGAGG GCATGCGGTG GTTGCAAAAT TTTAAATACC ATGACAGCGA TTTGAAAAAC	1200
GACCCTAAGG AATTTTACGA ACTCGCTAAG AACGATTTGT ATCGTGAAGA TATTGTCGTT	1260
TTTTCGCCCC ATGGGGACAC TTACACTTTA CCGGTGGGCG CGATCGCTTT AGATTTTCGCT	1320
TACATGGTGC ATAGTGATTT GGGCGATAAA GCCACGGACG CTTATATCAA TAGTAAAAAA	1380
GCCTTACTCA ATCAAGAATT AAGGAGTGGG GATGTGGTTA AAATCATTAA AGGCGATAAA	1440
GTAATACCTC GTTTCATTTG GATGGATCAG CTTAAACTT CTAAGGCTAA AAACCATTTG	1500
CGCATCCAAA GAAGAAACCG CTTGAAAGAA ATTGACACTA AGAGCATGAT CAATATCTTA	1560
GCGACTTTTT TTTGGGCGCT C	1581

(2) INFORMATION FOR SEQ ID NO:348:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

GTGGTGGTGG TTGAGAATAT AAAAGACGCT GTGCCTTTAG CGCAAAGCCT RATARAGGGG	60
GGTATTCCAA TCATAGAAGT AACTTTGCGA TCAAACGTGT CTTTAGAGGC CATAGAGCTT	120
ATCGCTAAGA ATGTGCCAAA AATGCGCGTG GGTGCTGGCA CGATACTCAA TCTCACTCAA	180
TTAGAGCAGG CTCAAATAG GGGGGCAGAG TTTTGTATTA GCCCGGGTCT TACGATAAAG	240

CTTTTAGAAC ACGCAAAGAA AAAAGACATG CCTTTAATAC CTGGGGTTTC TAGCAGCAGT	300
GAAGTCATGC AAGCTTTAGA ATTGGGTTAT AACGCTTTGA AATTTTCCC GCGGAGTAT	360
TGCGGGGGCC GT	372

(2) INFORMATION FOR SEQ ID NO:349:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...330
 - (D) OTHER INFORMATION: /note= " UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE--2 & 6-DIAMINOPIMELATE LIGASE"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

GTGGAAAAA TCAAACCCTA TGCCCCCTAAA GATAGCCCTT TAATAGACTA TTCTAGCCTA	60
GTTAGAAACG TCCAATCCAC TTTAAAGGC ACTTCTTTTG AAACGCTTAT CAATGGCGTT	120
TGGGAAAGCT TTGAAACGAA GGTTTTAGGG GAGTTTAACG CCTATAATAT CGCTTCAGCG	180
ATTTTAACCG CTAAGCATTT AGGCTTAGAG ACAGAAAGGA TCAAACGGCT TGTTTTTGAG	240
CTTAAGCCTA TTAACCATCG TTTGCAACTG TTGGAAGCGA ATCAAAAAAT CATTATAGAC	300
GATASCTTTA ATGGGAATTT AAAGGGCATG	330

(2) INFORMATION FOR SEQ ID NO:350:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1791 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...1791

(D) OTHER INFORMATION: /note= "heat shock protein C62.5 - chaperone-ATPase activity"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

ATGTCTAATC AAGAATACAC CTTCCAAACT GAAATCAACC AGCTTTTGGA TTTGATGATC	60
CACTCTTTGT ATTCTAATAA AGAGATTTTT TTAAGGGAGT TGATTTCTAA CGCGAGCGAC	120
GCTTTGGATA AGCTGAATTA TTTGATGCTA ACCGATGAGA AATTAAAAGG GCTGAATACC	180
ACGCCTAGCA TCCATTTGAG TTTTGATAGC CAAAAAAAAA CCTTAACGAT TAAAGACAAT	240
GGTATAGGCA TGGATAAAAG CGATCTCATC GAGCATTTAG GCACGATCGC TAAATCAGGC	300
ACGAAGAGTT TTTTAAGCGC TTTGAGTGGG GATAAGAAAA AAGATAGCGC CTTAATTGGC	360
CAATTTGGCG TGGGCTTTTA TTCGGCGTTC ATGGTAGCGA GTAAGATTGT CGTTCAAACC	420
AAAAAAGTTA CCAGTCATCA AGCTTATGCA TGGGTGAGCG ATGGTAAGGG CAAGTTTGAA	480
ATCAGCGAAT GCGTCAAAGA GGAGCAAGGC ACAGAAATCA CCCTCTTTTT AAAAGAAGAA	540
GATTCTCATT TTGCGAGCCG TTGGGAGATT GATAGCGTTG TTAAAAAGTA TTCTGAGCAT	600
ATCCCTTTCC CTATTTTTTT AACTTACACC GATACGAAAT TTGAGGGCGA AGGGGATAAT	660
AAAAAAGAAG TTAAAGAAGA AAAATGCGAT CAGATCAATC AAGCGAGCGC TTTATGGAAA	720
ATGAATAAGA GCGAATTGAA AGAAAAGGAT TACAAAGACT TTTACCAATC GTTTGCGCAT	780
GATAACAGCG AGCCTTTGAG CTATATCCAT AATAAAGTGG AAGGCTCTTT AGAATACACG	840
ACGCTTTTTT ATATCCCTAG CAAAGCGCCC TTTGATTTGT TTAGGGTGGA TTATAAAAGC	900
GGGGTCAAAC TTTATGTAA ACGGGTGTTT ATCACTGATG ATGACAAAGA ATTGTTGCCG	960
TCTTATTTGA GGTTTGTAA AGGCGTGATT GACAGCGAAG ATTTGCCCTT GAACGTGAGT	1020
CGTGAAATCT TACAGCAGAA TAAGATTTTA GCCAATATCC GTTCGGCTTC AGTGAAAAAG	1080
ATTTTAAGCG AGATTGAAAG GCTGAGCAAG GATAACAAGA ATTACCATAA ATTCTATGAG	1140
CCTTTTGGGA AAGTGTTAAA AGAAGGCTTG TATGGGGATT TTGAAAACAA AGAAAAACTT	1200
TTAGAATTGT TGAGATTCTA TTCTAAAGAC AAAGGAGAAT GGATTTCTTT AAAAGAATAC	1260
AAAGAAAATT TAAAAGAAAA TCAAAAAAGC ATTTACTACC TTTTAGGCGA AAATTTAGAC	1320
TTATTAAAAG CGTCCCCCCT TTTAGAAAAA TACGCTCAA AAGGCTATGA TGTTTTGTTA	1380

TTGAGCGATG AAATTGATGC GTTTGTGATG CCAGGCGTGA ATGAATACGA TAAAACGCCC	1440
TTTAGAGACG CTAGCCATAG TGAGAGTTTG AAAGAGCTTG GTTTGGCAGA AATCCATGAT	1500
GAGGTAAAG ATCAGTTTAA AGATTTAATC AAAGCGTTTG AAGAAAATCT TAAAGATGAG	1560
ATTAAGGGCG TAGAGCTTTC TGGTCATCTC ACTTCAGCGG TGGCTTTAAT AGGCGATGAA	1620
CCAAATGCGA TGATGGCTAA TTGGATGCGT CAAATGGGGC AAAGCGTGCC TGAAAGCAAG	1680
AAAACTTTAG AATTAAACCC TAACCATGCG ATTTTGCAA AACTCTTAAA ATGCGAAGAT	1740
AAAGAGCAGT TGAGCGCTTT TATCTGGTTG CTTTATGATG GCGGAAGCTT T	1791

(2) INFORMATION FOR SEQ ID NO:351:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

GTGAATTTAG GGGCTTACTA CACGCCCCCT TATTTAGTGG ATTGCGCTTA CAAGCTTTTA	60
AAAAAGCATG TTGGTATTGA AAACACACG CTTTTAGACA CCGCATGTGG TAATAAAGAG	120
TTTTTAAAGC TCCACCACCC TAAAAAATA GGAGCGGATA TTGACCCTAA GTGTGATGCT	180
TTAATAATAA ACGCTCTAGC CAATCCTAAA AGAGAAAATT ATGGCATTAG CCAAGATGAA	240
CCTTTAATCA TCGTGGGCAA TCCCCCTAT AACGATAGAA CTTCTTTTAT CAAACAAGAT	300
ATTAAAAATA AAGATTTTAT TTTTGAGATA GACAACGATT TGAAATCCCG AGATTAGGG	360
ATAAGTTTTT TAAAATCTTT TGCAATTTTA AAGCCGGCGT TTATTTGCGT GCTACACCCT	420
TTATCTTATC TCATCAAAGA AGCTAATTTT AAGCAATTTA AAGCTATT	468

(2) INFORMATION FOR SEQ ID NO:352:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

ATGAAAAGCA TTTTGCTCTT TATAATTTTT GTAGTTTGTC AGTTAGAAGG CAAAAAATTT	60
TCACAAGATA ATTTTAAGGT GGATTATAAC TACTATTTGC GCAAACAGGA TTTGCACATC	120
ATTAAAACGC AAAACGATTT GTCCAATGCC TGGTATCTCC CTCCACAAAA AGCCCCCAAA	180
GAACATTCTT GGGTGGATTT TGCTAAAAAA TATTTAAACA TGATGGATTA TCTAGGCACT	240
TATTTTTTGC CTTTTTATCA TAGTTTCACC CCCATTTTTC AATGGTACCA CCCTAATATC	300
AACCCCTACY AACGCAATGA GTTTAAGTTC CAAATCAGTT TTAGAGTGCC TGTATTTAGG	360
CATATTCTTT GGACTAAAGG CACGCTTTAT CTGGYTTATA CCCAACTAA CTGGTTTCAA	420
ATTTATAATG ACCCTCAATC CGCCCCCATG CGAATGATTA AATTTCATGC C	471

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

ATGGGCTTGA TGGGCGTGTC GCAAGGCTTA CCAAACACCA CTAGCAAGTT TGGTATTGAA	60
TTTGACTCTT TAGCTGATGT GGTGCTTTT GGAGTCGCCC CAAGCCTTAT TACTTACTTT	120
TATGTGGGGT ATAACCTTGG GCGTATAGGC ATGGCGGTGA GCGCGTTGTT TGTGATTTTT	180
GGAGCGATAC GATTAGCGCG ATTCAATATC AGCACCAACA CAAGCGATCC CTATTCTTTC	240
ATCGGTATCC CCATTCCTGC GGCGGCGGTA TTGGTGGTGC TTTGCGTGTT ATTAGATAAT	300

AAATACCATT TCTTAGAAGG CAATACCGAA AAGTTATTTT TAGGCTTTAT TGTCTTATTA	360
GGGGTGCTTA TGGTGAGCAA TATCCGCTAC CCTAATTTTA AAAAAGTCAA GTGGAATCTC	420
AAGCTTTTCA TCTTAGTGTT GATCTTTTTA TCGTTAGTGT TTGTGCGCCC TTTAGAGGCT	480
TTGAGCGTGT TTATGGGGTT GTATTTGATC TATGGCATCA TTCGGTGGAT CTTTTTAATG	540
GTAAAAATTA cTttTAATAA AAATAAAAGC GCA	573

(2) INFORMATION FOR SEQ ID NO:354:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

ATGATAGGAG TTTACCCCAA TTATTCCAAA AAGCAACTAA AACGCCCCTT AGTCATATTT	60
GTAAGTAGGG AGTTAGCGCT GGCTAATGGT ATTCTTACAG ACGCCTATGA CATTGAAGCA	120
AATCTTTACA TGAATGCTCG TATCGTTATG AARAATAATA AAAGGAAACA TTATGAGCAG	180
CGGGTTAATT TACATTTCRT TAGAAGTCTT GGTARCGTGT TTGATCACCG CTCTAATCAT	240
GTATTATGTG ATGAAAAAGA TCTATTACGC	270

(2) INFORMATION FOR SEQ ID NO:355:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 831 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

GTGAAAATAA CCATAATGAT TAAAGATTTT AACCACTATT GTAGAAAAAT AACGAGAGGG	60
TTTGTAAAAA TTCCACCAA AAAACAAGGA GCAAAAAAGA TGAAAAAAGC GGGTTTTCTT	120
TTTTTGGCGG CGATGGCTAT CATTGTTGTG AGTTTAAACG CCAAAGATCC GAATGTGTTG	180
CGTAAGATTG TTTTGTAGAA ATGTTTGCCT AATTATGAGA AAAATCAAAA TCCTTCACCA	240
TGCATAGAAG TCAAACCCGA CGCCGGCTAT GTGGTTTTAA AAGATATTAA CGGTCCGTTG	300
CAATATTTGT TGATGCCAAC GACTCACATT AGTGGCATTG AAAACCCTTT GTTGCTTGAT	360
CCTTCTACGC CTAACTTTTT TACTTGTCA TGGCAAGCGC GCGATTTTAT GAGTWAAAAA	420
TACGGAAAAC CCATTCCTGA TTATGCGATC TCTTTGACGA TCAATTCTAA AAAAGGGCGA	480
TCGCAAAACC ATTTTCACAT CCATATTTCT TGCATTAGCC TTGATGTGCG CAAACAGCTG	540
GATAATAATC TAAAAAATAT CAACAGCCGT TGGTCGCCAT TATCAGGTGG CTTGAACGGG	600
CATAAATATT TGGCGCGTCG GGTAACAGAG AGCGAATTAG CGCAAAAAAG CCCGTTTGTC	660
ATGCTTGCTA AAGAAGTGCC TAACGCGCAC AAACGCATGG GAGACTATGG CTTGGCGGTG	720
GTGCAACAGA GCGATAACTC CTTTGTCTTG TTAGCGACAC AATTTAACCC ATTGACTTTA	780
AATCGCGCTT CAGCCGAAGA GATTCAAGAT CATGAATGCG CGATTTTGCG T	831

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...174
- (D) OTHER INFORMATION: /note= "surface antigen"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

GTGCTAACGA GTGGGGACAT GATCACTTGT CCGTATTGCG GGCGTATTTT RTACGCTGAG	60
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AGTACGCATG AAAGTAACGC TCAACCTCCA AAAGAAAGCC AACCAAAAGA AAGCCAAGAA	120
GAAAGCCAAG AAGAAAGCCA AGAAGAAAGC CAAGAAGCCG TCCGTTTGAT TGTT	174

(2) INFORMATION FOR SEQ ID NO:357:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 837 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

ATGAAATTGA ATGACCCTTT CACAAGCCCT AATAAAGCCA AAAAAGAATT ATCGCCAAAA	60
GGCTTTAGGG GGGGGTTAGA GTCTGAAATT TTATTAGGCT TTGTCTTGCA AAAAGAAAGG	120
GTTTTTTTGC ACACGCATGA GCATTTGGAA TTAAGCCACG AAGAAGAAAC ACGCTTTTTT	180
GAATTGGTAG GAAAGCGTTT GAATGACTGC CCCATAGAGT ATTTATTAGG AAGCTGTGAT	240
TTTTATGGGC GCTCTTTTTT CGTGAATGAG CATGTTTTAA TCCCACGGCC TGAAACCGAG	300
ATTTTAGTCC AAAAAGCCCT TAATATTATT TCTCAATACC ATTTAAAAGA AATAGGCGAA	360
ATCGGCATAG GGAGCGGATG CGTGTCCGTG AGTTTGGCTT TAGAAAACCC TAATCTCTCT	420
ATTTATGCGA GCGATATTTT ACCAAAAGCT TTAGAAGTGG CGTTAAAAAA TATTGAACGC	480
TTTTGTCTAA AAGAGCGTGT TTTTTTAAAA CAAACGCGCC TTTGGGATCA TATGCCAACG	540
ATAGAAATGC TTGTCTCTAA CCCGCCCTAT ATCGCTAGAA ATTATCCTTT GGAAAAATCC	600
GTTCTCAAAG AACCGCACGA AGCCCTTTTT GGGGGGGTTA AAGGCGATGA AATCTTAAAA	660
GAAATCGTTT TTTTAGCCGC TAAATTAAAA ATCCCTTTTT TGGTTTGTGA AATGGGGTAT	720
GACCAGTTAA AGAGCTTGAA AGAATGCTTG GAGTTTTGCG GTTATGATGC AGAGTTTTAC	780
AAGGATTTGA GCGGCTTTGA TAGAGGGTTT GTGGGCGTTT TAAAAGTTT TTTAAGA	837

(2) INFORMATION FOR SEQ ID NO:358:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

ATGATTTCTT TCATTGGGTT TGAATGCTCC GCATTAAAAG TTTTTTTAAC TTTTGGTTAC 60

ATAGTTTTTA AAAGYTGCA CTATAGCGCT ATAAGACTAA TTGTTATA 108

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 387 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

GTGATCCAGT CTCACCCTAA ACAAACTCTA ATTGAAGATG AAAATTATTT TTATGCTAAC 60

AAGGGTCTTT ATAAACCAA CAAAGAAGCC TTTTAAAGG TTTATAAAAT CCCAGAGAGC 120

ATGCCCATAG AAAACGAGA AAGTTTAAGC AAGGTTTCTA AAATCTTTTT AGCGTTGCTT 180

TTTTTCATTT CTAGCATGCT TTTTGGGATC TTTTGGCGTT TGCCCAAACG ATTGGACACT 240

AAAATGAGTT TAGAGAGCGC GCACAAAAAC GAATTAGAAA ATGCATTCCA ACGATACGAT 300

GCGCTAGGGG TCGGTTTTGA AGACATTGCA GGGGTGAATG AAGTCAAAGA AGAATTACTA 360

GAAGTGATRG ATTWTTTWAA AAAACCC 387

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

ATGTTTGTAG TTAAATGGT GTTAGGGTTT TTGATCCTTT TAAGCCCTTT GTGCGCTACT	60
GGATTGGATA TTTCACAAAC AGACATTATA GAGCGTTCCT TAAATTCCT CTTGTTTGTG	120
GGGATTTTGT GGTATTTTTT GGCTAAAAGA TTGCGTTCAT TTTTGCATTC CAAAAGCCTT	180
GAAATCTCCA AACGCTTAGA AGAGATTCAA GCCCAACTTA AAGTGAGTAA AGAACATAAG	240
AAAAAECTCC TTAAAGAATT AGAGCAAGCC AAAGAAAAAG CTGAATTGAT TATTTCTGAT	300
GCGAATAAAG AAGCCCTACA CGATCACGCA AAAATACGAA TTACAAACCA AAATGGATGT	360
GGAAAATTTG ATCAAAAATT C	381

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 885 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

ATGAGGGTTT TAGAGTGGA ATATTGGTTA AATACTGATA AGTGGGATAC GCCCACCAAC	60
AAACCGCCTC AAACTTTTAA AATACAAATT TTAAAGATAC AAATAGGTAT AATCAATAAC	120
TTCAATCATT TAATCAAAGG GAGTTCTATG AAAAACGCTT TCAAAGCGTT TGCCTTGTTA	180
ATCGTATTTT TCTCAAACGC TCTATTAGCG CAGGATTTAA AAATCGCTGC TGCTGCTAAT	240
CTCACGCGCG CTTTAAAGC CCTTGTTAAA GAATTTCAAA AAGAACACCC AAAAGACGCT	300

ATTAACATTA GCTTTAATTC TTCAGGCAAA CTCTACGCTC AAATCGCTCA AAACGCCCCT	360
TTTGATTTAT TCATTTTCAGC GGATATTGCT AGACCCAAAA AACTTTATGA TGAAAAAATA	420
ACCCCTTTTA AAGAAGAAGT CTATGCTAAA GCGTGTTGG TTTTATGGAG TGAAAATCTA	480
AAAATGGATT CTTTAGAAAT TCTTAAAGAC CCTAAAATTA AACGTATCGC TATGGCTAAT	540
CCTAAACTAG CCCCTTATGG AAAAGCCAGC ATGGAAGTCT TGGATCGTTT AAAACTCACT	600
CCTAGTCTTA AATCTAAAAT CATTTATGGC GCTTCTATTT CTCAAGCCCA TCAATTCATC	660
GCCACCAAAA ACGCTCAAAT AGGCTTTGGA GCGTTATCTT TGATCGATAA AAAAGACAAA	720
AACCTCTCTT ATTTTCATCAT TGATAAAACC CTTTATAACC CTATTGAACA AGCCTTAATC	780
ATCACTAAAA ATGGGGCTAA TAACCCTTTA GCCAAAGTTT TTAAAGATTT TTTATTCAGC	840
CCTAAAGCTA GAGCTATCTT TAAAGAATAC GGCTATATTG TGGAT	885

(2) INFORMATION FOR SEQ ID NO:362:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

GTGGCTTTAT TAGAGCCAAG CGTGATGTAT CTTACCGAAA AGTATCAATA CTCTCGTTTT	60
AAGGTTACTT GGGGTCTTGT AGCGTTAATC TTTGTGGTAG GCGTGGTGTT GATTTTCTCG	120
CTCCATAAGG ATTATAAAGA CTATCTCACT TTCTTTGAAA AAAGTCTTTT TGATTGGTTG	180
GATTTTGCAT CAAGCACCAT TATCATSCCT TTAGGCGGGA TGRCAACCTT TATTTTATG	240
GGCTGGGTTT TGAAAAAAGA AAAATTGCGT CTTTGTAGCG CGCACTTTT AGGCCCTAAA	300
TTGTTTGCAA CTTGGTATTT CTTGCTTAAA TACATCACCC CTTTAATTGT GTTTTCCATT	360
TGGTTGAGCA AGATTTAT	378

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

GTGGGGCTTA TGAAAATAAG ATTTATGGGG CGGAGTGTTT TTGTGGGGGA TTTGGAACGC	60
ATTGAAGAAG TGGCTAGATT TGAAGAATTT TGGCTTTTAG GGGGGCAAAA AGCGATCAAA	120
GAGCCTAGAA GATTGGTTTT AGAAATCGCT TAAAACACC AGCTCAACAA GCTTTTAAAA	180
CGCGTTCAAA AGCATTTCAA AGAAGACGAA TTAGGAATTT TTAAACAAAT GCATGACAAA	240
AAAATTCAAA GCGTCGCCAC CAATTCCATA GGGCGTTTGT TTGATATAGT GCGGTTTAGT	300
TTGGGCGTGG TGGGAACGAT TAGTTTTGAA GCCGAGAGCG GGCAGGTTTT AGAAAATCTA	360
GCCCTACAAA GCGATGAGAT CGCTTTTAC CCTTTTGAAA TCAAAAACAG CGTGGTGCGT	420
TTGAAGGAAT TTTATCAAGC GTTTGAAAAG GATTGCGG TTTTAGAACC CAAACGCATC	480
GCTAAGAAAT TTTTAAACAG CTTAGTAGAA ATCATTACCG CTTTGATTGC GCCTTTTAAA	540
GGGCATGTCG TGGTGTGCAG TGGGGGCGTG TTTTGCAACC AATTGTTGTG CGAACAATTA	600
GCCAAGCGAT TGAAAAAGCT TCAAAGGGAG TATTTTTTCC ACAAGCATTT CCCCCCTAAT	660
GACAGYAGTA TCCCTGTCGG TCAAGCCTTA ATGGCGTATT TCAACCCTAC AATCATCAAA	720
AAAGGA	726

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 453 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

GTGAGCGATT CTAACGCTTT AAAGGAAGTG TTTTAAACA TCAGCGCTAA AGAAGATCAT	60
TGCGACGTTT TGATCAATTC CGCCGGTTAT GGGGTGTTTG GGAGCGTGGA AGACACGCCC	120
ATTGAAGAGG TTAAAAAGCA ATTTAGCGTG AATTTTTTCG CCCTTTGTGA AGTGGTGCAA	180
CTTTGTTTGC CCTTATTAAA AAACAAGCCT TATTCTAAGA TTTTCAATCT TTCTTCCATA	240
GCGGGGCGTG TGAGCATGCT CTTTTTAGGC CATTACAGCG CGAGTAAGCA TGCCTTAGAG	300
GCTTATAGCG ATGCCTTGCG TTTAGAGCTT AAGCCCTTTA ACGTTCAAGT GTGTTTGATT	360
GAGCCAGGCC CGGTGAAAAG CAATTGGGAA AAAACCGCTT TTGAAAATGA TGAGCGGAAA	420
GATAGCGTTT ATGCTTTGGA AGTGAATGCG GCT	453

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

GTGATAGTGG CGTGGCTTTT TAGGTTTAAA AGCATTGCGT TTTCTATTTT AATCACTCTG	60
TTGGTTATTT TAGTGGATAT TTGGGTGTAT AGCGATGTGC GCCAGTTTTT ATTGGACACT	120
TCTAGCTCTT TTATTTGGCT TTTAATCGCT TTACTAATCA AGTGGGGCGT GATTGTTATA	180
AGTGCGCGCA AATGCTACCA ATTCAGCCAA AAAATGTTTG CGTTAATCCA AAGAAAAAGG	240
CAAATCAGAG AGAATTTAAA AAACCGCTCC AATCGCAAAG ATGCTAAAAA TTTTGAAAAA	300
CTCTCTAACA TCGCTGAAGA AATCATTTCA AAAAAACAAG AAGAGTCCCA CCACAAAGAA	360
GATTCTAATG ATGAAAACCA CAAAGACAAG CTTTCTAACA TTACCGAAGA AATGATTCTC	420
AAAAAACAAG AGGAACTGAA AGCTAGAAAG GATAAGGGGG AT	462

(2) INFORMATION FOR SEQ ID NO:366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

ATGAACTACC CTAATCTACC TAACAGCGCT TTAGRGATAA GCGAACAGCC AGAAGTGAAA	60
GAAATCACTA ACGAGCTTTT AAAGCAATTA CAAAACGCTT TAAGGAGCAA CGCGCATTTT	120
AGCGAGCAAG TGGAATTAAG CCTTAAATGC ATCGTTAGGA TTTTAGAAGT GCTTTTGAGT	180
TTGGATTTTT TTAAGAATGC GAATGAGATT GATAGCAGTT TAAGAAATTC CATTGAGTGG	240
CTGACTAACG CCGGCGAGAG CTTGAAATTA AAAATGAAAG AATACGAGCG CTTTTTTAGC	300
GAGTTTAATA CGAGCATGCA TGCCAACGAG CAGGAAGTAA CCAATACCTT AAACGCTAAC	360
GCCGAGAACA TTAAAAGCGR AATTAAAARG CTAGAAAATC AATTGATAGA AACCACGACA	420
AGACTTTTAA CGAGCTATCA AATCTTTTTA AACCAAGCCA GAGATAACGC TAACAACCAA	480
ATCACAAAAA ACAAACCCR AAGCCTTGAA GCGATTACAC AAGCTAAAAA CAACAGC	537

(2) INFORMATION FOR SEQ ID NO:367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

GTGTTTGCCA CTGACAGCAG TAGCTTTTCT ATGGGGCTTA CCATGGCGAG TGCTTATGAY	60
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CCCATTTCAG GATCGCAAAA ACCCATTTGTG GGGCAAGCCC TTTTATTGTT AGCGATTTTA	120
ATTTTATTGG ATTTATCGTT CCACCATCAA ATCATTTTAT TTGTGGATCA CAGCTTAAAA	180
GCCGTCCCTT TAGGGCGATT TGTCTTTGAG CCAGAATTAG CTAAAAACAT TGTCAAAGCC	240
TTTTCACACT TGTTTGTTCAT AGGGTTTTCT ATGGCGTTCC CTATTTTATG CTTGGTGTTA	300
TTGAGCGATA TTATTTTTTG CATGATCATG AAAACCCACC CTCAATTCAA CCTGCTCGCT	360
ATCGGGTTTC CGGTTAAAAT TGCATCGGG TTTGTGGGCA TTATTTTAAT CGCTTCGGCT	420
ATCATGGGGC GTTTTAAAGA AGAAATCAGC CTGGCCTTTA GCGTTATTTRG TAAAATCTTT	480

(2) INFORMATION FOR SEQ ID NO:368:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

ATGTATGGCG TGAAAGAGAT TAAAGATAAA ATTGACAAGC AACTCCACAA TAACGATCAT	60
TTGTTTGAAG GGCTTTTTTG GGAAAAAGAA GATTTGAAAA AATTGGTGAG CATGTTTGGG	120
CAGTTGCGTT TCCAAAAGCG CTGGAGCCAA ACCCCAAGAG TGCCACAAAC CAGTGTCTA	180
GGGCATACTT TATGCGTGGC GATTATGGGG TATTTATTGA GTTTTGACTT GAAAGCTTGT	240
AAAAGCATGC GGATCAATCA TTTTGTGGG GGGCTTTTTC CA	282

(2) INFORMATION FOR SEQ ID NO:369:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 438 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

```
ATGACTTTAG ATGACTTATT AGGGGGGAGT TTGGACCCGC ATTGTTTTTG CAAACCCTTA      60
ATCAAAACCA AAAAAGACCA AGAAAGGCTC TTATCCCTTG CTTTAAAAGC CCACCCTAAA      120
ATCTCTTTTG GAWWGGACAG TGCCCCGCAT TTCATTTCTA AAAAGCATAG CGCTAACATC      180
CCGGCGGGCA TCTTTTCTGC CCCTATTTTG TTGCCTGCGT TGTGCGAACT TTTTGAAAAA      240
CACAACGCTT TAGAAAATTT GCAAGCCTTT ATCAGTGATA ACGCTAAAAA AATCTACGCG      300
CTAGACAATT TACCCAGTAA AAAAGCGCAT TTGTCTAAAA AACCTTTTAT AGTCCCTACG      360
CACACGCTTT GCTTGAATGA AAAAATCGCT ATCTTAAGAG GGGGCGAAAC GCTATCTTGG      420
AACCTTCAAG AAATCGCC                                     438
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(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

```
ATGGGCGTTT TGGGCATGTT CGCTTTTTTT TCATGGGTTT TTTTATTCAA GCACAATCTC      60
AGCCATAAAA TCCGCTTATA CCATGAAAAA AAGGATTTTG ACAAATTGCT CAAACAAATC      120
CTATCCCAAG ACACCCAAAA GACTTTTTTA AAAACAAAAT TTAAAAGCGA TCTCGCTAAA      180
AACCTCTCTC AAATCTTAGC CCGCTATGAT TTAAAAGCTG ATTTAAACAC GCCAAATAGC      240
GGGTGCGAAA AAGTGGATAA CCTTTTTTAA CATTACCACA ATATAGAAAA TAACACCCTT      300
GAGCCTAAAG ATCACGCTAA ACATTCCCTA GCTTATGAGC ATGCTTATTT TTCTAAACGC      360
TTGAAGGCTT TCATTCATAA CGATTGAAA AACGCCTTTG AAGTTTTAAC AAACGCGCAA      420
ATCCCTTTGG AATTACGCCG CTACGCTTAT AGAAATCGCC CAAAAGGCA GCAAAAAAGA      480
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(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

GTGAGTG TTC CTGCAACGAG TCGGAATTTA GGCCCCGGTT TTGATTGCTT GGGTTTGAGT	60
TTGAATTTAC GCAATCGTTT TTTTATTGAG CCTAGTAATA TCCATGCGGT GAAATTGGTT	120
GGGGAGGGTG AAGGGATCCC TAAATTTTAA ACCAACAATA TTTTCACCAA AGTGTTTTAT	180
GAGATTTTAA AAAAGCATGG GAATGACGGC TCGTTTAAAT TTTTATTGCA TAATAAAGTC	240
CCTATTACAA GGGGCATGGG GTCTAGCTCA GCGATGATTG TGGGGGCGGT CGCTTCAGCG	300
TTTGCGTTTT TAGGGTTTGC TTTTGATAGA GAAAACATTC TCAATACTGC TCTAATTTAT	360
GAAAACCACC CGGATAATAT CACCCCGGCG GTGTTTGGGG GGTATAATGC AGCGTTTGTG	420
GAAAAAAGA AAGTGATAAG TTTAAAAACC AAAATCCCTT CTTTTTTAAA AGCGGTGATG	480
GTGATCCCTA ATAGGGTCAT TTCTACCAAG CAATCGCGCC ATCTCTGCCC AAGCGTTACA	540
GCGTGCAAGA AAGCGTGTTT AACCTTTCGC ATGCGAGTT	579

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

GTGGCTAAAA ATTTGGTAGC GAGCGGGGTT TGCATAAAG CGACCGTGCA GCTTGCTTAT	60
GCGATTGGGG TGATAGAGCC TGTGTCTATT TATGTGAACA CGCATAACAC GAGCAAGCAT	120
TCAAGCGCGG AGTTGGAAAA ATGCGTGAAA TCGGTTTTCA AACTCACGCC AAAAGGCATC	180
ATTGAAAGCT TGGATTTGTT AAGACCCATT TATTCGCTCA CTTCAGCTTA TGGGCATTTT	240
GGGCGCGAGT TAGAAGAATT CACTTGGGAA AAGACTAACA AGGTTGAAGA GATTAAAGCG	300
TTCTTTAAGC GT	312

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

GTGCGTTTGT TTAGATTTGT GGGGTGGTAT TATTTCAAAT ACTTTTAAAT CGTGCTTTTA	60
GCTTTGGAAT TGTTTTTTGT AGGCATTGAC AGCCTGAAAT ACGCCGATAA AATGCCTGAT	120
TCTGCGAACA TGATCATTTT ATTTTTCACC TATGATATTT TATTCGCTCT CAATTACACC	180
TTGCCCATTT CCTTGCTTTT AGCGATGGTT TTATTTTATA TCACCTTCAT TAAATCCAAC	240
CAATACACCG CCCTGCTCTC TATTGGATTT TCCAAATGCC AGATTTTAAG CCCTATTTTT	300
TTGATTAGCC TGTTTTTCAC GGCTGTTTAT GTGGGGTTGA ACGCGACTCC TTTTGTGTAT	360
ATGGAAGAAA AAACGCAAAA TTTAATTTAT AAAGACAATT CTTTGAGCGT TTCAGAGCAT	420
TTGTTAGTGA AATACAACGA TGATTACGTG TATTTTGATA AGATTAATCC CTTATTGCAA	480
AAAGCCCAAA ATATCAAGGT TTTTCGCCTA AAAGATAAAA CTTTAGAATC TTATGCTGAA	540
GCTAAAGAAG CTTTTTTTGA AGACAAATAT TGGATTTTAC ATGACACTAC TATCTATGAG	600
ATGCCCTTGA GTTTTGAACT GGGCGCGAAC GCTTTAAACA CCACGCATTT AGAAACCTTT	660

AAAACGCTCA AAAATTTCCG CCCTAAAGTT TTAGACACCA TTTATCAAAA CAAGCCTGCG	720
GTTTCTATCA CAGACGCTCT TTTATCCTTG CATGCTTTAG TGCGCCAAAA CGCGGACACG	780
AAAAAAGTGC GCTCGTTTTT GTATGTGTTT GCGATTTTGC CCTTTTTTGT GCCGTTTTTA	840
AGCGTTTTAA TCGCTTATTT TTCGCCCAGT CTCGCCCCT ATGAAAACCT GGCTCTTTTA	900
GGGCTAAAGT TTATCATTAT CACGCTCGTT GTTTGGGGGC TATTCTTTGC TTTAGGGAAG	960
TTCAGCATTT CAGGGATACT CATTCTGAA ATAGGCGTTC TATCGCCCTT TTTCGTATTT	1020
CTAGCTCTCA GTCTTTGGTA TTTTAAAAAA CTTAATAAGA GATTG	1065

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

ATGATTTATG GCGTTTTAGA CGGCTTGTTT TTGGCTATTT TACAGGCTCA AAATTACCGC	60
TTCCATTTCGC TTTATTTGTT TGAAGAAAAT TTAGACTTGT TTAAATCAG TTGCTATTTT	120
GCGCGTTATG AAGATTTGAT TAAAAAAGGG GCTAACTTT TTATTCAAGG GTTTTTTAAC	180
CCTAATGAAT TGAAAATGGA TTTTTTGAAA CGCCCTATCA CGCATTCTTT TTTAAAGCTA	240
GAAATCATGC CCTATAAAAG CGCTTTTAAT TTGCGCATGC GAGAAAACAT TCAAAGCTAT	300
TACAAACAAG CCTTAAGGGG TTGGGGGAGT TTTGAAGACG AATTGCTAGG GTTAAAGAAC	360
ACGCTTAAAA ACTTACCCCT ATACCAAACC CTAAAAACCA AACCCAAAAA AATTAACGCC	420
CCCATTTGCG TGGTGGGTAA TGGGCCAAGC CTGGATTTAT TGTTAGATTT TTTAAAAGAA	480
AATGAAGAAA AATTCATCAT TTTTTCATGC GGAACCGCTT TAAAGCCTTT AAAAGCGCAT	540
GGCGTTAAAG TGGATTTTCA AATAGAAGTG GAGCGCATAG ACTATCTTAA GGAGGTTTTA	600
GAAAGAGCCC CCCTAGAAGA CACCCCTTA ATGGGCGCTA ACATGCTCAA TCCTAACGCT	660
TTTGATTTAG CCAAAGAAGC GTTGATGTTT ATGCGTGGGG GGAGCGCTTG CGCAGTA	717

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 867 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

ATGCTGGCGT TTTTAAAAC CCCTAGAAAC AGCGCTTTTG CTTTGGGTYT TTTCGTGGGG	60
GCGTTATTGT TTTACTGGTG CGCTTAAAG CTTTCGCATT CGGATTTTAC YTATTTATTG	120
CCCTTAATCA TTGTTTTAGT AGCGTTAGTT TATGGGGTTT TATTTTATTT GTTGCTCTAT	180
TTTGAAAACC CCTACTTCAG GCTTTTGAGT TTTTLAGGCT CTAGTTTTAT CCACCCTTTT	240
GGATTTGATT GGTTAGTCCC GGATAGCTTT TTTTCTTATA GCGTGTTTAG GGTGGATAAA	300
TTATCTTTAG GGCTTATTTT TTTAGCTTGC ATTTTTTTGA GCGCTCAAAA TCTTAAAAAA	360
TACAGAATGA TAGGGGTTTT ATTGCTGCTT GGCGCGTTGG ATTTTCATTT TTTTAAAATA	420
AGCGATTTAA AAGAGGTTGG AAATATTGAA TTAGTCTCTA CAAGAACGCC CCAAGATTTG	480
AAATTTGACT CAAATTACCT TAATAATATT GAAAACAACA TTCTTAAAGA AATCAAACCTC	540
GCTCAAAGCA AGCAAAAAAC CTTGATTGTT TTTCCAGAGA CCGCTTACCC TATCGCTTTA	600
GAAAACTCCC CTTTTAAAAC CCAACTAGAA GATTTAAGCG ACAAGATCGC CATTTTAATA	660
GGGACATTGC GCGCTCARGG CTATAGCCTT TATAACAGCT CGTTTTTATT TTCTAAAAAA	720
AGCGTTCAAA TCGCTGATAA AGTGATCTTA GCCCCCTTTG GCGAGATAAT GCCTTTACCG	780
GAGTTTCTTC AAAAACCCTT TGAAAAGCTC TTTTTTGCGA GAGCGCTTAT TTATACCGCA	840
ACGCTCCCCA TTTCAGCGAT TTTACAT	867

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

ATGAACGATC CTAAGCATGT GGTGTATGTT TGGCTGGACG CTTTATTGAA TTATGCGAGC	60
GCGTTAGGGT ATTTGAACGG TTTAGACAAT AAAATGGCGC ATTTTGAACG CGCTAGGCAT	120
ATTGTGGGTA AGGATATTTT ACGCTTCCAT GCCATTTATT GGCCAGCCTT TTTGATGAGT	180
TTGAATTTGC CCTTATTCAA ACAGCTCTGT GTGCATGGGT GGTGGACGAT AGAGGGCGTG	240
AAAATGAGTA AGAGCTTGGG TAATGTTTTA GACGCTCAAA AGCTCGCCAT GGAGTATGGG	300
ATTGAAGAAT TACGCTATTT TTTATTGCGT GAGGTGCCTT TTGGGCAAGA TGGGGATTTT	360
TCTAAAAAAG CGTTAGTAGA ACGGATTAAT GCGAATTTGA ATAACGATTT GGGGAATTTG	420
TTGAATCGTT TGCTAGGCAT GGCTAAAAAAG TATTTCAATT ATTCTCTAAA AAGCACCAAA	480
ATCACTGCGT ATTATCCTAA AGAGCTAGAA AAAGCACATC AAATTTTAGA TAACGCTAAT	540
TCTTTTGTGC CTAAATGCA ATTGCATAAG GCTTTAGAGG AATTGTTTAA TATTTATGAT	600
TTTTTGAATA AACTCATCGC TAAAGAAGAG CCGTGGGTCT TGCACAAAAA CAACGAATCA	660
GAAAAATTAG AAGCCTTATT GAGTTTGATC GCAAACACGC TACTACAATC AAGCTTCTTG	720
CTCTATGCGT TCATGCCAAA GAGCGCTATG AAATTAGCGA GCGCTTTTCG TGTAGAAATC	780
ACGCCCAATA ATTACGAACG CTTTTTTAAG GCTAAAAAAT TACAAGATAT GGTTTTACAA	840
GACACCGAGC CTTTATTTTC CAAAATTGAG AAAATTGAAA AGATTGAAAA GATTGAAAAG	900
ATTGAAAAGA TTGAAAAGG GGAGGAAGCC CTAGCAGAAA AAGCAGAAAA AAAAGAAAAA	960
GAAAAAGCCC CACCAACACA AGAAAATTAT ATTAGTATTG AGGATTTCAA GAAAGTAGAG	1020
ATTAAAGTGG GGCTTATCAA AGAAGCTCAA AGGATTGAAA AATCCAATAA ATTACTGCGC	1080
TTAAAAGTGG ATTTAGGCGA AAATCGTTTG AGGCAGATCA TCTCAGGGAT CGCTTTGGAT	1140
TATGAGCCTG AAAGCTTGGT GGGTCAAATG GTGTGCGTGG TGGCTAATTT AAAACCCGCA	1200
AAGCTTATGG GTGAAATGAG TGAGGGCATG ATTTTAGCGG TGCGAGATAA TGATAATCTG	1260
GCTTTAATCA GCCCTACCAG AGAAAAAATT GCAGGAAGTT TGATCAGC	1308

(2) INFORMATION FOR SEQ ID NO:377:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

ATGAAACGAC CGATCAGCAA ATTGAAACAA AACTTTTTTAC AATTCAAACA TTCTTTCAAC	60
AAACATTTAG ATAAGTACAG CCTTTATTAT AGGCTGTTCA ATATCAGCTC TATCGTTATA	120
GGTTTTTTTAA TAGCGCTTTT TTCTTATGGG GCAGGGGTGA TTTTAGTTTA TCCAATATTA	180
TTCTTGTTTG CTCTTATAAT AAAACCTAGC TTTTTTTTATT ACACTACTTA TCTTTTGCTA	240
CTCGTTTCTC TCAGCATAAT AAGCAAATAC TATCTCCTAA GCCACGCAAA TTCACAATG	300
AAGCTAATCA TGCTTATGAC TCAATGGCAA AATTGGTTCT TA	342

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

ATGGG

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(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

GTGTTCACTT ATTCCTTGGG GCAGGTTTTT TTTTCTCTAA GTATCGGTTT AGGGATCAAT	60
ATCACTTATG CTGCCGTTAC GGATAAAACG CAGAATTTGC TTAAAAGCAC GATTTGGGTG	120
GTTTTATCAG GRATTTTAAT TTCTCTGTG RCAGGGCTTA TGATTTTCAC TTTTGTGTTT	180
GAATATGGGG CTAATGTCTC ACAAGGCACA GGGTTAATCT TCACTTCTTT ACCGGTGGTT	240
TTTGGCCAAA TGGGAGCGAT AGGCGTTCCT TGTTTCAATT CTTTCTTGC TCGCGCTCGC	300
TTTTGCTGGC ATCACTTCTA CGGTGGCTTT ATTAGAGCCA AGCGTGATGT ATCTTACCGA	360
AAAGTATCAA TACTCTCGTT T	381

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 537 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

ATGAAACCAT TGCATTTTTT ACACCTGGAC AGAGAGCAAT CAGGCGATGT GGGTTTTATC	60
ATTAAAAACC TTATTTTTTT AGGGGTTTTT TCCTTATTGG GTTGGTTGAA TACCGAGTAT	120
TTTCTATGGC CTAGCATGCT GGAATTAAAA AAAATCCTTT TAGAAGAAAA TCGTAAAAAA	180
AGCGTTTTAG AATACGCGCA AAGGCATTTT GAAACAGCCC TAGCAAATA CCGCAATCAA	240
AAAGAAACCA GCGAATCTTT GTTAAAGATT TTTAATGATG AAGAGTCCAG GCGGATTTTA	300

GAAAAGATCT TAAAAAATG TTTTGACGCC TATAAAATCA AACCCCTTGCT CTCTCAAAAC	360
CCCTCCCAA AAACCCAATT TTTTATCATG GCTAGAGCGA GCGAATTGGA AAAAATTAT	420
CTTTTTTTCA CCTTAATCAA CAAGTATTTA CCGAGCGCTC AAAGCCAATT GCCCTTAAAG	480
ATTTCTAAAG ATAGCGACGG GTTGTGGTG CAATTTGGCG TGAGTATTGA TCTCCAA	537

(2) INFORMATION FOR SEQ ID NO:381:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 627 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

ATGAATGCAT TGAAGCGTGC GTGTTTAAGA TTGATGGGCG AAACCAATAC CGATGATTTA	60
ASCCCARYGA GCGACGCTTT CACACGGAGC GATATTCCTT TACACGCCAA AGCCATGCTA	120
AAAAACCGGA TTGAAAATTA CGAACAACGC ATTGAAGCCA TTAAACTAA AGGCGTTCCT	180
GTAGCGTATG TGGGCGATGT GGTGGGCACA GGAAGCTCTA GAAAAAGCGC GACTAACTCT	240
ATCATGTGGC ATTTTGGTAA GGACATTCCT TTTGTGCCTA ATAAAGGAG TGGAGGCATT	300
GTGATTGGGG GGGTGATCGC TCCGATTTTC TTTGCGACTT GTGAAGATAG CGGGGCGTTA	360
CCCATTGTGG CTGATGTAA GGATTGAAA GAGGGCGATA TCATTAAAAT CTACCCTTAT	420
AAAGGCGAAA TCACGCTGAA CGATAAGGTG GTTAGCACCT TTAAGCTAGA GCCTGAAACT	480
TTATTAGATG AAGTCAGGGC TTCTGGGCGT ATCCCCTTAA TCATTGGTAG GGGTTTGACC	540
AATAAAGCGC GTAAATTTTT GGGCCGGCGA ATCGGAAGCG TTCAAAAAC CTTCCGCCCC	600
TCAAGCGCGC TAAGGCTACA CTTTGCC	627

(2) INFORMATION FOR SEQ ID NO:382:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 702 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

ATGCTTTCAG CCCACCAACC TTTTAAAAAT TACCCTGATC TGATTAAAAA AGAGTTGCAA	60
GAGCATAACG CCTATGCGAG CGTCGCTAGT GGGGTGCCAG CGATGTGTGA TGGTATCACG	120
CAAGGTTATG AGGGAATGGA ATTGAGCTTG TTTAGTAGAG ATGTGATCGC ATTAAGCACC	180
SCCGTAGGGT TAAGCCATAA TGTTTTTGAC GGGGCGTTTT TTTTGGGCGT GTGCGATAAA	240
ATTGTGCCAG GCTTGCTCAT AGGAGCGTTA AGCTTTGGGA ATTTAGCGAG CGTGTTTGTG	300
CCAAGCGGGC CTATGGTGAG CGGGATAGAA AATTATAAAA AAGCCAAAGC GCGCCAAGAT	360
TTTGCAATGG GAAAGATCAA CAGAGAAGAG CTTTTAAAAG TGGAAATGCA AAGCTATCAT	420
GATGTGGGCA CTTGCACTTT TTATGGCACG GCTAATTCTA ATCAAATGAT GATGGAGTTT	480
ATGGGGTTGC ATGTGGCCAA TTCTAGCTTT ATCAACCCTA ACAACCCCTT ACGAAAGGTT	540
TTAGTAGAAG AGAGCGCTAA AAGATTAGCG AGCGGGAAAG TCCTGCCTTT AGCCAAACTC	600
ATTGATGAAA AAAGCATTCT TAACGCTCTT ATAGGCTTAA TGGCAACAGG GGGTTCTACT	660
AACCACACTT TGCATTTGAT CGCTATCGCA GATCTTGTGG GG	702

(2) INFORMATION FOR SEQ ID NO:383:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 795 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

ATGAAATTTT TAAAATTCTT TGCCAGTAGC GTAACCTAG ATGAAAAATT TTAAATGTTT	60
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CTTCTTTGCA ACGCTCTTTC TAACGCTTAC AAAAATAGCG ATTTGTTTTC TTTCTCTAAA      120
GGCTTTTTTAG GCGCTTTTTTT AATCGGGTTT GTGGTGTATT ATGGTTGCGC GCTAATCCCT      180
AAAAAACGCT TGAAATATTC ATTAGAATGG CTGTTTATAG GAAGCGGTAT TATTTTTAGC      240
GTGGCAGAAA TTTTACGCT GTTTATGTTT AAAATGCCTT TTTCCAAAGG CTTGATTGAC      300
ACGCTTTTAG CCACAAACAG CTCTGAAACG ATGGCGTTTA TAAAAAGCTA TAAAAATTAT      360
TTGCTTTACT ACGCTTTGAT TTTGATCGCT TTGTTGATCG CCATTAAAAT CATTCGCTTT      420
AGAGCGCTTG TGCCTGGTGT GATAGCGAGC GTTTTAGGGC TTTCTATCCT TACAATAGGG      480
AGCGTTCGTA ACATTAAACA CCTTACAAAG AACGATGCGA TTTTAAAAAG ATCACTCTTT      540
TCTCTTTCTT TAGCTAGGGG GTTTTATTCC GCTTATTTGA GTTTGTTTGA TCGCCAACAA      600
GCCATAAAAT TTTATAGCTT TTAAATAAT CTTTATTAC CAAGCGATTA TCTTTCTAGC      660
ACGGGCGATA TTTCAAATGT CGTCTTAGTC ATCGCGAAAG CGCGAGCAGA AATTTTCATGC      720
AACTCTATGG CTATAGCGTT CCTAATAATC CTTATSCGA GCGAACTCGC CAACGAGAGA      780
GAGAGAGAGA GAGAG                                                                795

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(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...509
- (D) OTHER INFORMATION: /note= "INTEGRAL MEMBRANE PROTEIN"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384

```

Met Cys Ser Gln Glu Ile Leu Ser Ser Leu Gln Thr Ile Ile Ala Glu
1           5           10           15
Gln Phe Ser Ile Asn Ile Ile Thr Gln Leu Ala Asn Lys Leu Thr Gln
          20           25           30
Val Lys Asn Leu Asn Phe Phe Glu Asn Lys Asp His Thr Ile Lys Leu
          35           40           45

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Asn	Thr	Ile	His	Asn	Gly	Leu	His	Ile	Arg	Pro	Leu	Asn	Tyr	Val	Ser	50	55	60
Asn	Leu	Phe	Phe	Asn	Leu	Gln	Arg	Ile	Ile	Gly	Leu	Ile	Ser	Leu	Phe	65	70	75
Gly	Ile	Leu	Phe	Ser	Ile	Ser	Ile	Tyr	Leu	Pro	Phe	Ile	Met	Ile	Phe	85	90	95
Ala	Thr	Val	Pro	Cys	Ile	Leu	Ile	Ser	Asn	His	Ile	Ala	Lys	Lys	His	100	105	110
Ser	Ala	Ser	Ile	Asp	Lys	Leu	Gln	Asp	Gln	Lys	Glu	Ser	Met	Gln	Asn	115	120	125
Tyr	Leu	Tyr	Ser	Gly	Leu	Asp	Asn	Gln	Lys	Asn	Lys	Asp	Asn	Leu	Leu	130	135	140
Phe	Asn	Phe	Met	Leu	Asn	Phe	His	His	Lys	Phe	Ile	Glu	Thr	Lys	Glu	145	150	155
Leu	Tyr	Leu	Asn	Asn	Phe	Val	Lys	Val	Ala	Gln	Lys	Asn	Leu	Ile	Phe	165	170	175
Thr	Ile	Tyr	Ala	Asp	Val	Leu	Ile	Thr	Thr	Leu	Ser	Ile	Ala	Leu	Phe	180	185	190
Phe	Leu	Met	Val	Phe	Ile	Ile	Leu	Ser	Lys	Leu	Ile	Gly	Val	Gly	Ala	195	200	205
Ile	Ala	Gly	Tyr	Ile	Gln	Ala	Phe	Ser	Ser	Thr	Gln	Gln	Gln	Leu	Gln	210	215	220
Asp	Leu	Ser	Phe	Tyr	Gly	Lys	Trp	Phe	Phe	Ala	Ile	Asn	Lys	Tyr	Phe	225	230	235
Glu	Asn	Tyr	Phe	Cys	Ile	Leu	Asp	Tyr	Lys	Ile	Pro	Lys	Pro	Glu	Thr	245	250	255
Gln	Ile	Lys	Leu	Glu	Glu	Lys	Ile	His	Ser	Ile	Thr	Phe	Glu	Asn	Ile	260	265	270
Ser	Phe	Ser	Tyr	Pro	Asn	Ser	Lys	Leu	Ile	Phe	Glu	Asn	Phe	Asn	Leu	275	280	285
Ser	Leu	His	Ser	Asn	Lys	Ile	Tyr	Ala	Leu	Val	Gly	Lys	Asn	Ala	Ser	290	295	300
Gly	Lys	Ser	Thr	Leu	Ile	Asn	Leu	Leu	Leu	Gly	Phe	Tyr	Thr	Pro	Asn	305	310	315
Ser	Gly	Gln	Ile	Ile	Ile	Asn	Asn	Lys	Tyr	Pro	Leu	Gln	Asp	Leu	Glu	325	330	335
Leu	Asn	Ser	Tyr	His	Gln	Gln	Met	Ser	Ala	Ile	Phe	Gln	Asp	Phe	Ser	340	345	350
Leu	Tyr	Ala	Gly	Tyr	Ser	Ile	Asp	Asp	Asn	Leu	Phe	Met	Gln	Asn	Asn			

355	360	365
Ile Thr Lys Glu Gln Leu Lys Gln Lys Arg Glu Ile Leu Lys Ser Phe 370 375 380		
Asp Glu Asn Phe Gln Asn Cys Leu Asn Asp Cys Asn Asn Thr Leu Phe 385 390 395 400		
Gly Ala Gln Tyr Asn Gly Val Asp Phe Ser Leu Gly Gln Lys Gln Arg 405 410 415		
Ile Ala Thr Met Arg Ala Phe Leu Lys Pro Ser Asn Cys Ile Val Leu 420 425 430		
Asp Glu Pro Ser Ser Ala Ile Asp Pro Ile Met Glu Lys Glu Phe Leu 435 440 445		
Asp Phe Ile Phe Lys Lys Ser Gln Ser Lys Met Ala Leu Ile Ile Thr 450 455 460		
His Arg Met Asn Ser Val Lys Gln Ala Asn Glu Ile Ile Val Leu Asp 465 470 475 480		
Gln Gly Lys Leu Ile Glu Gln Gly Asn Phe Glu Thr Leu Met Lys Lys 485 490 495		
Gln Gly Leu Phe Cys Glu Leu Phe Leu Lys Gln Gln Tyr 500 505		

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

Met Lys Gly Pro Ile Leu Trp Pro Ala Phe Ser Gln Phe Ser Asp Gln 1 5 10 15
Asp Leu Ser Asp Ile Val Ala Tyr Leu Thr Ser Ile Leu Pro Lys Asn 20 25 30
Leu Ser Asp Lys Glu Val Phe Ala Gln Ser Cys Gln Arg Cys His Ser 35 40 45
Leu Asp Tyr Ala Lys Asp Lys Ala Phe Ser Asp Pro Lys Asp Leu Ala 50 55 60

Asn Tyr Leu Gly Ser His Ala Pro Asp Leu Ser Met Met Ile Arg Ala
 65 70 75 80
 Lys Gly Glu His Gly Leu Asn Val Phe Ile Asn Asp Pro Gln Lys Leu
 85 90 95
 Leu Pro Gly Thr Ala Met Pro Arg Val Gly Leu Asn Glu Lys Ala Gln
 100 105 110
 Lys Gln Val Ile Ser Tyr Leu Glu Lys Ala Gly Asp Arg Lys Lys His
 115 120 125
 Glu Arg Asn Thr Leu Gly Ile Lys Ile Met Ile Phe Phe Ala Val Leu
 130 135 140
 Ser Phe Leu Ala Tyr Ala Gly Lys Glu Lys Phe Gly Ala Lys Cys Ile
 145 150 155 160
 Lys Phe Lys Lys Gly Gly Thr Trp Phe Tyr Asp Phe
 165 170

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...133
- (D) OTHER INFORMATION: /note= "biopolymer transport exbB protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

Met Glu Arg Lys Thr Leu Gln Ser Ile Leu Cys Leu Ile Lys Lys Glu
 1 5 10 15
 Met Met Arg Pro Lys Gly Ile Leu Met Asn Cys Cys Arg Thr Trp Lys
 20 25 30
 His Gln Val Leu Lys Gln Ser Thr Thr Gly Leu Val Val Leu Ser Ile
 35 40 45
 Ile Ser Ser Thr Ala Pro Phe Ile Gly Leu Phe Gly Thr Val Val Glu
 50 55 60
 Ile Leu Glu Ala Phe Asn Asn Leu Gly Ala Leu Gly Gln Ala Ser Phe
 65 70 75 80

Gly	Val	Ile	Ala	Pro	Ile	Ile	Ser	Lys	Ala	Leu	Ile	Ala	Thr	Ala	Ala	85	90	95
Gly	Ile	Leu	Ala	Ala	Ile	Pro	Ala	Tyr	Ser	Phe	Tyr	Leu	Ile	Leu	Lys	100	105	110
Arg	Lys	Val	Tyr	Asp	Leu	Ser	Val	Tyr	Val	Gln	Met	Gln	Val	Asp	Ile	115	120	125
Leu	Ser	Ser	Lys	Lys												130		

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

Met	His	Glu	Arg	Ile	Glu	Arg	Gly	Ile	Xaa	Asn	Asn	Glu	Cys	Lys	Glu	1	5	10	15
Ile	Phe	Gly	Asn	Glu	Leu	Lys	Gln	Arg	Lys	Thr	Lys	Leu	Ile	Glu	Asp	20	25	30	
Ile	Glu	Arg	Arg	Phe	Lys	Glu	Cys	Glu	Glu	Gln	Phe	Arg	Gly	Ser	Val	35	40	45	
Gly	Lys	Asn	Ile	Glu	Gln	Leu	Glu	Glu	Arg	Val	Lys	Asp	Ser	Leu	Ala	50	55	60	
Ile	Ile	Lys	Arg	Ile	Asn	Asn	Leu	Gly	Leu	Asn	Pro	Asn	Ser	Asn	Phe	65	70	75	80
Asn	Met	Asp	Ser	Gly	Ile	Asp	Thr	Ile	Gly	Leu	Phe	Ser	Ser	Ile	Gly	85	90	95	
Gly	Leu	Val	Leu	Leu	Leu	Thr	Pro	Val	Val	Gly	Glu	Phe	Ala	Leu		100	105	110	
Ile	Ala	Gly	Val	Gly	Leu	Ala	Leu	Val	Gly	Val	Gly	Lys	Ser	Ile	Trp	115	120	125	
Ser	Phe	Phe	Asp	Ser	Asp	Tyr	Lys	Lys	Ser	Gln	Gln	Arg	Lys	Glu	Val	130	135	140	
Asp	Lys	Asn	Leu	His	Gln	Ile	Cys	Glu	Lys	Leu	Cys	Arg	Met			145	150	155	

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

Met	Pro	Gly	Val	Tyr	Gln	Met	Ser	Ile	Glu	Pro	Leu	Leu	Lys	Glu	Cys
1				5					10					15	
Glu	Glu	Leu	Val	Gly	Leu	Gly	Ile	Lys	Ala	Val	Leu	Leu	Phe	Gly	Ile
			20					25					30		
Pro	Lys	His	Lys	Asp	Ala	Thr	Gly	Ser	His	Ala	Leu	Asn	Lys	Asp	His
		35					40					45			
Ile	Val	Ala	Lys	Ala	Thr	Arg	Glu	Ile	Lys	Lys	Arg	Phe	Lys	Asp	Leu
		50				55					60				
Ile	Val	Ile	Ala	Asp	Leu	Cys	Phe	Cys	Glu	Tyr	Thr	Asp	His	Gly	His
65				70						75				80	
Cys	Gly	Ile	Leu	Glu	Asn	Ala	Ser	Val	Ser	Asn	Asp	Lys	Thr	Leu	Lys
			85						90					95	
Ile	Leu	Asn	Leu	Gln	Gly	Leu	Ile	Leu	Leu	Lys	Ala	Val	Trp	Ile	Phe
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...65
- (D) OTHER INFORMATION: /note= "FLAGELLAR HOOK-ASSOCIATED"

PROTEIN 1 HAP1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Val	Glu	Asn	Asn	Lys	Ser	Leu	Lys	His	Ala	Asn	Glu	Leu	Arg	Asp	Lys
1				5					10					15	
Arg	Asp	Glu	Leu	Glu	Phe	His	Leu	Arg	Glu	Leu	Phe	Gly	Gly	Asn	Val
			20					25					30		
Phe	Lys	Ser	Ser	Ile	Lys	Thr	His	Ser	Leu	Thr	Asp	Lys	Asp	Ser	Ala
			35				40					45			
Asp	Phe	Asp	Glu	Ser	Tyr	Asn	Leu	Asn	Ile	Gly	His	Gly	Xaa	Asn	Xaa
	50					55				60					
Ile															
65															

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Met	Gln	Glu	Phe	Ser	Leu	Trp	Cys	Asp	Phe	Ile	Glu	Arg	Asp	Phe	Leu
1				5					10					15	
Glu	Asn	Asp	Phe	Leu	Lys	Leu	Ile	Asn	Lys	Gly	Ala	Ile	Cys	Gly	Xaa
			20					25					30		
Thr	Ser	Asn	Pro	Ser	Leu	Phe	Cys	Glu	Ala	Ile	Thr	Lys	Ser	Ala	Phe
			35				40					45			
Tyr	Gln	Asp	Glu	Ile	Ala	Lys	Xaa	Gln	Arg	Gln	Lys	Ser			
	50					55				60					

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...619

(D) OTHER INFORMATION: /note= "INVOLVED IN F PILUS ASSEMBLY"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

```
Val Phe Val Ala Ser Lys Gln Ala Asp Glu Gln Lys Lys Leu Val Ile
1          5          10          15

Glu Gln Glu Val Gln Lys Arg Gln Phe Gln Lys Ile Glu Glu Leu Lys
20          25          30

Ala Asp Met Gln Lys Gly Val Asn Pro Phe Phe Lys Val Leu Phe Asp
35          40          45

Gly Gly Asn Arg Leu Phe Gly Phe Pro Glu Thr Phe Ile Tyr Ser Ser
50          55          60

Ile Phe Ile Leu Phe Val Thr Ile Val Leu Ser Val Ile Leu Phe Gln
65          70          75          80

Ala Tyr Glu Pro Val Leu Ile Val Ala Ile Val Ile Val Leu Val Ala
85          90          95

Leu Gly Phe Lys Lys Asp Tyr Arg Leu Tyr Gln Arg Met Glu Arg Ala
100         105         110

Met Lys Phe Lys Lys Pro Phe Leu Phe Lys Gly Val Lys Asn Lys Ala
115         120         125

Phe Met Ser Ile Phe Ser Met Lys Pro Ser Lys Glu Met Ala Asn Asp
130         135         140

Ile His Leu Asn Pro Asn Arg Glu Asp Arg Leu Val Ser Ala Ala Asn
145         150         155         160

Ser Tyr Leu Ala Asn Asn Tyr Glu Cys Phe Leu Asp Asp Gly Val Ile
165         170         175

Leu Thr Asn Asn Tyr Ser Leu Leu Gly Thr Ile Lys Leu Gly Gly Ile
180         185         190

Asp Phe Leu Thr Thr Ser Lys Lys Asp Leu Ile Glu Leu His Ala Ser
195         200         205

Ile Tyr Ser Val Phe Arg Asn Phe Val Thr Pro Glu Phe Lys Phe Tyr
210         215         220

Phe His Thr Val Lys Lys Lys Ile Val Ile Asp Glu Thr Asn Arg Asp
225         230         235         240

Tyr Gly Leu Ile Phe Ser Asn Asp Phe Met Arg Ala Tyr Asn Glu Lys
```

245										250					255				
Gln	Lys	Arg	Glu	Ser	Phe	Tyr	Asp	Ile	Ser	Phe	Tyr	Leu	Thr	Ile	Glu				
			260					265					270						
Gln	Asp	Leu	Leu	Asp	Thr	Leu	Asn	Glu	Pro	Val	Met	Asn	Lys	Lys	His				
		275					280					285							
Phe	Ala	Asp	Asn	Asn	Phe	Glu	Glu	Phe	Gln	Arg	Ile	Ile	Arg	Ala	Lys				
	290					295				300									
Leu	Glu	Asn	Phe	Lys	Asp	Arg	Ile	Glu	Leu	Ile	Glu	Glu	Leu	Leu	Ser				
305					310					315					320				
Lys	Tyr	His	Pro	Thr	Arg	Leu	Lys	Glu	Tyr	Thr	Lys	Asp	Gly	Ile	Ile				
				325				330						335					
Tyr	Ser	Lys	Gln	Cys	Glu	Phe	Tyr	Asn	Phe	Leu	Val	Gly	Met	Asn	Glu				
			340					345					350						
Ala	Pro	Phe	Ile	Cys	Asn	Arg	Lys	Asp	Leu	Tyr	Leu	Lys	Glu	Lys	Met				
		355					360					365							
His	Gly	Gly	Val	Lys	Glu	Val	Tyr	Phe	Ala	Asn	Lys	His	Gly	Lys	Ile				
	370					375				380									
Leu	Asn	Asp	Asp	Leu	Ser	Glu	Lys	Tyr	Phe	Ser	Ala	Ile	Glu	Ile	Ser				
385					390					395					400				
Glu	Tyr	Ala	Pro	Lys	Ser	Gln	Ser	Asp	Leu	Phe	Asp	Lys	Ile	Asn	Ala				
			405					410						415					
Leu	Asp	Ser	Glu	Phe	Ile	Phe	Met	His	Ala	Tyr	Ser	Pro	Lys	Asn	Ser				
			420					425					430						
Gln	Val	Leu	Lys	Asp	Lys	Leu	Ala	Phe	Thr	Ser	Arg	Arg	Ile	Ile	Ile				
	435						440					445							
Ser	Gly	Gly	Ser	Lys	Glu	Gln	Gly	Met	Thr	Leu	Gly	Cys	Leu	Ser	Glu				
	450					455					460								
Leu	Val	Gly	Asn	Gly	Asp	Ile	Thr	Leu	Gly	Ser	Tyr	Gly	Asn	Ser	Leu				
465					470					475					480				
Val	Leu	Phe	Ala	Asp	Ser	Phe	Glu	Lys	Met	Lys	Gln	Ser	Val	Lys	Glu				
			485					490						495					
Cys	Val	Ser	Ser	Leu	Asn	Ala	Lys	Gly	Phe	Leu	Ala	Asn	Ala	Ala	Thr				
			500					505					510						
Phe	Ser	Met	Glu	Asn	Tyr	Phe	Phe	Ala	Lys	His	Cys	Ser	Phe	Ile	Thr				
		515					520					525							
Leu	Pro	Phe	Ile	Phe	Asp	Val	Thr	Ser	Asn	Asn	Phe	Ala	Asp	Phe	Ile				
	530					535					540								
Ala	Met	Arg	Ala	Met	Ser	Phe	Asp	Gly	Lys	Glu	Asp	Asn	Asn	Ala	Trp				
545					550					555				560					

Gly Asn Ser Val Met Thr Leu Lys Ser Glu Ile Asn Ser Pro Phe Tyr
 565 570 575
 Leu Asn Phe His Met Pro Thr Asp Phe Gly Ser Ala Ser Ala Gly His
 580 585 590
 Thr Leu Ile Leu Gly Ser Thr Gly Ser Gly Lys Asn Ser Val Tyr Val
 595 600 605
 His Asp Ser Lys Arg Tyr Gly Ala Ile Cys Leu
 610 615

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

Val Lys Thr Ser Cys Leu Val Thr Ile Gly Arg Ile Arg Gly Val Phe
 1 5 10 15
 Ile Ile Lys Ala Gln Leu Leu Leu Arg Glu Gly Gly Phe Met Asn Phe
 20 25 30
 Thr Ala Tyr Asn Thr Lys Thr Pro Gly His Leu His Leu Tyr Val His
 35 40 45
 Lys Gly His Thr Glu Leu Gly Glu Gly Glu Arg Leu Ile Lys Thr Leu
 50 55 60
 Ser Met Lys Leu Ala Gln Gly Leu Pro Lys Glu Trp Arg Val Phe Pro
 65 70 75 80
 Ser Asn Glu Trp Pro Lys Glu Phe Asn Ile Leu Ala Leu Pro Tyr Glu
 85 90 95
 Val Phe Ala Lys Glu Arg Gly Ser Ser Trp Ala Lys His Leu
 100 105 110

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...68
 - (D) OTHER INFORMATION: /note= "H+-transporting ATP synthase alpha chain homolog"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

```

Val Ala Lys Asp Ile Ile Ser Glu Ser Gln Asn Leu Cys Ala Arg Lys
1           5           10           15
Phe Arg Arg Leu Tyr Ala Leu Leu Lys Glu Asn Glu Met Leu Ile Arg
          20           25           30
Ile Gly Ser Tyr Gln Met Gly Asn Asp Lys Glu Leu Asp Glu Ala Ile
          35           40           45
Lys Lys Lys Ala Leu Met Glu Gln Phe Leu Val Gln Asp Glu Asn Ala
          50           55           60
Leu Xaa Ala Phe
65

```

(2) INFORMATION FOR SEQ ID NO:394:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 446 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

```

Met Lys Ser Arg Pro Ile Leu Ala Gln Ala Tyr Ala Leu Gln Met Met
1           5           10           15
Val Lys Gln Ile Ala Phe Leu Glu Thr Ile Leu Val Glu Asn Glu Gln
          20           25           30
Asp Ala Leu Ile Leu Glu Asn Ser Leu Ile Lys Gln Leu Lys Pro Lys
          35           40           45
Tyr Asn Ile Leu Leu Arg Asp Asp Lys Thr Tyr Pro Tyr Ile Tyr Met

```

50				55				60							
Asp 65	Phe	Ser	Ile	Asp	Phe 70	Pro	Ile	Pro	Leu	Ile 75	Thr	Arg	Lys	Ile	Leu 80
Lys	Gln	Pro	Gly	Val 85	Lys	Tyr	Phe	Gly	Pro	Phe	Thr	Ser	Gly	Ala	Lys
Asp	Ile	Leu	Asp 100	Ser	Leu	Tyr	Glu	Leu	Leu	Pro	Leu	Val	Gln	Lys	Lys
Asn	Cys	Ile 115	Lys	Asp	Lys	Lys	Ala 120	Cys	Met	Phe	Tyr	Gln	Ile	Glu	Arg
Cys	Lys	Ala	Pro	Cys	Glu	Asp 135	Lys	Ile	Thr	Lys	Glu	Glu	Tyr	Leu	Lys
Ile 145	Ala	Lys	Glu	Cys	Leu 150	Glu	Met	Ile	Glu	Asn 155	Lys	Asp	Arg	Leu	Ile 160
Lys	Glu	Leu	Glu	Leu 165	Lys	Met	Glu	Arg	Leu	Ser	Ser	Asn	Leu	Arg	Phe
Glu	Glu	Ala	Leu 180	Ile	Tyr	Arg	Asp	Arg 185	Ile	Ala	Lys	Ile	Gln	Lys	Ile
Ala	Pro	Phe 195	Thr	Cys	Met	Asp	Leu 200	Ala	Lys	Leu	Tyr	Asp 205	Leu	Asp	Ile
Phe	Ala	Phe	Tyr	Gly	Gly	Asn 215	Asn	Lys	Ala	Val	Leu	Val	Lys	Met	Phe
Met 225	Arg	Gly	Gly	Lys	Ile 230	Ile	Ser	Ser	Ala	Phe 235	Glu	Lys	Ile	His	Ser 240
Leu	Asn	Gly	Phe	Asp 245	Thr	Asp	Glu	Ala	Met	Lys	Gln	Ala	Ile	Ile	Asn
His	Tyr	Gln	Ser 260	His	Leu	Pro	Leu	Met 265	Pro	Glu	Gln	Ile	Leu	Leu	Ser
Ala	Cys	Ser	Asn	Glu	Thr	Leu	Lys 280	Glu	Leu	Gln	Glu	Phe 285	Ile	Ser	His
Gln	Tyr	Ser	Lys	Lys	Ile	Ala 295	Leu	Ser	Ile	Pro	Lys	Lys	Gly	Asp	Lys
Leu 305	Ala	Leu	Ile	Glu	Ile 310	Ala	Met	Lys	Asn	Ala 315	Gln	Glu	Ile	Phe	Ser 320
Gln	Glu	Lys	Thr	Ser 325	Asn	Glu	Asp	Arg	Ile	Leu	Glu	Glu	Ala	Arg	Ser
Leu	Phe	Asn	Leu 340	Glu	Cys	Val	Pro	Tyr 345	Arg	Val	Glu	Ile	Phe	Asp	Thr
Ser	His	His 355	Ser	Asn	Ser	Gln	Cys 360	Val	Gly	Gly	Met	Val	Val	Tyr	Glu

Asn Asn Ala Phe Gln Lys Asp Ser Tyr Arg Arg Tyr His Leu Lys Gly
 370 375 380
 Ser Asn Glu Tyr Asp Gln Met Ser Glu Leu Leu Thr Arg Arg Ala Leu
 385 390 395 400
 Asp Phe Ala Lys Glu Pro Pro Pro Asn Leu Trp Val Ile Asp Gly Gly
 405 410 415
 Arg Ala Gln Leu Asn Ile Ala Leu Glu Ile Leu Lys Ser Ser Gly Ser
 420 425 430
 Phe Val Glu Val Ile Ala Ile Ser Lys Glu Lys Arg Gly Phe
 435 440 445

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...84
- (D) OTHER INFORMATION: /note= "oligopeptide permease membrane protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

Val Ser Leu Gly Ala Phe Gln Gly Tyr Tyr Gly Gly Leu Val Asp Leu
 1 5 10 15
 Val Gly Gln Arg Leu Ser Glu Ile Trp Ser Ala Ile Pro Met Leu Phe
 20 25 30
 Leu Leu Ile Val Ile Ser Ser Ala Phe Asn Ser Asn Phe Trp Ile Ile
 35 40 45
 Leu Phe Leu Val Leu Leu Phe Ser Trp Met Gly Leu Ser Gln Val Val
 50 55 60
 Arg Thr Glu Phe Leu Lys Ala Arg Asn Met Asp Tyr Thr Lys Ala Ala
 65 70 75 80
 Arg Ala Leu Gly

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: /note= "hypothetical abc transporter in bcr 5'region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

```
Met Ser Glu Ala Tyr Phe Leu His His Lys Asn Ala Ser Gln Val Ser
1              5              10              15
Leu Asn Glu Gln Val Leu Asn Val Met Lys Gln Val Gln Leu Asp Glu
              20              25              30
Asn Phe Trp Asn Val Ser Leu Met
              35              40
```

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

```
Val Ile Leu Ile Phe Ile Ile Val Val Glu Asp Gln Lys Gly Ile Phe
1              5              10              15
Pro Ile Ala Ala Ser Lys Arg Lys Ser Gln Ser Ser Val Ile Ile Glu
              20              25              30
Asp Val Cys Phe Ser Lys Glu Asp Phe Val Glu Gly Ala Lys Ala Ile
              35              40              45
Glu Gly Leu Leu Lys Lys His Gly Phe Lys Asp Asn Gly Ile Ile Phe
```

50	55	60
Gly His Ala Leu Ser	Gly Asn Leu His Phe	Val Val Thr Pro Ile Leu
65	70	75 80
Glu Asn Glu Ala Glu	Arg Lys Ala Phe	Glu Asn Leu Val Ser Glu Met
	85	90 95
Phe Leu Met Val Ser	Lys Ser Ser Gly	Ser Ile Lys Ala Glu His Gly
	100	105 110
Thr Gly Arg Met Val	Ala Pro Phe Val	Glu Met Glu Trp Gly Glu Lys
	115	120 125
Ala Tyr Lys Ile His	Lys Gln Ile Lys	Glu Leu Phe Asp Pro Asn Gly
	130	135 140
Leu Leu Asn Pro Asp	Val Ile Ile Thr	Asn Asp Lys Glu Ile His Thr
145	150	155 160
Lys Asn Leu Lys Ser	Ile Tyr Pro Ile	Glu Glu His Leu Asp Met Cys
	165	170 175
Met Glu Cys Gly Phe	Cys Glu Arg Ile	Cys Pro Ser Lys Asp Leu Ser
	180	185 190
Leu Thr Pro Arg Gln	Arg Ile Val Ile	His Arg Glu Val Glu Arg Leu
	195	200 205
Lys Glu Arg Val Ser	His Gly His Asp	Glu Asp Gln Val Leu Leu Asp
	210	215 220
Glu Leu Leu Lys Glu	Ser Glu Tyr Leu	Ala His Ala Thr Cys Ala Val
225	230	235 240
Cys His Met Cys Ser	Thr Leu Cys Pro	Leu Gly Ile Asp Thr Gly Xaa
	245	250 255
Ile Ala Leu Asn His	Tyr Gln Lys Asn	Pro Lys Gly Glu Lys Ile Ala
	260	265 270
Ser Lys Ile Leu Lys	Ser His Ala Asn	Asp His Lys Arg Gly Ser Phe
	275	280 285
Phe Phe Lys Xaa Arg	Phe Arg Gly Phe	Lys Asn Ser
	290	295 300

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

Met	Lys	Glu	Lys	Asn	Phe	Trp	Pro	Leu	Gly	Ile	Met	Ser	Val	Leu	Ile
1				5					10					15	
Phe	Gly	Leu	Gly	Ile	Val	Val	Phe	Leu	Val	Val	Phe	Ala	Leu	Lys	Asn
			20					25					30		
Ser	Pro	Lys	Asn	Asp	Leu	Val	Tyr	Phe	Lys	Gly	His	Asn	Glu	Val	Asp
		35					40					45			
Leu	Asn	Phe	Asn	Ala	Met	Leu	Lys	Thr	Tyr	Glu	Asn	Phe	Lys	Ser	Asn
	50					55					60				
Tyr	Arg	Phe	Ser	Val	Gly	Leu	Lys	Pro	Leu	Thr	Glu	Ser	Pro	Lys	Thr
65					70					75					80
Pro	Ile	Leu	Pro	Tyr	Phe	Ser	Lys	Gly	Thr	His	Gly	Asp	Lys	Lys	Ile
				85					90					95	
Gln	Glu	Asn	Leu	Leu	Asn	Asn	Ala	Leu	Ile	Leu	Glu	Lys	Ser	Asn	Thr
			100					105					110		
Leu	Tyr	Ala	Gln	Leu	Gln	Pro	Leu	Lys	Pro	Ala	Leu	Asp	Ser	Pro	Asn
		115					120					125			
Ile	Gln	Val	Tyr	Leu	Ala	Phe	Tyr	Pro	Ser	Gln	Ser	Gln	Pro	Arg	Leu
	130					135					140				
Leu	Gly	Thr	Leu	Asp	Cys	Lys	Asn	Ala	Cys	Glu	Pro	Leu	Lys	Phe	Asp
145					150					155					160
Leu	Leu	Glu	Gly	Asp	Lys	Val	Gly	Arg	Tyr	Lys	Ile	Leu	Phe	Lys	Phe
				165				170					175		
Val	Phe	Lys	Asn	Lys	Glu	Glu	Leu	Ile	Leu	Glu	Gln	Leu	Leu	Phe	Leu
			180					185					190		
Ser	Ser	Met	Ala	Cys	Met	Gly	Ile	Ser	Ile	Leu	Lys	Asn	Ala	Lys	Ala
		195					200					205			
Phe	Phe	Lys	Tyr	Lys	Ile										
	210														

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

```
Met Pro Ile Lys Gly Ser Phe Leu Ala Arg Asn Arg Leu Val Ile Ala
1          5          10          15
Leu Thr Asp Ala Val Ile Ile Pro Gln Ala Asp Leu Lys Ser Gly Ser
20          25          30
Met Ser Ser Ala Arg Leu Ala Gln Lys Tyr Gln Lys Pro Leu Phe Val
35          40          45
Leu Pro Gln Arg Leu Asn Glu Ser Asp Gly Thr Asn Glu Leu Leu Glu
50          55          60
Lys Gly Gln Ala Gln Gly Ile Phe Asn Ile Gln Asn Phe Ile Asn Thr
65          70          75          80
Leu Leu Lys Asp Tyr His Leu Lys Glu Met Pro Glu Met Lys Asp Glu
85          90          95
Phe Leu Glu Tyr Cys Ala Lys Asn Pro Ser Tyr Glu Glu Ala Tyr Leu
100         105         110
Lys Phe Gly Asp Lys Leu Leu Glu Tyr Glu Leu Leu Gly Lys Ile Lys
115         120         125
Arg Ile Asn His Leu Val Val Leu Ala
130         135
```

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...272

(D) OTHER INFORMATION: /note= "ATP-BINDING PROTEIN ABC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

```
Met Val Val Glu Leu Lys Asn Ile Glu Lys Ile Tyr Glu Asn Gly Phe
1          5          10          15
```

His Ala Leu Lys Gly Val Asn Leu Glu Leu Lys Lys Gly Asp Ile Leu
 20 25 30
 Gly Val Ile Gly Tyr Ser Gly Ala Gly Lys Ser Thr Leu Ile Arg Leu
 35 40 45
 Ile Asn Cys Leu Glu Arg Pro Ser Ser Gly Glu Val Leu Val Asn Gly
 50 55 60
 Val Asn Leu Leu Asn Leu Lys Pro Lys Glu Leu Gln Lys Ala Arg Gln
 65 70 75 80
 Lys Ile Gly Met Ile Phe Gln His Phe Asn Leu Leu Ser Ala Lys Asn
 85 90 95
 Val Phe Glu Asn Val Ala Phe Ala Leu Glu Ile Ala Arg Trp Glu Lys
 100 105 110
 Thr Lys Ile Lys Ser Arg Val His Glu Leu Leu Glu Leu Val Gly Leu
 115 120 125
 Glu Asp Lys Val His Phe Tyr Pro Lys Gln Leu Ser Gly Gly Gln Lys
 130 135 140
 Gln Arg Val Ala Ile Ala Arg Ser Leu Ala Asn Cys Pro Asn Leu Leu
 145 150 155 160
 Leu Cys Asp Glu Ala Thr Ser Ala Leu Asp Ser Lys Thr Thr His Ser
 165 170 175
 Ile Leu Thr Leu Leu Ser Gly Ile Gln Lys Lys Phe Asp Leu Ser Ile
 180 185 190
 Val Phe Ile Thr His Gln Ile Glu Val Val Lys Glu Leu Cys Asn Gln
 195 200 205
 Met Cys Val Ile Ser Ser Gly Glu Ile Val Glu Arg Gly Ser Val Glu
 210 215 220
 Glu Ile Phe Ala Asn Pro Lys His Ala Val Thr Lys Glu Leu Leu Gly
 225 230 235 240
 Ile Lys Asn Glu His Ala Asp Gln Lys Ser Gln Asp Ile Tyr Arg Ile
 245 250 255
 Val Phe Leu Gly Glu His Leu Asp Glu Pro Ile Ile Ser Xaa Phe Xaa
 260 265 270

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Leu	Xaa	Pro	Met	Lys	Val	Ile	Gln	Val	Phe	Leu	Phe	Ser	Asn	Pro	Phe	
1				5					10					15		
Cys	Ala	Ile	Val	Pro	Asn	Thr	Glu	Pro	Glu	His	Leu	Glu	His	Tyr	Asp	
			20					25					30			
His	Asp	Leu	Glu	Arg	Phe	Phe	Phe	Ala	Tyr	Lys	Tyr	Phe	Leu	Asp	His	
		35					40					45				
Ala	Gln	Lys	Arg	Val	Ile	Tyr	Lys	Glu	Asp	Pro	Phe	Leu	Lys	Asn	Tyr	
	50					55					60					
Ser	Lys	Asp	Ala	Ile	Val	Leu	Glu	Lys	Lys	Asp	Ile	Tyr	Asn	Ile	Gln	
65					70					75					80	
Tyr	Ile	Leu	Lys	Asp	Gly	Glu	Pro	Tyr	Thr	Ser	Phe	Glu	Leu	Lys	Asn	
				85					90					95		
Leu	Gly	Ala	Phe	Leu	Val	Trp	Gly	Leu	Gly	Glu	His	Asn	Ala	Thr	Asn	
			100					105					110			
Ala	Ser	Leu	Ala	Ile	Leu	Ser	Ala	Leu	Asp	Glu	Leu	Asn	Leu	Glu	Glu	
		115					120					125				
Ile	Arg	Asn	Asn	Xaa	Leu	Asn	Phe	Lys	Gly	Ile	Lys	Lys	Arg	Phe	Asp	
	130					135						140				
Ile	Leu	Gln	Lys	Asn	Asn	Leu	Ile	Leu	Ile	Asp	Asp	Tyr	Ala	His	His	
145					150					155					160	
Pro	Thr	Glu	Ile	Gly	Xaa	Thr	Leu	Lys	Ser	Ala	Arg	Ile	Tyr	Ala	Asn	
				165					170					175		
Leu	Leu	Asn	Thr	Gln	Glu	Lys	Ile	Ile	Val	Ile	Trp	Gln	Ala	His	Lys	
			180					185					190			
Tyr	Ser	Arg	Leu	Met	Asp	Asn	Leu	Glu	Glu	Phe	Lys	Lys	Cys	Phe	Leu	
		195				200						205				
Glu	His	Cys	Asp	Arg	Leu	Ile	Ile	Leu	Pro	Val	Tyr	Ser	Ala	Ser	Glu	
	210					215					220					
Val	Lys	Arg	Asp	Ile	Asp	Leu	Lys	Ala	His	Phe	Lys	His	Tyr	Asn	Pro	
225					230					235					240	
Thr	Phe	Ile	Asp	Arg	Val	Arg	Lys	Lys	Gly	Asp	Phe	Leu	Glu	Leu	Leu	
				245					250					255		
Val	Asn	Asp	Asn	Val	Val	Glu	Thr	Ile	Glu	Lys	Gly	Phe	Val	Ile	Gly	
			260					265					270			

Phe Gly Ala Gly Asp Ile Thr Tyr Gln Leu Arg Gly Glu Met
 275 280 285

(2) INFORMATION FOR SEQ ID NO:402:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Met	Gly	Ala	Leu	Ile	Ala	Met	Phe	Phe	Leu	Met	Leu	Ile	Lys	Lys	Thr
1				5					10					15	
Ile	Ala	Tyr	Lys	Glu	Asp	Lys	Lys	Ser	Ala	Ala	Leu	Lys	Val	Val	Pro
			20					25					30		
Tyr	Leu	Val	Ala	Leu	Met	Ser	Leu	Ala	Phe	Ser	Trp	Tyr	Leu	Ile	Val
		35					40					45			
Lys	Val	Leu	Lys	Arg	Leu	Tyr	Ala	Val	Ser	Phe	Glu	Ile	Gln	Leu	Ala
	50					55				60					
Cys	Gly	Cys	Val	Leu	Ala	Leu	Leu	Ile	Phe	Ile	Leu	Phe	Lys	Arg	Phe
65					70					75					80
Val	Leu	Lys	Lys	Ala	Pro	Gln	Leu	Glu	Asn	Ser	His	Glu	Ser	Val	Asn
				85					90					95	
Glu	Leu	Phe	Asn	Val	Pro	Leu	Ile	Phe	Ala						
				100					105						

(2) INFORMATION FOR SEQ ID NO:403:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

Met Ile Lys Arg Ile Ala Cys Ile Leu Ser Leu Ser Ala Ser Leu Ala
 1 5 10 15
 Leu Ala Gly Glu Val Asn Gly Phe Phe Met Gly Ala Gly Tyr Gln Gln
 20 25 30
 Gly Arg Tyr Gly Pro Tyr Asn Ser Asn Tyr Ser Asp Trp Arg His Gly
 35 40 45
 Asn Asp Leu Tyr Gly Leu Asn Phe Lys Leu Gly Phe Val Gly Phe Ala
 50 55 60
 Asn Lys Trp Phe Gly Ala Arg Val Tyr Gly Phe Leu Asp Trp Phe Asn
 65 70 75 80
 Thr Ser Gly Thr Glu His Thr Lys Thr Asn Leu Leu Thr Tyr Gly Gly
 85 90 95
 Gly Gly Asp Leu Ile Val Asn Leu Ile Pro Leu Asp Lys Phe Ala Leu
 100 105 110
 Gly Leu Ile Gly Gly Val Gln Leu Ala Gly Asn Thr Trp Met Phe Pro
 115 120 125
 Tyr Asp Val Asn Gln Thr Arg Phe Gln Phe Leu Trp Asn Leu Gly Gly
 130 135 140
 Arg Met Arg Val Gly Asp Thr Val Arg Leu Lys Arg Ala
 145 150 155

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...278
- (D) OTHER INFORMATION: /note= "FLAGELLAR BIOSYNTHETIC PROTEIN FLHB"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

Met Tyr Arg His Val Leu Lys Asp Phe Ser Leu Asp Phe Ser Lys Glu
 1 5 10 15
 Ser Val Gln Glu Leu Phe Asn Gln Leu Ala Lys Asp Thr Phe Leu Leu

20					25					30						
Leu	Leu	Pro	Val	Leu	Ile	Ile	Leu	Met	Val	Val	Ala	Phe	Leu	Ser	Asn	
35					40					45						
Val	Leu	Gln	Phe	Gly	Trp	Leu	Phe	Ala	Pro	Lys	Val	Ile	Glu	Pro	Lys	
50					55					60						
Phe	Ser	Lys	Ile	Asn	Pro	Ile	Asn	Gly	Val	Lys	Asn	Leu	Phe	Ser	Leu	
65					70					75					80	
Lys	Lys	Ile	Leu	Asp	Gly	Ser	Leu	Ile	Thr	Leu	Lys	Val	Phe	Leu	Ala	
85					90					95						
Phe	Phe	Leu	Gly	Phe	Phe	Ile	Phe	Ser	Leu	Phe	Leu	Gly	Glu	Leu	Asn	
100					105					110						
His	Ala	Ala	Leu	Leu	Asn	Leu	Gln	Gly	Gln	Leu	Leu	Trp	Phe	Lys	Ser	
115					120					125						
Lys	Ala	Leu	Trp	Leu	Ile	Ser	Ser	Leu	Leu	Phe	Leu	Phe	Phe	Val	Leu	
130					135					140						
Ala	Phe	Val	Asp	Leu	Ile	Ile	Lys	Arg	Arg	Gln	Tyr	Thr	Asn	Ser	Leu	
145					150					155					160	
Lys	Met	Thr	Lys	Gln	Glu	Val	Lys	Asp	Glu	Tyr	Lys	Gln	Gln	Glu	Gly	
165					170					175						
Asn	Pro	Glu	Ile	Lys	Ala	Lys	Ile	Arg	Gln	Met	Met	Val	Lys	Asn	Ala	
180					185					190						
Thr	Asn	Lys	Met	Met	Gln	Glu	Ile	Pro	Lys	Ser	Asn	Val	Val	Val	Thr	
195					200					205						
Asn	Pro	Thr	His	Tyr	Ala	Val	Ala	Leu	Lys	Phe	Asp	Glu	Glu	His	Pro	
210					215					220						
Val	Pro	Val	Val	Val	Ala	Lys	Gly	Thr	Asp	Tyr	Leu	Ala	Ile	Arg	Ile	
225					230					235					240	
Lys	Gly	Ile	Ala	Arg	Glu	His	Asp	Ile	Glu	Ile	Ile	Glu	Asn	Lys	Thr	
245					250					255						
Leu	Ala	Arg	Glu	Leu	Tyr	Arg	Asp	Val	Lys	Leu	Asn	Ala	Thr	Ile	Pro	
260					265					270						
Glu	Glu	Leu	Phe	Glu	Arg											
275																

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

```

Met Asn Thr Xaa Pro Leu Ile Ala Thr Leu Leu Gln Ala Pro Leu His
1           5           10           15
Val Leu Gly Ile Arg Glu Pro Val Ser Phe Gln Pro Phe Tyr Pro Lys
          20           25           30
Thr Glu Lys Pro Asn Arg Pro Gln Lys Phe Ala His Val Ser Ser Met
          35           40           45
Pro Ser Leu Glu Phe Leu Glu Lys Leu Val Ile Arg Tyr Leu Leu Glu
          50           55           60
Asp Arg Ser Leu Leu Asp Leu Ala Val Gly Tyr Ile His Ser Gly Val
65           70           75           80
Phe Leu His Lys Lys Gln Glu Phe Asp Ala Leu Cys Gln Glu Lys Leu
          85           90           95
Asp Asp Pro Lys Leu Val Ala Leu Leu Leu Asp Ala Asn Leu Pro Leu
          100          105          110
Lys Lys Gly Gly Phe Glu Lys Glu
          115          120

```

(2) INFORMATION FOR SEQ ID NO:406:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 226 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

```

Met Gly Gln Ala Phe Phe Lys Lys Ile Val Gly Cys Phe Cys Leu Gly
1           5           10           15
Tyr Leu Phe Leu Ser Ser Ala Ile Glu Ala Val Ala Leu Asp Ile Lys
          20           25           30
Asn Phe Asn Arg Gly Arg Val Lys Val Val Asn Lys Lys Ile Ala Tyr
          35           40           45

```

Leu Gly Asp Glu Lys Pro Ile Thr Ile Trp Thr Ser Leu Asp Asn Val
 50 55 60
 Thr Val Ile Gln Leu Glu Lys Asp Glu Thr Ile Ser Tyr Ile Thr Thr
 65 70 75 80
 Gly Phe Asn Lys Gly Trp Ser Ile Val Pro Asn Ser Asn His Ile Phe
 85 90 95
 Ile Gln Pro Lys Ser Val Lys Ser Asn Leu Met Phe Glu Lys Glu Ala
 100 105 110
 Val Asn Phe Ala Leu Met Thr Arg Asp Tyr Gln Glu Phe Leu Lys Thr
 115 120 125
 Lys Lys Leu Ile Val Asp Ala Pro Asp Pro Lys Glu Leu Glu Glu Gln
 130 135 140
 Lys Lys Ala Leu Glu Lys Glu Lys Glu Ala Lys Glu Gln Ala Gln Lys
 145 150 155 160
 Ala Gln Lys Asp Lys Arg Glu Lys Arg Lys Glu Glu Arg Ala Lys Asn
 165 170 175
 Arg Ala Asn Leu Glu Asn Leu Thr Asn Ala Met Ser Asn Pro Gln Asn
 180 185 190
 Leu Ser Asn Asn Lys Asn Leu Ser Glu Leu Ile Lys Gln Gln Arg Glu
 195 200 205
 Asn Glu Leu Asp Gln Met Glu Arg Thr Arg Gly His Ala Arg Ala Gly
 210 215 220
 Ser Ser
 225

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

Leu Leu Leu Phe Phe Leu Leu Lys Gly Val Val Phe Ser Leu Gly Phe
 1 5 10 15
 Phe Ser Phe Phe Glu Glu Val Ser Gly Ser Phe Xaa Ala Val Ser Leu

20

25

30

Xaa Val Leu Ala Leu Val Met Gly Ser Ser Xaa Gly Leu Glu Glu Phe
 35 40 45

Cys Val Leu Glu Glu Leu Ile Asn Ser Gly Leu Ser Val
 50 55 60

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...50
- (D) OTHER INFORMATION: /note= "homology to NITROGEN FIXATION;
 TRANSMEMBRANE [Rhizo. meliloti]"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

Met Asn Thr Glu Ile Leu Thr Ile Met Leu Val Val Ser Val Leu Met
 1 5 10 15

Gly Leu Val Gly Leu Ile Ala Phe Leu Trp Gly Val Lys Ser Gly Gln
 20 25 30

Phe Asp Asp Glu Lys Arg Met Leu Glu Ser Val Leu Tyr Asp Ala Arg
 35 40 45

Ala Thr
 50

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

Met Gly Phe Leu Lys Val Leu Lys His Asp Ala Leu Gly Gln Val Gly
1 5 10 15
Asn Ile Val Ile Gly Asn Phe Leu Ile Thr Leu Thr Val Leu Ala Val
20 25 30
Cys Phe Ser Ser Gln Ser Ala Glu Glu Thr Thr Met Leu Thr Leu Ser
35 40 45
Tyr Thr Leu Phe Phe Ile Leu Gly Ala Phe Leu Leu Val Ala Ile Ser
50 55 60
Val Gly Ala Ile Lys Asn Leu Asn Ala Leu Phe Ser Lys Arg Gly Val
65 70 75 80
Leu Ser Phe Ser Leu Pro Ile Ser Leu Glu Ser Leu Leu Leu Pro Lys
85 90 95
Ile Leu Leu Pro Xaa Val Phe Phe Tyr Leu Gln Phe Val Leu Val Cys
100 105 110
Gly Glu Arg Ala Phe Gly Leu Leu Pro Phe
115 120

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

Met Leu Lys Thr His Leu Ser Ser Ala Arg Gly Val Val Val Leu Ser
1 5 10 15
Lys Ile Leu Pro Val Asn Val Val Leu Met Val Ser Val Arg Leu Phe
20 25 30
Glu Lys Glu Leu Lys Arg Lys Pro Tyr Tyr Ile Ile Ala Ser Ala His
35 40 45
Ser Asp Glu Gly Leu Glu Lys Leu Lys Lys Xaa Gly Xaa Asp Met Val
50 55 60
Xaa Xaa Pro Thr Lys Leu Met Ala Gln Arg Val Ser Ala Asn Xaa Trp
65 70 75 80

Cys	Xaa	Leu	Asp	Met	Glu	Asn	Ile	Leu	Glu	Arg	Phe	Ile	Asn	Lys	Lys	
				85					90					95		
Asp	Thr	Leu	Leu	Asp	Leu	Glu	Glu	Val	Ile	Val	Pro	Lys	Thr	Ser	Trp	
			100					105					110			
Leu	Val	Leu	Arg	Lys	Leu	Lys	Glu	Ala	His	Phe	Arg	Glu	Ile	Ala	Lys	
		115					120					125				
Ala	Phe	Val	Ile	Gly	Ile	Thr	Gln	Lys	Asp	Gly	Lys	Tyr	Ile	Pro	Met	
	130					135					140					
Pro	Asp	Gly	Glu	Thr	Ile	Ile	Ala	Ser	Glu	Ser	Lys	Leu	Leu	Met	Val	
145					150					155					160	
Gly	Thr	Ser	Glu	Gly	Val	Ala	Thr	Cys	Lys	Gln	Leu	Ile	Thr	Ser	His	
			165						170					175		
Gln	Lys	Pro	Lys	Glu	Val	Asp	Tyr	Ile	Ser	Leu						
			180					185								

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

Met	Phe	Val	Ala	Ala	Gly	Leu	Gly	Ala	Tyr	Ala	Ile	Ala	Leu	Phe	His	
1				5					10					15		
Leu	Phe	Thr	His	Ala	Phe	Phe	Lys	Ser	Leu	Leu	Phe	Leu	Gly	Ser	Gly	
			20					25					30			
Asn	Val	Met	His	Ala	Met	Glu	Asp	Asn	Leu	Asp	Ile	Thr	Lys	Met	Gly	
		35					40					45				
Ala	Leu	Tyr	Lys	Pro	Met	Arg	Ile	Thr	Ala	Val	Phe	Met	Ile	Ile	Gly	
	50					55					60					
Ser	Val	Ala	Leu	Cys	Gly	Ile	Tyr	Pro	Phe	Ala	Gly	Tyr	Phe	Ser	Lys	
65					70				75					80		
Asp	Lys	Ile	Leu	Glu	Val	Ala	Phe	Gly	Met	His	His	His	Ile	Leu	Trp	
			85					90						95		
Phe	Val	Leu	Leu	Ile	Gly	Ala	Ile	Phe	Thr	Ala	Phe	Tyr	Ser	Phe	Arg	
		100					105						110			

Leu Ile Met Leu Val Phe Phe Ala Pro Lys Gln His Glu Ile Asn His
 115 120 125

Pro Pro
 130

(2) INFORMATION FOR SEQ ID NO:412:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 183 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

Met Phe Ile Ser Ser Ser Tyr Thr Leu Ser Phe Val Trp Leu Phe Leu
 1 5 10 15

Ile Phe Phe Phe Phe Lys Asn Lys Pro Leu Gly Leu Arg Phe Ser Leu
 20 25 30

Ser Leu Ile Ser Val Ile Leu Ser Asn Ile Ala Leu Lys Asp Ser Leu
 35 40 45

Ser Leu Asn Glu Phe Leu Ser Ser Phe Thr Ala Pro Leu Ser Pro Phe
 50 55 60

Ser Cys Leu Leu Ile Leu Ala Tyr Ala Ser Phe Ser Cys His Ile Leu
 65 70 75 80

Lys Lys Pro Pro Leu Glu Thr Leu Gln Ser Tyr Ser Val Met Leu Phe
 85 90 95

Phe Asn Leu Leu Leu Thr Asp Ile Leu Gly Phe Leu Pro Phe Ser
 100 105 110

Ile Tyr His His Phe Met Ala Ser Leu Ile Phe Ser Ala Leu Phe Cys
 115 120 125

Ser Ser Leu Phe Leu Ser Ser Pro Leu Leu Gly Val Ile Ala Leu Val
 130 135 140

Ala Leu Ser Ser Ser Leu Leu Met Arg Ser Asn Phe Gln Ile Leu Asp
 145 150 155 160

Ser Leu Leu Asp Phe Pro Leu Phe Leu Phe Val Phe Phe Lys Thr Leu
 165 170 175

Tyr Leu Ala Lys Lys Arg Leu

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

Val	Gly	Ser	Phe	Leu	Phe	Val	Gly	Pro	Ser	Gly	Val	Gly	Lys	Thr	Glu			
1				5				10					15					
Leu	Ala	Lys	Glu	Leu	Ala	Leu	Asn	Leu	Xaa	Leu	His	Phe	Glu	Arg	Phe			
			20				25						30					
Asp	Met	Ser	Glu	Tyr	Lys	Glu	Ala	His	Ser	Val	Ala	Lys	Leu	Ile	Gly			
		35				40					45							
Ser	Pro	Ser	Gly	Tyr	Val	Gly	Phe	Glu	Gln	Gly	Gly	Leu	Leu	Val	Asn			
	50					55					60							
Ala	Ile	Lys	Lys	His	Pro	His	Cys	Leu	Leu	Leu	Leu	Asp	Glu	Ile	Glu			
65				70						75				80				
Lys	Ala	His	Pro	Asn	Val	Tyr	Asp	Leu	Leu	Leu	Gln	Val	Met	Xaa	Asn			
			85					90						95				
Ala	Thr	Leu	Ser	Asp	Asn	Leu	Gly	Asn	Lys	Ala	Ser	Phe	Lys	His	Val			
		100					105						110					
Ile	Leu	Ile	Met	Thr	Xaa	Xaa	Val	Gly	Ser	Lys	Asp	Lys	Asp	Thr	Leu			
	115						120					125						
Gly	Phe	Phe	Ser	Thr	Lys	Asn	Ala	Lys	Tyr	Asp	Arg	Ala	Val	Lys	Glu			
	130					135				140								
Leu	Leu	Thr	Pro	Glu	Leu	Arg	Ser	Arg	Ile	Asp	Ala	Ile	Val	Pro	Phe			
145				150					155					160				
Asn	Ala	Leu	Ser	Leu	Glu	Asp	Phe	Glu	Thr	His	Cys	Phe	Cys	Gly	Ile			
			165					170					175					
Gly	Arg	Val	Lys	Ser	Pro	Ser	Thr	Arg	Ala	Arg	Arg	Asp	Leu	Lys	Ile			
		180						185					190					
Pro																		

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Met	Arg	Leu	Asp	Tyr	Ala	Leu	Phe	Asn	Gln	His	Leu	Ala	Asn	Ser	Arg	
1				5					10					15		
Glu	Lys	Ala	Lys	Ala	Leu	Val	Leu	Lys	Lys	Gln	Val	Leu	Val	Asn	Lys	
			20					25					30			
Met	Val	Val	Ser	Lys	Pro	Ser	Phe	Ile	Val	Lys	Glu	Gly	Asp	Gln	Ile	
		35					40					45				
Glu	Leu	Ile	Ala	Pro	Asn	Leu	Phe	Val	Ser	Arg	Ala	Gly	Glu	Lys	Leu	
	50					55					60					
Gly	Ala	Phe	Leu	Glu	Asp	His	Phe	Ile	Asp	Phe	Lys	Glu	Lys	Val	Val	
65					70					75					80	
Leu	Asp	Val	Gly	Ala	Ser	Lys	Gly	Gly	Phe	Ser	Gln	Val	Ala	Leu	Leu	
				85					90					95		
Lys	Gly	Ala	Lys	Lys	Val	Leu	Cys	Val	Asp	Val	Gly	Lys	Met	Gln	Leu	
			100					105					110			
Asp	Glu	Ser	Leu	Lys	Asn	Asp	Gln	Arg	Ile	Glu	Cys	Tyr	Glu	Glu	Cys	
		115					120					125				
Asp	Ile	Arg	Gly	Phe	Lys	Thr	Pro	Glu	Lys	Ile	Asp	Leu	Ala	Leu	Cys	
	130					135					140					
Asp	Val	Ser	Phe	Ile	Ser	Leu	Tyr	Cys	Ile	Leu	Glu	Ala	Ile	Leu	Pro	
145					150					155					160	
Leu	Ser	Gly	Glu	Phe	Leu	Thr	Leu	Phe	Lys	Pro	Gln	Phe	Glu	Val	Gly	
				165					170					175		
Arg	Thr	Ile	Lys	Arg	Asn	Lys	Lys	Gly	Val	Val	Met	Asp	Lys	Glu	Ala	
			180					185					190			
Ile	Leu	Asn	Ala	Leu	Glu	Asn	Phe	Lys	Asn	His	Leu	Lys	Thr	Lys	Asp	
	195						200					205				
Phe	Gln	Ile	Leu	Thr	Ile	Gln	Glu	Ser	Leu	Val	Lys	Gly	Lys	Asn	Gly	
	210					215					220					

Asn Val Glu Phe Phe Ile His Phe Lys Arg Ala
 225 230 235

(2) INFORMATION FOR SEQ ID NO:415:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

Met	Ser	Leu	Pro	Pro	Val	Cys	Ile	Leu	Lys	Asp	Val	Asn	His	Leu	Leu
1				5					10					15	
Gln	Val	Leu	His	Ser	Leu	Val	Ala	Leu	Gly	Asn	Ser	Met	Leu	Val	Ile
			20						25					30	
Glu	His	Asn	Leu	Asp	Ile	Ile	Lys	Asn	Ala	Asp	Tyr	Ile	Ile	Asp	Met
		35					40					45			
Gly	Pro	Asp	Gly	Gly	Asp	Lys	Gly	Gly	Lys	Val	Ile	Ala	Ser	Gly	Thr
	50					55					60				
Pro	Leu	Glu	Val	Ala	Gln	Asn	Cys	Glu	Lys	Thr	Gln	Ser	Tyr	Thr	Gly
65					70					75					80
Lys	Phe	Leu	Ala	Leu	Glu	Leu	Lys								
															85

(2) INFORMATION FOR SEQ ID NO:416:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

Met	Gln	Asn	Arg	Ser	His	Glu	Ile	Gln	Gly	Val	Ser	His	Ile	Lys	Asn
1				5					10					15	

Asn Tyr Lys Phe Phe Thr Lys Glu Leu Asp Asn Tyr Ile Ser Lys Gly
 20 25 30
 Tyr Arg Ile Glu Glu Ile Tyr Gly Ala Phe Leu Trp Leu Lys Ile Val
 35 40 45
 Ala Ile Gly Leu Glu Leu Gly Glu Asp Asp Pro Gln Val Val Phe Glu
 50 55 60
 Ser Ile Asn Ala Thr Gly Val Gln Leu Lys Gly Leu Asp Leu Ile Arg
 65 70 75 80
 Asn Tyr Leu Met Met Gly Glu Asn Xaa Asp Asn Gln Asn Arg Leu Tyr
 85 90 95
 Asn Thr Tyr Trp Val Pro Leu Glu Asn Trp Leu Gly Glu
 100 105

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

Met Asp Thr Ile Lys Ser Ile Pro Ile Arg Thr Phe Ile Leu Leu Tyr
 1 5 10 15
 Lys Ser Ser Pro Lys Cys Val Val Leu Ala Ser Ile Thr Val Leu Phe
 20 25 30
 Val Gly Ile Leu Xaa Ser Leu Asn Ile Leu Val Met Ile Lys Leu Ile
 35 40 45
 Asp Ile Val Val Asn Leu Leu Gln Lys His Thr His Phe Glu Tyr Ser
 50 55 60
 Leu Leu Leu Pro Thr Leu Leu Leu Trp Gly Ala Leu Leu Phe Leu Thr
 65 70 75 80
 His Val Phe Ser Gly Asn Phe Ile Lys Leu Ala Asn His Tyr Cys Arg
 85 90 95
 Thr Ile Phe Tyr Lys Tyr His His Ser Ala Cys
 100 105

(2) INFORMATION FOR SEQ ID NO:418:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418

```

Met Ile Phe Tyr Thr Thr Ile Lys Glu Pro Leu Lys Asn Leu Gln Tyr
1           5           10           15
Arg Tyr Ala Gln Phe Phe Gly Lys Ile Lys Pro Cys Ser Phe Leu Glu
          20           25           30
Ser Leu Lys Ser Cys Phe Phe Gln Thr Tyr Ser Phe Ser Leu Thr Arg
          35           40           45
Lys Gln Asp Phe Lys Ser His Leu Arg His Phe Ile Asp Ser Ala His
          50           55           60
Ser Asn Ala Leu Val Gly Asn Leu Tyr Arg Ala Leu Phe Ile Gly Asp
65           70           75           80
Ser Leu Asn Lys Asp Leu Arg Asp Arg Ala Asn Ala Leu Gly Ile Asn
          85           90           95
His Leu Leu Ala Ile Ser Gly Phe His Leu Gly Ile Leu Ser Ala Ser
          100          105          110
Val Tyr Phe Leu Phe Ser Leu Phe Tyr Thr Pro Leu Gln Lys Arg Tyr
          115          120          125
Phe Pro Tyr Arg Asn Ala Phe Xaa
          130          135

```

(2) INFORMATION FOR SEQ ID NO:419:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

Met Asn Lys Pro Phe Leu Ile Leu Leu Ile Ala Leu Ile Ala Phe Ser
 1 5 10 15
 Gly Cys Asn Met Arg Lys Tyr Phe Lys Pro Ala Lys His Gln Ile Lys
 20 25 30
 Ala Lys Arg Ile Ser Leu Thr Ile Cys Lys Lys Ala Ser Phe Arg Leu
 35 40 45
 Ile Val Met Glu Pro Phe
 50

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

Met Ala Ala Trp Asn Thr Leu Val Glu Lys Ile Ile Ala Pro Lys His
 1 5 10 15
 Lys Val Lys Ile Gly Phe Val Gly Lys Tyr Leu Ser Leu Lys Glu Ser
 20 25 30
 Tyr Lys Ser Leu Ile Glu Ala Leu Ile His Ala Gly Ala His Leu Asp
 35 40 45
 Thr Gln Val Asn Ile Glu Trp Leu Asp Ser Glu Asn Phe Asn Glu Lys
 50 55 60
 Thr Asp Leu Glu Gly Val Asp Ala Ile Leu Val Pro Gly Gly Phe Gly
 65 70 75 80
 Glu Arg Gly Ile Glu Gly Lys Ile Cys Ala Ile Gln Arg Ala Arg Leu
 85 90 95
 Glu Lys Leu Pro Phe Leu Gly Ile Cys Leu Gly Met Gln Leu Ala Ile
 100 105 110
 Val Glu Phe Cys Arg Lys Cys Phe Arg Leu Glu Arg Gly
 115 120 125

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

Met	Thr	Lys	Ala	Phe	Val	Pro	Leu	Ser	Leu	Leu	Val	Ser	Ala	Ile	Leu	
1				5					10					15		
Leu	Ala	Phe	Ser	Leu	Ile	Leu	Ile	Pro	Thr	Ser	Lys	Ser	Ala	Tyr	Tyr	
			20					25					30			
Gly	Phe	Leu	Arg	Gln	Lys	Lys	Asp	Lys	Ile	Asp	Ile	Asn	Ile	Arg	Ala	
		35					40					45				
Gly	Glu	Phe	Gly	Gln	Lys	Leu	Gly	Asp	Trp	Leu	Val	Tyr	Val	Asp	Lys	
	50					55					60					
Thr	Glu	Asn	Asn	Ser	Tyr	Asp	Asn	Leu	Val	Leu	Phe	Ser	Asn	Lys	Ser	
65				70						75				80		
Leu	Ser	Gln	Glu	Ser	Phe	Ile	Leu	Ala	Gln	Lys	Gly	Asn	Ile	Asn	Asn	
				85					90					95		
Gln	Asn	Gly	Val	Phe	Glu	Leu	Asn	Leu	Tyr	Asn	Gly	His	Ala	Tyr	Phe	
		100						105					110			
Thr	Gln	Gly	Asp	Lys	Met	Arg	Lys	Val	Asp	Phe	Glu	Glu	Leu	His	Leu	
	115						120					125				
Arg	Asn	Lys	Leu	Lys	Ser	Phe	Asn	Ser	Asn	Asp	Ala	Ala	Tyr	Leu	Gln	
	130					135					140					
Gly	Thr	Asp	Tyr	Leu	Gly	Tyr	Trp	Lys	Lys	Ala	Phe	Gly	Lys	Asn	Ala	
145				150						155				160		
Asn	Lys	Asn	Gln	Lys	Arg	Arg	Phe	Ser	Gln	Ala	Ile	Leu	Val	Ser	Leu	
				165					170					175		
Phe	Pro	Leu	Ala	Ser	Val	Phe	Leu	Ile	Pro	Leu	Phe	Gly	Ile	Ala	Asn	
		180					185						190			
Pro	Arg	Phe	Lys	Thr	Asn	Trp	Ser	Tyr	Phe	Xaa	Val	Leu	Gly	Ala	Val	
	195						200					205				
Gly	Val	Tyr	Phe	Leu	Met	Val	His	Val	Ile	Ser	Thr	Asp	Leu	Phe	Leu	
	210					215					220					
Met	Thr	Phe	Phe	Phe	Pro	Phe	Ile	Trp	Ala	Phe	Ile	Ser	Tyr	Leu	Leu	
225					230					235				240		

Phe Arg Lys Phe Ile Leu Lys Arg Tyr
245

(2) INFORMATION FOR SEQ ID NO:422:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 86 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

Met	Ser	Lys	Ser	Ala	Ile	Phe	Val	Leu	Ser	Gly	Phe	Leu	Ala	Phe	Leu
1				5					10					15	
Leu	Tyr	Ala	Leu	Leu	Leu	Tyr	Gly	Leu	Leu	Leu	Glu	Arg	His	Asn	Lys
			20					25					30		
Glu	Ala	Glu	Lys	Ile	Leu	Leu	Asp	Leu	Asn	Lys	Lys	Asp	Glu	Gln	Ala
			35				40					45			
Ile	Asp	Leu	Asn	Leu	Glu	Asp	Leu	Pro	Ser	Glu	Lys	Lys	Asn	Glu	Lys
	50					55				60					
Ile	Lys	Lys	Val	Thr	Glu	Lys	Gln	Asp	Asp	Phe	Leu	Glu	Pro	Lys	Arg
65				70						75				80	
Arg	Thr	Gln	Arg	Gly	Ala										
				85											

(2) INFORMATION FOR SEQ ID NO:423:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

Val	Met	Ala	Gln	Ser	Leu	Leu	Val	His	Ala	Phe	Phe	Ala	Ala	Leu	Leu
1				5				10						15	

Ala	Leu	Ala	Phe	Met	Ile	Asn	Leu	Tyr	Thr	Leu	Phe	Lys	Glu	Lys	Asn
			20					25					30		
Phe	Ile	Gln	Leu	Asn	Arg	Lys	Ile	Tyr	Leu	Val	Met	Pro	Ala	Ile	Tyr
		35					40					45			
Ile	Leu	Leu	Ser	Ile	Ala	Leu	Leu	Ser	Gly	Val	Phe	Ile	Trp	Ala	Met
	50					55					60				
Gln	Gln	Phe	Glu	Phe	Ser	Phe	Ser	Ala	Val	Val	Met	Leu	Leu	Gly	Leu
65					70					75					80
Leu	Leu	Met	Leu	Ile	Ala	Glu	Ile	Lys	Arg	His	Lys	Ser	Val	Lys	Phe
				85					90					95	
Ala	Ile	Thr	Lys	Lys	Glu	Arg	Met	Lys	Ala	Tyr	Ile	Lys	Lys	Ala	Lys
			100					105					110		
Ile	Leu	Tyr	Phe	Leu	Glu	Thr	Ile	Leu	Ile	Ile	Val	Leu	Met	Gly	Ile
		115					120						125		

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Val	Arg	Asn	Val	Val	Leu	Phe	Ile	Leu	Thr	Ala	Ile	Phe	Leu	Ala	Phe
1				5					10					15	
Met	Leu	Leu	Val	Ser	Tyr	Cys	Met	Pro	His	Tyr	Ser	Val	Ala	Val	Ile
			20					25					30		
Ser	Gly	Val	Glu	Val	Lys	Arg	Met	Asn	Glu	Asn	Glu	Asn	Thr	Pro	Asn
		35					40					45			
Asn	Lys	Glu	Val	Lys	Thr	Leu	Ala	Arg	Asp	Val	Tyr	Phe	Val	Gln	Thr
	50					55					60				
Tyr	Asp	Pro	Lys	Asp	Gln	Lys	Ser	Val	Thr	Val	Tyr	Arg	Asn	Glu	Asp
65				70						75					80
Thr	Arg	Phe	Gly	Phe	Pro	Phe	Tyr	Phe	Lys	Phe	Asn	Ser			
				85					90						

(2) INFORMATION FOR SEQ ID NO:425:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

```

Met Phe Lys Lys Ile Ile Phe Leu Cys Val Phe Leu Ile Gly Gly Phe
1           5           10           15
Val Ile Pro Pro Leu Glu Ala Met Pro Ile Leu Arg Asn Lys Thr Pro
          20           25           30
Lys Lys Asn Tyr Gln Glu Ala His Glu Lys Leu Tyr Arg Ser Ile Ile
          35           40           45
Asn Arg Gln Xaa Xaa Thr Arg Lys Lys Ser Gly Trp Tyr Phe Leu Gly
          50           55           60
Gly Val Gly Ala Val Glu Ala Ile Lys Asp Tyr Gln Gly Lys Glu Met
65           70           75           80
Lys Asp Trp Met Pro Arg Ser Ile
          85
  
```

(2) INFORMATION FOR SEQ ID NO:426:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

```

Val His Phe Thr Cys Ile Phe Leu Thr Leu Leu Lys Trp Ile Leu Pro
1           5           10           15
Ala Lys Asn Lys Gln Ala Cys Lys Lys Ala Thr Asn Gln Ile His Ser
          20           25           30
Arg Xaa Ala Lys His Pro Ala Lys Tyr Pro Pro Ser Ser Ile Asn Pro
          35           40           45
  
```

Ser Ile Gln Ala Gly Ile Gln Gly Val Met Gln Gly Phe Gly Ala Leu
50 55 60

Ser Ser Xaa Leu Glu Xaa Pro Xaa Phe Val Xaa Xaa Ala Lys Cys Gly
65 70 75 80

Trp Ile Gly Gly Phe Glu His Tyr Leu Ser Pro Leu Tyr Gly Trp Gly
85 90 95

Lys Ile His Asp Gly Ala His Cys Asp Leu Met Gln Lys Asp Ala Asn
100 105 110

Gly Arg Gly Ile Gly Leu Glu Lys Gly Leu Pro Pro Phe Lys Gly Leu
115 120 125

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

Met Gln Lys Phe Phe Ser Arg Phe Arg Arg Trp Ala Leu Pro Phe Tyr
1 5 10 15

Phe Val Ser Ala Leu Ala Ala Ile Asp Ile Asp Glu Val Thr Glu Ala
20 25 30

Gln Ala Asn Ser Ile Lys Leu Ser Asp Gln Leu Val Ser Leu Ser Asp
35 40 45

Lys Leu Leu Glu Lys Ala Val Asp Arg Gly Arg Asn Thr Asp His Leu
50 55 60

Lys Asp Leu Asn Asp Leu His Glu Lys Ile Lys His Leu Arg Leu Ile
65 70 75 80

Leu Glu Pro Lys Pro Lys Gly Lys Glu Asp Ser Pro Asn Leu Gly Gly
85 90 95

Asn Lys Asp Met Lys Thr Val Glu Ile Gly Ser Gly
100 105

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

```
Val Ile Leu Ala Phe Ala Phe Gly Met Ser Leu Leu Gly Leu Ala Gly
1           5           10           15
Met Phe Ile Asp Ile Pro Phe Leu Ser Thr Gly Val His Ile Pro Arg
20           25           30
Lys Glu Asp Ile Leu Trp Ile Ser Leu Ile Gly Ile Ser Gly Thr Leu
35           40           45
Gly Gln Tyr Phe Leu Thr Tyr Ala Tyr Met Asn Ala Pro Ala Gly Ile
50           55           60
Ile Ala Pro Ile Glu Tyr Thr Arg Ile Val Trp Gly Leu Leu Phe Gly
65           70           75           80
Leu Tyr Leu Gly Asp Thr Phe Leu Asp Leu Lys Ser Ser Leu Gly Val
85           90           95
Ala Leu Ile Leu Cys Ser Gly Leu Leu Ile Ala Leu Pro Ala Leu Leu
100          105          110
Lys Glu Leu Lys Lys Ile
115
```

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

```
Met Ile Tyr Leu Gly Lys Lys Asn Phe Asn Ala Leu Leu Lys Gly Ala
1           5           10           15
Tyr Leu Met Asp Glu His Phe Arg Asn Ala Pro Phe Glu Ser Asn Leu
```

20	25	30
Pro Val Leu Met Gly Leu Ile Trp Arg Val Val Tyr Leu Thr Phe Phe		
35	40	45

Pro Ile Gln Lys Ala Thr
50

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...288
- (D) OTHER INFORMATION: /note= "HYPOTHETICAL ABC TRANSPORTER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

Met	Ala	Ala	Lys	Ser	Lys	Ala	Xaa	Thr	Leu	Lys	Val	Phe	Ser	Lys	Phe
1				5					10					15	
Phe	Ser	Asn	Phe	Lys	Ile	Thr	Lys	Leu	Lys	Asp	Asn	His	Glu	Glu	Ala
			20					25					30		
His	Lys	Leu	Phe	Gly	Glu	Asn	Ser	Arg	Lys	Ala	His	Asp	Thr	Glu	Ile
		35					40					45			
Ile	Tyr	Ser	Thr	Leu	Gln	Val	Val	Pro	Arg	Tyr	Ser	Ile	Glu	Thr	Val
	50					55					60				
Gly	Phe	Ser	Leu	Leu	Ile	Leu	Ala	Val	Ala	Tyr	Ile	Leu	Phe	Lys	Tyr
65					70				75					80	
Gly	Glu	Ala	Arg	Met	Val	Leu	Pro	Thr	Ile	Ser	Met	Tyr	Ala	Leu	Ala
			85					90						95	
Leu	Tyr	Arg	Ile	Leu	Pro	Ser	Val	Thr	Gly	Val	Ile	Ser	Tyr	Tyr	Asn
		100						105					110		
Glu	Ile	Ala	Tyr	Asn	Gln	Leu	Ala	Thr	Asn	Val	Val	Phe	Lys	Ser	Leu
	115					120						125			
Ser	Lys	Thr	Ile	Val	Glu	Glu	Asp	Leu	Val	Pro	Leu	Asp	Phe	Asn	Glu
	130					135				140					
Lys	Ile	Thr	Leu	Gln	Asn	Ile	Ser	Phe	Ala	Tyr	Lys	Ser	Lys	His	Pro

145		150		155		160									
Val	Leu	Lys	Asn	Phe	Asn	Leu	Thr	Ile	Gln	Lys	Gly	Gln	Lys	Ile	Ala
				165					170					175	
Leu	Ile	Gly	His	Ser	Gly	Cys	Gly	Lys	Ser	Thr	Leu	Ala	Asp	Ile	Ile
			180					185					190		
Met	Gly	Leu	Thr	Tyr	Pro	Lys	Ser	Gly	Glu	Ile	Phe	Ile	Asp	Asn	Thr
		195					200					205			
Leu	Leu	Thr	Ser	Glu	Asn	Arg	Arg	Ser	Trp	Arg	Lys	Lys	Ile	Gly	Tyr
	210					215					220				
Ile	Pro	Gln	Asn	Ile	Tyr	Leu	Phe	Asp	Gly	Thr	Val	Gly	Asp	Asn	Ile
225					230					235					240
Ala	Phe	Gly	Ser	Ala	Ile	Asp	Glu	Lys	Arg	Leu	Ile	Lys	Val	Cys	Lys
				245					250					255	
Met	Ala	His	Ile	Tyr	Asp	Phe	Leu	Cys	Glu	His	Glu	Gly	Leu	Lys	Thr
			260					265					270		
Gln	Val	Gly	Glu	Gly	Ala	Leu	Ser	Leu	Ala	Ala	Val	Lys	Asn	Ser	Ala
		275					280					285			

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

Met	Ala	Phe	Gln	Val	Asn	Thr	Asn	Ile	Asn	Ala	Met	Asn	Ala	His	Val
1				5				10						15	
Gln	Ser	Ala	Leu	Thr	Gln	Asn	Ala	Leu	Lys	Thr	Ser	Leu	Glu	Arg	Leu
			20					25					30		
Ser	Ser	Gly	Leu	Arg	Ile	Asn	Lys	Ala	Ala	Asp	Asp	Ala	Ser	Gly	Met
		35					40					45			
Thr	Val	Ala	Asp	Ser	Leu	Arg	Ser	Gln	Ala	Ser	Ser	Leu	Gly	Gln	Ala
	50					55					60				
Ile	Ala	Asn	Thr	Asn	Asp	Gly	Met	Gly	Ile	Ile	Gln	Val	Ala	Asp	Lys
65					70				75					80	

Ala	Met	Asp	Glu	Gln	Leu	Lys	Ile	Leu	Asp	Thr	Val	Lys	Val	Lys	Ala	
				85					90					95		
Thr	Gln	Ala	Ala	Gln	Asp	Gly	Gln	Thr	Thr	Glu	Ser	Arg	Lys	Ala	Ile	
			100					105					110			
Gln	Ser	Asp	Ile	Val	Arg	Leu	Ile	Gln	Gly	Leu	Asp	Asn	Ile	Gly	Asn	
		115					120					125				
Thr	Thr	Thr	Tyr	Asn	Gly	Gln	Ala	Leu	Leu	Ser	Gly	Gln	Phe	Thr	Asn	
		130				135					140					
Lys	Glu	Phe	Gln	Val	Gly	Ala	Tyr	Ser	Asn	Gln	Ser	Ile	Lys	Ala	Ser	
145					150					155					160	
Ile	Gly	Ser	Thr	Thr	Ser	Asp	Lys	Ile	Gly	Gln	Val	Arg	Ile	Ala	Thr	
				165					170					175		
Gly	Ala	Leu	Ile	Thr	Ala	Ser	Gly	Asp	Ile	Ser	Leu	Thr	Phe	Lys	Gln	
		180						185					190			
Val	Asp	Gly	Val	Asn	Asp	Val	Thr	Leu	Glu	Ser	Val	Lys	Val	Ser	Ser	
		195					200					205				
Ser	Ala	Gly	Thr	Gly	Ile	Gly	Val	Leu	Ala	Glu	Val	Ile	Asn	Lys	Asn	
		210				215					220					
Ser	Asn	Arg	Thr	Gly	Val	Lys	Ala	Tyr	Ala	Ser	Val	Ile	Thr	Thr	Ser	
225					230					235					240	
Asp	Val	Ala	Val	Gln	Ser	Gly	Ser	Leu	Ser	Asn	Leu	Thr	Leu	Asn	Gly	
				245					250					255		
Ile	His	Leu	Gly	Asn	Ile	Ala	Asp	Ile	Lys	Xaa	Asn	Asp	Ser	Asp	Gly	
		260						265					270			
Arg	Leu	Val	Thr	Ala	Ile	Asn	Ala	Val	Thr	Ser	Glu	Thr	Gly	Val	Xaa	
		275					280					285				
Ala	Tyr	Thr	Asp	Gln	Lys	Gly	Arg	Leu	Asn	Leu	Arg	Ser	Ile	Gly		
	290					295					300					

(2) INFORMATION FOR SEQ ID NO:432:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

Met	Leu	Asp	Ile	Trp	Ile	Asp	Met	Ile	Ile	Cys	Ile	Phe	Tyr	Leu	Leu	1	5	10	15
Phe	Phe	Thr	Thr	Pro	Tyr	Ile	Val	Gly	Asp	Ile	Leu	Gln	Leu	Lys	Phe	20	25	30	
Ile	Arg	Gln	Lys	Leu	Cys	Glu	Lys	Pro	Val	Leu	Leu	Pro	Gln	Lys	Asp	35	40	45	
Tyr	Glu	Glu	Ala	Gly	Asn	Tyr	Ala	Ile	Arg	Lys	Met	Gln	Leu	Ser	Ile	50	55	60	
Ile	Ser	Gln	Ile	Leu	Asp	Gly	Val	Ile	Phe	Ala	Gly	Trp	Val	Phe	Phe	65	70	75	80
Gly	Leu	Thr	His	Leu	Glu	Asp	Leu	Thr	His	Tyr	Leu	Asn	Leu	Pro	Glu	85	90	95	
Thr	Leu	Gly	Tyr	Leu	Val	Phe	Ala	Leu	Leu	Phe	Leu	Ala	Ile	Gln	Ser	100	105	110	
Val	Leu	Ala	Leu	Pro	Ile	Ser	Tyr	Tyr	Thr	Thr	Met	His	Leu	Asp	Lys	115	120	125	
Glu	Phe	Gly	Phe	Ser	Lys	Val	Ser	Leu	Ser	Leu	Phe	Phe	Lys	Asp	Phe	130	135	140	
Phe	Lys	Gly	Leu	Leu	Leu	Thr	Leu	Gly	Val	Gly	Leu	Leu	Leu	Ile	Tyr	145	150	155	160
Thr	Leu	Ile	Met	Ile	Ile	Glu	His	Val	Glu	His	Trp	Glu	Ile	Ser	Ser	165	170	175	
Phe	Phe	Val	Val	Phe	Val	Phe	Met	Ile	Leu	Ala	Asn	Leu	Phe	Leu	Pro	180	185	190	

(2) INFORMATION FOR SEQ ID NO:433:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 168 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...168
 - (D) OTHER INFORMATION: /note= "VIRULENCE FACTOR MVIN"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

Met Leu Lys Lys Ile Phe Leu Thr Asn Ser Leu Gly Ile Leu Cys Ser
 1 5 10 15
 Arg Ile Phe Gly Phe Leu Arg Asp Leu Met Met Ala Asn Ile Leu Gly
 20 25 30
 Ala Gly Val Tyr Ser Asp Ile Phe Phe Val Ala Phe Lys Leu Pro Asn
 35 40 45
 Leu Phe Arg Arg Ile Phe Ala Glu Gly Ser Phe Ser Gln Ser Phe Leu
 50 55 60
 Pro Ser Phe Ile Arg Ser Ser Ile Lys Gly Gly Phe Ala Ser Leu Val
 65 70 75 80
 Gly Leu Ile Phe Cys Gly Val Leu Phe Met Trp Cys Leu Leu Val Ala
 85 90 95
 Leu Asn Pro Leu Trp Leu Thr Lys Leu Leu Ala Tyr Gly Phe Asp Glu
 100 105 110
 Glu Thr Leu Lys Leu Cys Thr Pro Ile Val Ala Ile Asn Phe Trp Tyr
 115 120 125
 Leu Leu Leu Val Phe Ile Thr Thr Phe Leu Gly Ala Leu Leu Gln Tyr
 130 135 140
 Lys His Ser Phe Phe Ala Ala Leu Met Arg Lys Leu Thr Gln Phe Met
 145 150 155 160
 His Asp Phe Ser Pro Phe Asp Phe
 165

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Met Asn Leu Glu Val Ala Leu Lys Ala Phe Glu Thr Leu Leu Pro Cys
 1 5 10 15
 Asn Lys Gln Glu Val Leu Lys Asn Leu Lys Pro Leu Asp Leu Ile Gly
 20 25 30
 Arg Cys Glu Leu Leu Ser Pro Asn Ile Leu Ile Asp Val Gly His Asn

35	40	45
Pro His Ser Ala Lys Ala Leu Lys Glu Glu Ile Lys Arg Ile Phe Asn		
50	55	60
Ala Pro Ile Val Leu Ile Tyr Asn Cys Tyr Gln Asp Lys Asp Ala Phe		
65	70	75
Leu Val Leu Glu Ile Leu Lys Ser Val Val Lys Lys Val Leu Ile Leu		
	85	90
Glu Leu His Asn Glu Arg Ile Ile Gln Leu Glu Lys Leu Lys Gly Ile		
	100	105
Leu Glu Thr Leu Gly Leu Glu His Ala Leu Phe Glu Glu Leu Lys Glu		
	115	120
Asn Glu Asn Tyr Leu Val Tyr Gly Ser Phe Leu Val Ala Asn Ala Phe		
130	135	140
Tyr Glu Arg Tyr Pro Lys Lys Arg Asp		
145	150	

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

Met Phe Phe Lys Thr Tyr Gln Lys Leu Leu Gly Ala Ser Cys Leu Ala		
1	5	10
Leu Tyr Leu Val Gly Cys Gly Asn Gly Gly Gly Gly Glu Ser Pro Val		
	20	25
Glu Met Ile Xaa Asn Ser Glu Gly Thr Phe Gln Ile Asp Ser Lys Ala		
35	40	45
Asp Ser Ile Thr Ile Gln Gly Val Lys Leu Asn Arg Gly Asn Cys Ala		
50	55	60
Val Asn Phe Val Pro Val Ser Glu Thr Phe Gln Met Gly Val Leu Ser		
65	70	75
Gln Val Thr Pro Ile Ser Ile Gln Asp Phe Lys Asp Met Ala Ser Thr		
	85	90
		95

Tyr Lys Ile Phe Asp Gln Lys Lys Gly Leu Ala Asn Ile Ala Asn Lys
 100 105 110
 Ile Ser Gln Leu Glu Gln Lys Gly Val Met Met Lys Pro Xaa Thr Leu
 115 120 125
 Asn Phe Gly Glu Ser Leu Lys Gly Ile Ser Gln Gly Cys Asn Ile Ile
 130 135 140
 Glu Ala Glu Ile Gln Thr Asp Lys Gly Ala Trp Thr Phe Asn Phe Asp
 145 150 155 160
 Lys

(2) INFORMATION FOR SEQ ID NO:436:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...59
 - (D) OTHER INFORMATION: /note= "beginning of protein???"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

Met Ala Ile Gly Phe Pro Leu Val Phe Gly Ile Leu Leu Thr Leu Phe
 1 5 10 15
 Ser Arg Ser Tyr Trp Arg Glu Phe Gly Gly Val Ser Gly Val Leu Trp
 20 25 30
 Arg Ala Ser Gly Phe Ser Gly Ala Lys Val Glu Arg Asn Leu Glu Arg
 35 40 45
 Asp Pro His Ala Phe Phe Thr His Cys Asp Phe
 50 55

(2) INFORMATION FOR SEQ ID NO:437:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

Met	Lys	Lys	Lys	Ala	Lys	Val	Phe	Trp	Cys	Cys	Phe	Lys	Met	Ile	Arg
1				5					10					15	
Trp	Leu	Tyr	Leu	Ala	Val	Phe	Phe	Leu	Leu	Ser	Val	Ser	Asp	Ala	Lys
			20					25					30		
Glu	Ile	Ala	Met	Gln	Arg	Phe	Asp	Lys	Gln	Asn	His	Lys	Ile	Phe	Glu
		35					40					45			
Ile	Leu	Ala	Asp	Lys	Val	Ser	Ala	Lys	Asp	Asn	Val	Ile	Thr	Ala	Ser
	50					55					60				
Gly	Asn	Ala	Ile	Leu	Leu	Asn	Tyr	Asp	Val	Tyr	Ile	Leu	Ala	Asp	Lys
65					70					75					80
Val	Arg	Tyr	Asp	Thr	Lys	Thr	Lys	Glu	Ala	Leu	Leu	Glu	Gly	Asn	Ile
				85					90					95	
Lys	Val	Tyr	Arg	Gly	Glu	Gly	Leu	Leu	Val	Lys	Thr	Asp	Tyr	Val	Lys
			100					105						110	
Leu	Ser	Leu	Asn	Glu	Lys	Tyr	Glu	Ile	Ile	Phe	Pro	Phe	Tyr	Val	Gln
		115					120					125			
Asp	Ser	Val	Ser	Gly	Ile	Trp	Val	Ser	Ala	Asp	Ile	Ala	Ser	Gly	Lys
	130					135					140				
Asp	Gln	Lys	Tyr	Lys	Ile	Lys	Asn	Met	Ser	Ala	Ser	Gly	Cys	Ser	Ile
145					150					155					160
Asp	Asn	Pro	Ile	Trp	His	Val	Asn	Ala	Thr	Ser	Gly	Ser	Phe	Asn	Met
				165					170					175	
Gln	Lys	Ser	His	Leu	Ser	Met	Trp	Asn	Pro	Lys	Ile	Tyr	Val	Gly	Asp
			180						185					190	
Ile	Pro	Val	Leu	Tyr	Leu	Pro	Tyr	Ile	Phe	Met	Ser	Thr	Ser	Asn	Lys
		195					200					205			
Arg	Thr	Thr	Gly	Phe	Leu	Tyr	Pro	Glu	Phe	Gly	Thr	Ser	Thr		
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

```
Met Leu Asp Phe Asp Leu Val Leu Phe Gly Ala Thr Gly Asp Leu Ala
1           5           10           15
Met Arg Lys Leu Phe Val Ser Leu Tyr Glu Ile Tyr Ile Ser Phe Met
          20           25           30
Val Leu Lys Thr Ile Leu Gly Leu Ser His Arg Gly Val Arg Ser Tyr
          35           40           45
Pro Met Lys Ser Phe
          50
```

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...109

(D) OTHER INFORMATION: /note= "alkylphosphonate uptake genes A
through Q"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

```
Met Gln Asp Leu Pro Pro Cys Pro Lys Arg Asn Asp Ala Tyr Thr Tyr
1           5           10           15
His Asp Gly Thr Gln Phe Val Cys Ser Ser Cys Leu Tyr Glu Trp Asn
          20           25           30
Gly Asn Glu Ile Ser Asn Glu Glu Leu Ile Val Lys Asp Cys His Asn
          35           40           45
Asn Leu Leu Gln Asn Gly Asp Ser Val Ile Leu Ile Lys Asp Leu Lys
          50           55           60
Val Lys Gly Ser Ser Leu Val Leu Lys Lys Gly Thr Lys Ile Lys Asn
          65           70           75           80
```

Ile Lys Leu Val Asn Ser Asp His Asn Val Asp Cys Lys Val Glu Gly
85 . 90 95

Gln Ser Leu Ser Leu Lys Ser Glu Phe Leu Lys Lys Ala
100 105

(2) INFORMATION FOR SEQ ID NO:440:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...73
 - (D) OTHER INFORMATION: /note= "outer membrane 30.2K protein"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

Val Asp Gly Ala Ile Ile Thr Gly Asn Tyr Ala Leu Gln Ala Lys Leu
1 5 10 15

Thr Gly Ala Leu Phe Ser Glu Asp Lys Asp Ser Pro Tyr Ala Asn Leu
20 25 30

Val Ala Ser Arg Glu Asp Asn Ala Gln Asp Glu Ala Ile Lys Ala Leu
35 40 45

Ile Glu Ala Leu Gln Ser Glu Lys Thr Arg Lys Phe Ile Leu Asp Thr
50 55 60

Tyr Lys Gly Ala Ile Ile Pro Ala Phe
65 70

(2) INFORMATION FOR SEQ ID NO:441:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

Val	Phe	Thr	Met	Leu	Val	Leu	Val	Leu	Ser	Asp	Asn	Phe	Leu	Gly	Leu	
1				5					10					15		
Phe	Ile	Gly	Trp	Glu	Gly	Val	Gly	Leu	Cys	Ser	Tyr	Leu	Leu	Ile	Gly	
			20					25					30			
Phe	Trp	Tyr	His	Lys	Lys	Ser	Ala	Asn	Asn	Ala	Ser	Ile	Glu	Ala	Phe	
			35				40					45				
Val	Met	Asn	Arg	Ile	Thr	Asp	Leu	Gly	Met	Leu	Met	Gly	Ile	Ile	Leu	
	50					55					60					
Ile	Phe	Trp	Asn	Phe	Gly	Thr	Leu	Gln	Tyr	Lys	Glu	Val	Phe	Ser	Met	
65					70					75					80	
Leu	Asn	Asn	Ala	Asp	Tyr	Ser	Met	Leu	Phe	Tyr	Ile	Ser	Val	Phe	Leu	
				85					90					95		
Phe	Ile	Gly	Ala	Met	Gly	Lys	Ser	Ala	Gln	Phe	Pro	Met	His	Thr	Trp	
			100					105					110			
Leu	Ala	Asn	Ala	Met	Glu	Gly	Pro	Thr	Pro	Val	Ser	Ala	Leu	Ile	His	
		115					120					125				
Ala	Thr	Thr	Met	Val	Thr	Ala	Gly	Val	Tyr	Leu	Ile	Ile	Arg	Ala	Asn	
	130						135				140					
Pro	Leu	Tyr	Ser	Ala	Val	Phe	Glu	Val	Gly	Tyr	Phe	Ile	Ala	Cys	Leu	
145					150					155					160	
Gly	Ala	Phe	Val	Ala	Leu	Phe	Gly	Ala	Ser	Met	Ala	Leu	Val	Asn	Lys	
				165					170					175		
Asp	Leu	Lys	Arg	Ile	Val	Glu	Tyr	Ser	Thr	Leu	Ser	Gln	Leu	Gly	Leu	
			180					185					190			
Tyr	Val	Cys	Ser	Gly	Arg	Ala	Trp	Gly	Leu	Cys	Asp	Arg	Ala	Phe	Pro	
		195					200					205				
Pro	Leu	Tyr	Ala	Cys	Val	Leu	Gln	Ile	Pro	Pro	Phe	Leu	Arg	Leu	Arg	
	210						215				220					
Gln	Cys	His	Ala	Cys	Asp	Gly	Arg	Gln	Ser	Gly	Tyr	Tyr				
225					230					235						

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

Val	Cys	Leu	Gly	Leu	Ala	Asp	Val	Met	Val	Val	Leu	Ser	Leu	His	Leu
1				5					10					15	
Asn	Leu	Asn	Pro	Thr	Asn	Pro	Lys	Trp	Leu	Asn	Arg	Asp	Arg	Leu	Val
			20					25					30		
Phe	Ser	Gly	Gly	His	Ala	Ser	Ala	Leu	Val	Tyr	Ser	Leu	Leu	His	Leu
		35					40					45			
Trp	Gly	Phe	Asp	Leu	Ser	Leu	Asp	Asp	Leu	Lys	Arg	Phe	Arg	Gln	Leu
	50					55					60				
His	Ser	Lys	Thr	Pro	Gly	His	Pro	Glu	Leu	His	His	Thr	Glu	Gly	Ile
65					70					75					80
Glu	Ile	Thr	Thr	Xaa	Phe	Arg	Ala	Arg	Phe	Cys					
				85					90						

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1...97

(D) OTHER INFORMATION: /note= "chloramphenicol resistance protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

Met	Met	Ile	Thr	Lys	Gln	Ser	Tyr	Gln	Arg	Phe	Ala	Leu	Met	Arg	Val
1				5					10					15	
Phe	Val	Phe	Ser	Leu	Ser	Ala	Phe	Ile	Phe	Asn	Thr	Thr	Glu	Phe	Val
			20					25					30		
Pro	Val	Ala	Leu	Leu	Ser	Asp	Ile	Ala	Lys	Ser	Phe	Glu	Met	Glu	Ser
		35					40					45			
Ala	Thr	Val	Gly	Leu	Met	Ile	Thr	Ala	Tyr	Ala	Trp	Val	Val	Ser	Leu
	50					55				60					

Gly Ser Leu Pro Leu Met Leu Leu Ser Ala Lys Ile Glu Arg Lys Arg
65 70 75 80
Leu Leu Leu Phe Leu Phe Ala Leu Phe Ile Phe Ser His Ile Leu Ser
85 90 95
Arg

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

Met Lys Leu Arg Ala Ser Val Leu Ile Gly Val Ala Ile Leu Cys Leu
1 5 10 15
Ile Leu Ser Ala Cys Ser Asn Tyr Ala Lys Lys Val Val Lys Gln Lys
20 25 30
Asn His Val Tyr Thr Pro Val Tyr Asn Glu Leu Ile Glu Lys Tyr Ser
35 40 45
Glu Ile Pro Leu Asn Asp Lys Leu Lys Asp Thr Pro Phe Met Val Gln
50 55 60
Val Lys Leu Pro Asn Tyr Lys Asp Tyr Leu Leu Asp Asn Lys Gln Val
65 70 75 80
Val Leu Thr Phe Lys Leu Val His His Ser Lys Lys Ile Thr Leu Ile
85 90 95
Gly Asp Ala Asn Lys Ile Leu Gln Tyr Lys Asn Tyr Phe Gln Ala Asn
100 105 110
Gly Ala Arg Ser Asp Ile Asp Phe Tyr Leu Gln Pro Thr Leu Asn Gln
115 120 125
Lys Gly Val Val Met Ile Ala Ser Asn Tyr Asn Asp Asn Pro Asn Asn
130 135 140
Lys Glu Lys Pro Gln Thr Phe Asp Val Leu Gln Gly Ser Gln Pro Met
145 150 155 160
Leu Gly Ala Asn Thr Lys Asn Leu His Gly Tyr Asp Val Ser Gly Ala

165	170	175
Asn Asn Lys Gln Val Ile Asn Glu Val Ala Arg Glu Lys Ala Gln Leu		
180	185	190
Glu Lys Ile Asn Gln Tyr Tyr Lys Thr Leu Leu Gln Asp Lys Glu Gln		
195	200	205
Glu Tyr Thr Thr Arg Lys Asn Asn Gln Arg Glu Ile Leu Glu Thr Leu		
210	215	220
Ser Asn Arg Ala Gly Tyr Gln Met Arg Gln Asn Val Ile Ser Ser Glu		
225	230	235
Ile Phe Lys Asn Gly Asn Leu Asn Met Gln Ala Lys Glu Glu Glu Val		
245	250	255
Arg Glu Lys Leu Gln Glu Glu Arg Glu Asn Glu Tyr Leu Arg Asn Gln		
260	265	270
Ile Arg Ser Leu Leu Ser Gly Lys		
275	280	

(2) INFORMATION FOR SEQ ID NO:445:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

Met Thr Thr Pro Met Ile Ile Ile Ser Leu Glu Met Gly Leu Ser Leu		
1	5	10
Val Pro Met Arg Gln Cys Leu Val Cys Gln Ala Leu Ala Arg Ser Ile		
20	25	30
Ser Trp Asn Gly Leu Gly Gly Asn Val Arg Asn Thr Lys Val Tyr Gly		
35	40	45
Lys Phe Ala Ala Tyr His His Leu Gln Lys Tyr Leu Leu Ile Asp Leu		
50	55	60
Ile Ala Arg Phe Lys Thr Gln Gly Gly Tyr Ile Phe Arg Tyr Asn Thr		
65	70	75
Asp Asp Tyr Leu Pro Leu Asn Ser Thr Phe Tyr Met Gly Gly Val Thr		
85	90	95

Thr Val Arg Gly Phe Arg Asn Gly Ser Ile Thr Pro Lys Asp Glu Phe
 100 105 110
 Gly Leu Trp Leu Gly Gly Asp Gly Ile Phe Thr Xaa Ser Thr Glu Leu
 115 120 125
 Ser Tyr Gly Val Leu Lys Ala Ala Lys Met Arg Leu Ala Trp Phe Phe
 130 135 140
 Asp Phe Gly Phe Leu Thr Phe Xaa Thr Pro Thr Arg Gly Ser Phe Phe
 145 150 155 160
 Tyr Asn Ala Xaa Thr Thr Thr Ala Asn Phe Lys Asp Tyr Xaa Val Val
 165 170 175
 Gly Xaa Xaa Phe Glu Xaa Ala Thr Trp Arg Ala
 180 185

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

Met Trp Leu Asp His Ile Ala Lys Glu Ile Arg Ser Leu Val Glu Asn
 1 5 10 15
 Asp Ile Glu Val Gly Ile Val Ile Gly Gly Gly Asn Ile Ile Arg Gly
 20 25 30
 Val Ser Ala Ala Leu Gly Gly Ile Ile Arg Arg Thr Ser Gly Asp Tyr
 35 40 45
 Met Gly Met Leu Ala Thr Val Ile Lys Arg
 50 55

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...85

(D) OTHER INFORMATION: /note= "variable antigen from Treponema"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

```
Val His Asn Phe His Trp Asn Val Lys Gly Thr Asp Phe Phe Asn Val
1           5           10           15
His Lys Ala Thr Glu Glu Ile Tyr Glu Gly Phe Ala Asp Met Phe Asp
          20           25           30
Asp Leu Ala Glu Arg Ile Val Gln Leu Gly His His Pro Leu Val Thr
          35           40           45
Leu Ser Glu Ala Ile Lys Leu Thr Arg Val Lys Glu Glu Thr Lys Thr
          50           55           60
Ser Phe His Ser Lys Asp Ile Phe Lys Glu Ile Leu Glu Asp Tyr Lys
65           70           75           80
His Leu Glu Lys Glu
          85
```

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...90

(D) OTHER INFORMATION: /note= "HYPERSENSITIVITY RESPONSE
SECRETION PROTEIN"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

```
Met Asn Lys Thr Ile Lys Ala Ala Ala Leu Ala Tyr Asn Met Gly Gln
1           5           10           15
Asp His Ala Pro Lys Val Ile Ala Ser Gly Val Gly Glu Val Ala Lys
          20           25           30
```

Arg Ile Ile Gln Lys Ala Lys Glu Tyr Asp Ile Ala Leu Phe Ser Asn
35 40 45

Pro Met Leu Val Asp Ser Leu Leu Lys Val Glu Leu Asp Cys Ala Ile
50 55 60

Pro Glu Glu Leu Tyr Glu Ser Val Val Gln Val Phe Leu Trp Leu Asn
65 70 75 80

Ser Val Glu Asn Asn Ala Gln Met Ser Lys
85 90

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

Met Gln Ala Leu Lys Ser Leu Leu Glu Val Ile Thr Lys Leu Gln Asn
1 5 10 15

Leu Gly Gly Tyr Leu Met His Ile Ala Ile Phe Ile Ile Phe Ile Trp
20 25 30

Ile Gly Gly Leu Lys Phe Val Pro Tyr Glu Ala Glu Gly Ile Ala Pro
35 40 45

Phe Val Xaa Asn Ser Pro Phe Phe Ser Phe Met Tyr Lys Phe Glu Lys
50 55 60

Pro Ala Tyr Lys Gln His Lys Met Ser Glu Ser Gln Ser Met Gln Glu
65 70 75 80

Glu Met Gln Asp Asn Pro Lys Ile Val Glu Asn Lys Xaa Trp His Lys
85 90 95

Glu Asn Arg Thr Ser Phe Ser Gly
100

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...172
 - (D) OTHER INFORMATION: /note= "sensor protein"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

Met	Gly	Lys	Ile	Ser	Ala	His	Leu	Ala	His	Glu	Ile	Arg	Asn	Pro	Val	1	5	10	15
Gly	Ser	Ile	Ser	Leu	Leu	Ala	Ser	Val	Leu	Leu	Lys	His	Ala	Asn	Glu	20	25	30	
Lys	Thr	Lys	Pro	Ile	Val	Val	Glu	Leu	Gln	Lys	Ala	Leu	Trp	Arg	Val	35	40	45	
Glu	Arg	Ile	Ile	Lys	Ala	Thr	Leu	Leu	Phe	Ser	Lys	Gly	Ile	Gln	Ala	50	55	60	
Asn	Arg	Thr	Lys	Gln	Ser	Leu	Lys	Thr	Leu	Glu	Ser	Asp	Leu	Lys	Glu	65	70	75	80
Ala	Leu	Asn	Cys	Tyr	Thr	Tyr	Ser	Lys	Asp	Ile	Asp	Phe	Leu	Phe	Asn	85	90	95	
Phe	Ser	Asp	Glu	Glu	Gly	Phe	Phe	Asp	Phe	Asp	Leu	Met	Gly	Ile	Val	100	105	110	
Leu	Gln	Asn	Phe	Leu	Tyr	Asn	Ala	Ile	Asp	Ala	Ile	Glu	Ala	Leu	Glu	115	120	125	
Glu	Ser	Glu	Gln	Gly	Gln	Val	Lys	Ile	Glu	Ala	Phe	Ile	Gln	Asn	Glu	130	135	140	
Phe	Ile	Val	Phe	Thr	Ile	Ile	Asp	Asn	Gly	Lys	Glu	Val	Glu	Asn	Lys	145	150	155	160
Ser	Ala	Leu	Phe	Glu	Pro	Phe	Glu	Thr	Thr	Lys	Leu	165	170						

(2) INFORMATION FOR SEQ ID NO:451:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 212 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...212
(D) OTHER INFORMATION: /note= "L-lactate permease"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

```
Val Ser Glu Phe His Gln Val Tyr Asp Pro Leu Gly Asn Ile Trp Leu
1           5           10           15

Ser Ala Leu Val Ala Leu Leu Pro Ile Leu Leu Phe Phe Leu Ser Leu
20           25           30

Met Val Phe Lys Leu Lys Gly Tyr Thr Ala Ala Phe Leu Ser Val Ala
35           40           45

Leu Ser Ala Ile Ile Ala Val Leu Val Tyr Lys Met Pro Val Ser Met
50           55           60

Val Gly Ser Ser Phe Leu Tyr Gly Phe Leu Tyr Gly Leu Trp Leu Phe
65           70           75           80

Ala Trp Ile Ile Ile Ala Ala Ile Phe Leu Tyr Lys Leu Ser Val Lys
85           90           95

Ser Gly Tyr Phe Glu Ile Leu Lys Glu Ser Val Gln Ser Ile Thr Leu
100          105          110

Asp His Arg Ile Leu Val Ile Leu Ile Gly Phe Cys Phe Gly Ser Phe
115          120          125

Leu Glu Gly Ala Ile Gly Phe Gly Gly Pro Ile Ala Ile Thr Ala Ala
130          135          140

Ile Leu Val Gly Leu Gly Leu Ser Pro Leu Tyr Ser Ala Gly Leu Cys
145          150          155          160

Leu Ile Ala Asn Thr Ala Pro Val Ala Phe Gly Ala Val Gly Ile Pro
165          170          175

Ile Ser Ala Met Ala Ser Ala Val Gly Val Pro Ala Ile Leu Ile Ser
180          185          190

Ala Met Thr Gly Lys Ile Leu Phe Phe Val Ser Leu Leu Val Pro Phe
195          200          205

Phe Ile Val Phe
210
```

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...182

(D) OTHER INFORMATION: /note= "INVOLVED IN PENICILLIN TOLERANCE-
has signal peptide seq."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

Met	Glu	Ile	Lys	Met	Ala	Lys	Asp	Tyr	Gly	Phe	Cys	Phe	Gly	Val	Lys	
1				5					10					15		
Arg	Ala	Ile	Gln	Ile	Ala	Glu	Lys	Asn	Gln	Asn	Ser	Leu	Ile	Phe	Gly	
			20					25					30			
Ser	Leu	Ile	His	Asn	Ala	Lys	Glu	Ile	Asn	Arg	Leu	Glu	Lys	Asn	Phe	
			35					40					45			
Asn	Val	Lys	Ile	Glu	Glu	Asp	Pro	Lys	Lys	Ile	Pro	Lys	Asn	Lys	Ser	
			50				55					60				
Val	Ile	Ile	Arg	Thr	His	Gly	Ile	Pro	Lys	Gln	Asp	Leu	Glu	Tyr	Leu	
65					70					75					80	
Lys	Asn	Lys	Gly	Val	Lys	Ile	Thr	Asp	Ala	Thr	Cys	Pro	Tyr	Val	Ile	
				85					90						95	
Lys	Pro	Gln	Gln	Ile	Val	Glu	Ser	Met	Ser	Lys	Glu	Gly	Tyr	Gln	Ile	
			100					105						110		
Val	Leu	Phe	Gly	Asp	Ile	Asn	His	Pro	Glu	Val	Lys	Gly	Val	Ile	Ser	
			115				120						125			
Tyr	Ala	Thr	Asn	Gln	Ala	Leu	Val	Gly	Asn	Ser	Leu	Glu	Glu	Leu	Gln	
			130				135					140				
Glu	Lys	Lys	Leu	Gln	Arg	Lys	Val	Ala	Leu	Val	Ser	Gln	Thr	Thr	Gln	
145					150					155					160	
Ala	Asn	Pro	Lys	Thr	Leu	Ala	Asn	Arg	Phe	Leu	Phe	Gly	Gly	Xaa	Cys	
				165					170						175	
Thr	Glu	Val	Arg	Ile	Phe											
				180												

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...224

(D) OTHER INFORMATION: /note= "molybdenum transport system permease"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

Met	Asp	His	Glu	Phe	Leu	Ile	Thr	Met	Arg	Leu	Ser	Phe	Ser	Leu	Ala
1				5					10					15	
Leu	Ile	Thr	Thr	Leu	Ile	Leu	Leu	Pro	Ile	Gly	Ile	Phe	Leu	Gly	Tyr
			20					25					30		
Phe	Leu	Ser	Leu	Lys	Arg	Asn	Leu	Leu	Thr	Ser	Leu	Thr	Glu	Thr	Leu
			35				40					45			
Val	Tyr	Met	Pro	Leu	Val	Leu	Pro	Pro	Ser	Val	Leu	Gly	Phe	Tyr	Leu
	50					55					60				
Leu	Leu	Ile	Phe	Ser	Pro	Ser	Ser	Phe	Leu	Gly	Ala	Phe	Leu	Gln	Asp
65					70					75				80	
Val	Leu	Asn	Val	Lys	Leu	Val	Phe	Ser	Phe	Gln	Gly	Leu	Ile	Leu	Gly
				85					90					95	
Ser	Val	Ile	Phe	Ser	Leu	Pro	Phe	Met	Val	Ser	Pro	Ile	Lys	Ser	Ala
			100					105					110		
Leu	Ile	Ser	Leu	Pro	Thr	Ser	Leu	Lys	Glu	Ala	Ser	Tyr	Ser	Leu	Gly
			115				120					125			
Lys	Gly	Glu	Tyr	Tyr	Thr	Leu	Phe	Phe	Val	Leu	Leu	Pro	Asn	Ile	Lys
	130						135					140			
Pro	Ser	Val	Leu	Met	Ala	Ile	Ile	Thr	Thr	Phe	Met	His	Thr	Ile	Gly
145					150					155				160	
Glu	Phe	Gly	Val	Val	Met	Met	Leu	Gly	Gly	Asp	Ile	Leu	Gly	Glu	Thr
				165					170					175	
Arg	Val	Ala	Ser	Ile	Thr	Ile	Phe	Asn	Glu	Ala	Glu	Ala	Leu	Asn	Tyr
			180					185					190		
Ser	Lys	Ala	His	Gln	Tyr	Ala	Leu	Thr	Leu	Thr	Leu	Ile	Ser	Phe	Ser
			195				200					205			

Leu Leu Phe Val Thr Leu Phe Leu Asn Lys Lys Gln Ser Ser Phe Leu
 210 215 220

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

Met His Pro Ile Met Phe Ala Tyr Ile Ala Asn Ala Leu Ala Gln Ala
 1 5 10 15
 Arg Lys Ile Asn Gly Thr Leu Cys Met Ala Phe Gln Lys Ile Ser Gln
 20 25 30
 Val Lys Glu Leu Gly Ile Asp Lys Ala Lys Ser Leu Ile Gly Asn Leu
 35 40 45
 Ser Gln Val Ile Ile Tyr Pro Thr Lys Asp Thr Asp Glu Leu Ile Glu
 50 55 60
 Cys Gly Val Pro Leu Ser Asp Ser Glu Ile Asn Phe Leu His Asn Thr
 65 70 75 80
 Asp Met Arg Ala Arg Gln Val Leu Val Lys Asn Ile Val Thr Asn Ala
 85 90 95
 Ser Ala Phe Ile Glu Ile Asp Leu Lys Lys Ile Cys Lys Asn Tyr Phe
 100 105 110
 Ile Phe Leu Ile Ala Met Leu Val Ile Glu Lys Ser Ser Met Ile Leu
 115 120 125
 Lys Lys Gln
 130

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

```
Met Cys Leu Thr Gly Gly Leu Met Arg Trp Leu Lys Ser Val Lys Pro
1           5           10           15
Glu Arg Ile Leu His Ser Val Val Glu Phe Val Asp Ile Ala Gly Leu
          20           25           30
Ile Lys Gly Ala Ser Lys Gly Glu Gly Leu Gly Asn Gln Phe Leu Ala
          35           40           45
Asn Ile Lys Glu Cys Glu Val Ile Leu Gln Val Val Arg Cys Phe Glu
          50           55           60
Asp Asp Asn Asn His Ala Cys Glu Arg
65           70
```

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

```
Met His Val Ala Cys Leu Leu Ala Leu Gly Asp Asn Leu Ile Thr Leu
1           5           10           15
Ser Leu Leu Lys Glu Ile Ala Ser Lys Gln Gln Gln Ser Leu Lys Ile
          20           25           30
Leu Gly Thr His Leu Thr Leu Lys Ile Ala Lys Leu Leu Glu Cys Glu
          35           40           45
Lys His Phe Glu Ile Ile Pro Val Phe Glu Asn Ile Pro Ala Phe Tyr
          50           55           60
Asp Leu Lys Lys Gln Gly Val Phe Trp Ala Met Lys Asp Phe Leu Trp
65           70           75           80
Leu Leu Lys Gln Leu Lys Asn Ile Lys Ser Asn Val
          85           90
```

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

Met	Lys	Lys	Lys	Pro	Leu	Met	Trp	Arg	Ile	Cys	Ala	Leu	Arg	Arg	Leu		
1				5					10					15			
Leu	Leu	Gly	Phe	Lys	Arg	Glu	Arg	Glu	Leu	Leu	Ser	Phe	Ala	Lys	His		
			20					25					30				
Trp	Asn	Ile	Pro	Thr	Ile	Val	Val	Phe	Thr	His	Thr	Gln	Ala	Glu	Ala		
		35					40					45					
Gly	Asp	Ala	Phe	Val	Gln	Glu	Thr	Lys	Gly	Ile	Ile	Asp	Glu	Glu	Trp		
	50					55					60						
Gly	Phe	Lys	Gly	Phe	Val	Arg	Ala	Tyr	Val	Arg	Val	Asn	Ser	Val	Ala		
65					70					75					80		
Phe	Ser	Phe	Arg	Gly	Leu	Lys	Val	Pro	Val	Glu	Gly	Leu	Glu	Glu	Leu		
				85					90						95		
Val	Asp	Glu	Thr	Lys	Lys	Cys	Leu	Ser	Asp	Ala	Glu	Lys	Asn	Lys	Lys		
			100					105					110				
Arg	His	Phe	Leu	Ser	Ile	Gln	Arg	Val	Lys	Ile	Gln	Glu	Arg	Lys	Gln		
		115					120					125					
Ala	Met	Ile	Glu	Glu	Cys	Lys	Thr	Ile	Ile	His	Val	Ala	Ser	Gly	Ala		
	130					135					140						
Ala	Gly	Val	Ala	Gly	Leu	Ile	Pro	Ile	Pro	Phe	Ser	Asp	Ala	Leu	Ala		
145					150					155					160		
Ile	Ala	Pro	Ile	Gln	Ala	Gly	Met	Ile	Tyr	Lys	Met	Asn	Asp	Ala	Phe		
				165					170					175			
Gly	Met	Asp	Leu	Asp	Lys	Ser	Val	Gly	Ala	Ser	Leu	Val	Ala	Gly	Leu		
			180					185					190				
Leu	Gly	Val	Asn	Cys	Arg	Ala	Ser	Gly	Glu	Asp	Ser	Arg					
		195					200					205					

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...41

(D) OTHER INFORMATION: /note= "chemotaxis protein chew"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

```
Val Leu Gly Val Xaa Asn Leu Arg Gly Asn Val Phe Pro Leu Ile Ser  
1           5           10           15  
Leu Arg Leu Lys Phe Gly Leu Lys Ala Glu Lys Gln Asn Lys Asp Thr  
          20           25           30  
Arg Tyr Leu Val Val Arg His Asn Asp  
          35           40
```

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

```
Val Lys Ser Val Phe Ser Glu Glu Lys Glu Thr Pro Val Thr Lys Glu  
1           5           10           15  
Asn Gly Ser Tyr Leu Ile Ala Tyr Asp Pro Leu Asp Gly Ser Ser Val  
          20           25           30  
Met Glu Ala Asn Phe Leu Val Gly Thr Ile Ile Gly Val Tyr Glu Lys  
          35           40           45  
Asp Tyr Lys Ala Gln Asn Leu Val Ala Ser Leu Tyr Val Val Phe Gly  
          50           55           60  
His Lys Ile Glu Leu Val Val Ala Leu Glu Glu Val Tyr Arg Tyr Ala  
65           70           75           80
```

Phe Tyr Gln Asn Lys Phe His Phe Ile Glu Thr Ile Val Leu Glu Asn
 85 90 95
 Lys Gly Lys Ile Ile Ala Ser Gly Gly Asn Gln Lys Asp Phe Ser Leu
 100 105 110
 Gly Leu Lys Lys Ala Leu Glu Gly Phe Phe Ala Glu Asn Tyr Arg Leu
 115 120 125
 Arg Tyr Ser Gly Ser Met Val Ala Asp Val His His Val Leu Val Lys
 130 135 140
 Lys Gly Gly Met Phe Ser Tyr Pro Gln Lys Lys Leu Arg Lys Leu Phe
 145 150 155 160
 Glu Val Phe Pro Leu Ala Leu Met Val Glu Lys Ala Lys Gly Glu Ala
 165 170 175
 Phe Tyr Phe Asp Lys Gly Val Lys Lys Arg Leu Leu Asp Gln Ser Val
 180 185 190
 Glu Ser Tyr His Glu Lys Ser Glu Cys Tyr Leu Ala Ser Pro His Glu
 195 200 205
 Ala Gln Ile Leu Glu Lys His Leu Lys Gly Glu
 210 215

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

Met Lys Ser Ile Gly Glu Val Met Ala Ile Gly Gly Asn Phe Leu Glu
 1 5 10 15
 Ala Leu Gln Lys Ala Leu Cys Ser Leu Glu Asn Asn Trp Leu Gly Phe
 20 25 30
 Glu Ser Leu Ser Lys Asp Leu Glu Ala Ile Lys Lys Glu Ile Arg Arg
 35 40 45
 Pro Asn Pro Lys Arg Leu Leu Tyr Ile Ala Asp Ala Phe Arg Leu Gly
 50 55 60
 Val Ser Val Asp Glu Val Phe Glu Leu Cys Gln Ile Asp Arg Trp Phe

65		70		75		80
Leu Ser Gln Ile	Gln Lys Leu Val Lys	Ala Glu Glu Gly Ile	Asn Ser			
	85	90	95			
Ser Val Leu Thr	Asp Ala Lys Lys	Leu Arg Gly Leu Lys	Asn Leu Gly			
	100	105	110			
Phe Ser Asp Ala	Arg Ile Ala Thr Lys	Ile Lys Glu Asn	Glu Asn Leu			
	115	120	125			
Glu Val Ser Pro	Phe Glu Val Glu Leu	Ala Arg Ser Asn	Leu Gln Ile			
	130	135	140			
Ala Pro His Phe	Glu Glu Val Asp Thr	Cys Ala Ala Glu	Phe Leu Ser			
	145	150	155	160		
Leu Thr Leu Ile	Cys Ile Pro Pro Met	Pro Leu Thr Leu	Cys Pro Leu			
	165	170	175			
Leu Glu Thr Asn	Lys Lys Asn Lys Lys	Arg Lys Ser				
	180	185				

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...231
- (D) OTHER INFORMATION: /note= "transmembrane receptor"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

Met Phe Gly Asn Lys Gln Leu Gln Leu Gln Ile Ser Gln Lys Asp Ser		
1	5	10 15
Glu Ile Ala Glu Leu Lys Lys Glu Val Asn Leu Tyr Gln Ser Leu Leu		
	20	25 30
Asn Leu Cys Leu His Glu Gly Phe Val Gly Ile Lys Asn Asn Lys Val		
	35	40 45
Val Phe Lys Ser Gly Asn Leu Ala Ser Leu Asn Asn Leu Glu Glu Gln		
	50	55 60
Ser Val His Phe Lys Glu Asn Ala Glu Ser Val Asn Leu Gln Gly Val		

65		70		75		80
Ser Tyr Ser Leu Lys	Ser Gln Asn Ile	Asp Gly Val Gln Tyr Phe Ser				
	85	90			95	
Leu Ala Lys Lys Thr Gly Gly Val Gly Glu Tyr His Lys Asn Asp Leu						
	100	105			110	
Phe Lys Thr Phe Cys Thr Ser Leu Lys Glu Gly Leu Glu Asn Ala Gln						
	115	120			125	
Glu Ser Met Gln Tyr Phe His Gln Glu Thr Gly Leu Leu Leu Asn Ala						
	130	135			140	
Ala Lys Asn Gly Glu Glu His Ser Asn Glu Gly Leu Ile Thr Val Asn						
	145	150			155	160
Lys Thr Gly Gln Asp Ile Glu Ser Leu Tyr Glu Lys Met Gln Asn Ala						
	165	170			175	
Thr Ser Leu Ala Asp Ser Leu Asn Gln Arg Ser Asn Glu Ile Thr Gln						
	180	185			190	
Val Ile Ser Leu Ile Asp Asp Ile Ala Glu Gln Thr Asn Leu Leu Ala						
	195	200			205	
Leu Asn Ala Ala Ile Glu Ala Ala Arg Ala Val Asn Met Ala Glu Gly						
	210	215			220	
Leu Arg Trp Trp Leu Met Arg						
	225	230				

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

Met Trp Ile Met Ser Ser Leu Ser Ser Ser Phe Phe His Ser Leu Phe									
1		5				10			15
Phe Ile Lys Ser Asn Pro Gly Gln Leu Leu Lys Gly Trp Gly Ser Lys									
	20				25			30	
Ile Phe Phe Ile Asn Arg Lys Phe Val Leu Ala Gln Tyr Asn Pro Ser									
	35			40				45	

Val Ser Ile Phe Ile Leu Leu Asn Arg Val Phe Gly Val Gly Val
 50 55 60

(2) INFORMATION FOR SEQ ID NO:463:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 182 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

Met	Gln	Phe	Glu	Glu	Met	Lys	Glu	Leu	Ala	His	Gln	Ile	Gly	Val	Phe	1	5	10	15
Tyr	His	Val	Gly	Val	Asp	Gly	Ile	Ala	Leu	Phe	Leu	Leu	Leu	Leu	Asn	20	25	30	
Ala	Ile	Val	Val	Leu	Leu	Ser	Val	Val	Tyr	Val	Lys	Glu	Arg	Arg	Lys	35	40	45	
Asp	Phe	Val	Ile	Cys	Leu	Leu	Leu	Xaa	Gly	Ile	Leu	Met	Gly	Val		50	55	60	
Phe	Ser	Ser	Leu	Asn	Val	Ile	Phe	Phe	Tyr	Ala	Phe	Trp	Glu	Ile	Ser	65	70	75	80
Leu	Leu	Pro	Val	Leu	Tyr	Leu	Ile	Gly	Arg	Phe	Gly	Arg	Asn	Asn	Lys	85	90	95	
Ile	Tyr	Ser	Gly	Met	Lys	Phe	Phe	Leu	Tyr	Thr	Phe	Leu	Ala	Ser	Leu	100	105	110	
Cys	Met	Leu	Leu	Gly	Ile	Leu	Tyr	Ile	Gly	Tyr	Asp	Tyr	Ala	Asn	Asn	115	120	125	
Tyr	Gly	Met	Met	Ser	Phe	Asp	Ile	Leu	Asp	Trp	Tyr	Gln	Leu	Asn	Phe	130	135	140	
Ser	Ser	Gly	Ile	Lys	Thr	Trp	Leu	Phe	Val	Ala	Phe	Leu	Ile	Gly	Ile	145	150	155	160
Ala	Val	Lys	Ile	Pro	Leu	Phe	Pro	Phe	Thr	His	Gly	Cys	Leu	Met	Arg	165	170	175	
Ile	Leu	Thr	Pro	Pro	Leu											180			

(2) INFORMATION FOR SEQ ID NO:464:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

```
Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys Ser
1           5           10           15
Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu Ser
          20           25           30
Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu Leu
          35           40           45
His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr Ile
          50           55           60
Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr Glu
65           70           75           80
Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys Ser
          85           90           95
Glu Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Xaa Glu Gln
          100          105          110
Phe Xaa Ala Gln
          115
```

(2) INFORMATION FOR SEQ ID NO:465:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...153
 (D) OTHER INFORMATION: /note= "Outer membrane 30K protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

Val Gly Ala Asn Pro Val Pro His Ala Gln Ile Leu Gln Ser Val Val
1 5 10 15
Asp Asp Leu Lys Glu Lys Gly Ile Lys Leu Val Ile Val Ser Phe Thr
 20 25 30
Asp Tyr Val Leu Pro Asn Leu Ala Leu Asn Asp Gly Ser Leu Asp Ala
 35 40 45
Asn Tyr Phe Gln His Arg Pro Tyr Leu Asp Arg Phe Asn Leu Asp Arg
 50 55 60
Lys Met His Leu Val Gly Leu Ala Asn Ile His Val Glu Pro Leu Arg
65 70 75 80
Phe Tyr Ser Gln Lys Ile Thr Asp Ile Lys Asn Leu Lys Lys Gly Ser
 85 90 95
Val Ile Ala Val Pro Asn Asp Pro Ala Asn Gln Gly Arg Ala Leu Ile
 100 105 110
Leu Leu His Lys Gln Gly Leu Ile Ala Leu Lys Asp Pro Ser Asn Leu
 115 120 125
Tyr Ala Thr Glu Phe Asp Ile Val Lys Asn Pro Tyr Asn Ile Lys Ile
 130 135 140
Lys Pro Leu Glu Ala Ala Val Ile Ala
145 150

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

Met Gly Leu Val Ala Ser Gly Ile Asn Asp Glu Glu Leu Leu Lys Trp
1 5 10 15
Leu Gln Ala Phe Gly Leu Lys Met Gly Leu Cys Phe Gln Val Leu Asp
 20 25 30
Asp Ile Ile Asp Val Thr Gln Asp Glu Lys Glu
 35 40

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

Met	Met	Lys	Asn	Lys	Arg	Ser	Gln	Asn	Ser	Pro	Tyr	Val	Thr	Pro	Asp	
1			5					10						15		
Asn	Pro	Tyr	Leu	Thr	Leu	Glu	Lys	Ala	Leu	Gly	Tyr	Ser	Phe	Lys	Asp	
			20					25					30			
Lys	Arg	Leu	Leu	Glu	Gln	Ala	Leu	Thr	His	Lys	Ser	Cys	Lys	Leu	Ala	
			35				40					45				
Leu	Asn	Asn	Glu	Arg	Leu	Glu	Phe	Leu	Gly	Asp	Ala	Val	Leu	Gly	Leu	
	50					55				60						
Val	Ile	Gly	Glu	Leu	Leu	Tyr	His	Lys	Phe	Xaa	Xaa	Xaa	Asp	Gly	Gly	
65				70						75				80		
Lys	Leu	Ser	Lys	Leu	Arg	Ala	Ser	Ile	Val	Ser	Ala	His	Gly	Phe	Thr	
				85				90						95		
Lys	Leu	Ala	Lys	Ala	Ile	Ala	Leu	Gln	Asp	Tyr	Leu	Arg	Val	Ser	Ser	
			100					105					110			
Ser	Glu	Glu	Ile	Ser	Lys	Gly	Arg	Glu	Lys	Pro	Ser	Ile	Leu	Ser	Ser	
			115				120					125				
Ala	Phe	Glu	Ala	Leu	Met	Ala	Gly	Val	Tyr	Leu	Glu	Ala	Gly	Leu	Ala	
	130					135					140					
Lys	Val	Arg	Lys	Ile	Ile	Gln	Asn	Leu	Leu	Asn	Arg	Ala	Tyr	Lys	Arg	
145				150						155					160	
Leu	Asp	Leu	Glu	His	Leu	Phe	Met	Asp	Tyr	Lys	Thr	Ala	Leu	Gln	Glu	
				165					170					175		
Leu	Thr	Gln	Xaa	Gln	Phe	Cys	Val	Ile	Pro	Thr	Tyr	Gln	Leu	Leu	Gln	
			180					185					190			
Glu	Lys	Gly	Pro	Asp	His	His	Lys	Glu	Phe	Glu	Met	Ala	Leu	Tyr	Ile	
			195				200				205					
Gln	Asp	Lys	Met	Tyr	Ala	Thr	Ala	Lys	Gly	Lys	Ser	Lys	Lys	Glu	Ala	

210		215		220
Glu Gln Gln Cys Ala Tyr Gln Ala Leu Gln Asn Leu Arg Lys Pro Asn				
225		230	235	240

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...209

(D) OTHER INFORMATION: /note= "integral protein in inner membrane"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

Met Gly Phe Asn Arg Leu Val Asp Arg Asp Ile Asp Lys Asp Asn Pro			
1	5	10	15
Arg Thr Lys Asn Arg Pro Ser Val Asp Gly Arg Ile Ser Val Lys Gly			
	20	25	30
Met Val Ile Phe Ser Val Ser Asn Ala Leu Leu Phe Val Gly Val Ser			
	35	40	45
Tyr Phe Ile Asn Pro Leu Ala Phe Lys Leu Ser Leu Pro Phe Leu Ile			
	50	55	60
Ile Leu Gly Gly Tyr Ser Tyr Phe Lys Arg Phe Ser Ser Leu Ala His			
65	70	75	80
Phe Val Val Gly Leu Ala Leu Gly Leu Ala Pro Ile Ala Gly Ser Val			
	85	90	95
Ala Val Leu Gly Asp Ile Pro Leu Trp Asn Val Phe Leu Ala Leu Gly			
	100	105	110
Val Met Leu Trp Val Ala Gly Phe Asp Leu Leu Tyr Ser Leu Gln Asp			
	115	120	125
Met Glu Phe Asp Lys Glu Arg Gly Leu Phe Ser Ile Pro Ser Gln Leu			
	130	135	140
Gly Glu Lys Trp Cys Leu Asn Leu Ser Arg Leu Ser His Leu Val Ala			
145	150	155	160

Leu Ile Cys Trp Leu Cys Phe Val Lys Cys Tyr His Gly Gly Leu Phe
165 170 175

Ala Tyr Leu Gly Leu Gly Val Ser Ala Leu Ile Leu Leu Tyr Glu Gln
180 185 190

Ile Leu Val Ala Arg Asp Tyr Lys Asn Ile Pro Lys Ser Leu Phe Cys
195 200 205

Glu

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...95
- (D) OTHER INFORMATION: /note= "MAGNESIUM AND COBALT TRANSPORT PROTEIN"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

Val Glu Gln Asn Lys Ile Ile Lys Leu Phe Thr Val Ala Thr Met Ala
1 5 10 15

Met Met Pro Pro Thr Leu Ile Gly Thr Ile Asn Gly Met Asn Phe Lys
20 25 30

Phe Met Pro Glu Leu Glu Trp Gln Tyr Gly Tyr Leu Phe Ala Leu Ile
35 40 45

Val Met Ala Ile Ser Thr Ile Leu Pro Val Ile Tyr Phe Lys Lys Lys
50 55 60

Gly Leu Val Val Ala Phe His Gly Ile Phe Ile Leu Thr Leu Arg Arg
65 70 75 80

Ser Phe Tyr Thr Ala Trp His Ser Leu Leu Gly Tyr Ala Thr Leu
85 90 95

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

(2) INFORMATION FOR SEQ ID NO:472:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47

Met Ala Met Leu Tyr Cys Met Arg Leu Leu Met Pro Ile Leu Gly Ala
1 5 10 15

Ile Lys Gly Gly Asp Ile Gly Glu Trp Phe Pro Asp Asn Asp Pro Lys
20 25 30

Tyr Lys Asn Ala Ser Ser Lys Glu Leu Leu Lys Ile Val Leu Asp Phe

35	40	45
Ser Gln Ser Ile Gly Phe Glu Leu Leu Glu Met Gly Ala Thr Ile Phe		
50	55	60
Ser Glu Ile Pro Lys Ile Thr Pro Tyr Lys Pro Ala Ile Leu Glu Asn		
65	70	75
Leu Ser Gln Leu Leu Gly Leu Glu Lys Ser Gln Ile Ser Leu Lys Ala		
85	90	95

(2) INFORMATION FOR SEQ ID NO:473:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1178 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...1178
 - (D) OTHER INFORMATION: /note= "cytotoxicity associated immunodominant antigen [H.pylori]"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

Met Ile Pro Asn Leu Asp Ile Glu Gly Glu Thr Met Thr Asn Glu Ala		
1	5	10
Ile Asn Gln Gln Pro Gln Thr Glu Ala Ala Phe Asn Pro Gln Gln Phe		
20	25	30
Ile Asn Asn Leu Gln Val Ala Phe Ile Lys Val Asp Asn Val Val Ala		
35	40	45
Ser Phe Asp Pro Asn Gln Lys Pro Ile Val Asp Lys Asn Asp Arg Asp		
50	55	60
Asn Arg Gln Ala Phe Glu Lys Ile Ser Gln Leu Arg Glu Glu Phe Ala		
65	70	75
Asn Lys Ala Ile Lys Asn Pro Thr Lys Lys Asn Gln Tyr Phe Ser Ser		
85	90	95
Phe Ile Ser Lys Ser Asn Asp Leu Ile Asp Lys Asp Asn Leu Ile Asp		
100	105	110
Thr Gly Ser Ser Ile Lys Ser Phe Gln Lys Phe Gly Thr Gln Arg Tyr		
115	120	125

Gln	Ile	Phe	Met	Asn	Trp	Val	Ser	His	Gln	Asn	Asp	Pro	Ser	Lys	Ile	130	135	140
Asn	Thr	Gln	Lys	Ile	Arg	Gly	Phe	Met	Glu	Asn	Ile	Ile	Gln	Pro	Pro	145	150	155
Ile	Ser	Asp	Asp	Lys	Glu	Lys	Ala	Glu	Phe	Leu	Arg	Ser	Ala	Lys	Gln	165	170	175
Ala	Phe	Ala	Gly	Ile	Ile	Ile	Gly	Asn	Gln	Ile	Arg	Ser	Asp	Gln	Lys	180	185	190
Phe	Met	Gly	Val	Phe	Asp	Glu	Ser	Leu	Lys	Glu	Arg	Gln	Glu	Ala	Glu	195	200	205
Lys	Asn	Gly	Glu	Pro	Asn	Gly	Asp	Pro	Thr	Gly	Gly	Asp	Trp	Leu	Asp	210	215	220
Ile	Phe	Leu	Ser	Phe	Val	Phe	Asn	Lys	Lys	Gln	Ser	Ser	Asp	Leu	Lys	225	230	235
Glu	Thr	Leu	Asn	Gln	Glu	Pro	Val	Pro	His	Val	Gln	Pro	Asp	Val	Ala	245	250	255
Thr	Thr	Thr	Thr	Asp	Ile	Gln	Ser	Leu	Pro	Pro	Glu	Ala	Arg	Asp	Leu	260	265	270
Leu	Asp	Glu	Arg	Gly	Asn	Phe	Ser	Lys	Phe	Thr	Leu	Gly	Asp	Met	Asn	275	280	285
Met	Leu	Asp	Val	Glu	Gly	Val	Ala	Asp	Ile	Asp	Pro	Asn	Tyr	Lys	Phe	290	295	300
Asn	Gln	Leu	Leu	Ile	His	Asn	Asn	Ala	Leu	Ser	Ser	Val	Leu	Met	Gly	305	310	315
Ser	His	Asn	Gly	Ile	Glu	Pro	Glu	Lys	Val	Ser	Leu	Leu	Tyr	Gly	Asn	325	330	335
Asn	Gly	Gly	Pro	Glu	Ala	Arg	His	Asp	Trp	Asn	Ala	Thr	Val	Gly	Tyr	340	345	350
Lys	Asn	Gln	Arg	Gly	Asp	Asn	Val	Ala	Thr	Leu	Ile	Asn	Val	His	Met	355	360	365
Lys	Asn	Gly	Ser	Gly	Leu	Val	Ile	Ala	Gly	Gly	Glu	Lys	Gly	Ile	Asn	370	375	380
Asn	Pro	Ser	Phe	Tyr	Leu	Tyr	Lys	Glu	Asp	Gln	Leu	Thr	Gly	Ser	Gln	385	390	395
Arg	Ala	Leu	Ser	Gln	Glu	Glu	Ile	Gln	Asn	Lys	Val	Asp	Phe	Met	Glu	405	410	415
Phe	Leu	Ala	Gln	Asn	Asn	Ala	Lys	Leu	Asp	Asn	Leu	Ser	Lys	Lys	Glu	420	425	430
Lys	Glu	Lys	Phe	Gln	Asn	Glu	Ile	Glu	Asp	Phe	Gln	Lys	Asp	Ser	Lys			

435	440	445
Ala Tyr Leu Asp Ala Leu Gly Asn Asp His Ile Ala Phe Val Ser Lys 450 455 460		
Lys Asp Lys Lys His Leu Ala Leu Val Ala Glu Phe Gly Asn Gly Glu 465 470 475 480		
Leu Ser Tyr Thr Leu Lys Asp Tyr Gly Lys Lys Ala Asp Lys Ala Leu 485 490 495		
Asp Arg Glu Ala Lys Thr Thr Leu Gln Gly Ser Leu Lys His Asp Gly 500 505 510		
Val Met Phe Val Asp Tyr Ser Asn Phe Lys Tyr Thr Asn Ala Ser Lys 515 520 525		
Ser Pro Asp Lys Gly Val Gly Ala Thr Asn Gly Val Ser His Leu Glu 530 535 540		
Ala Gly Phe Ser Lys Val Ala Val Phe Asn Leu Pro Asn Leu Asn Asn 545 550 555 560		
Leu Ala Ile Thr Ser Val Val Arg Gln Asp Leu Glu Asp Lys Leu Ile 565 570 575		
Ala Lys Gly Leu Ser Pro Gln Glu Ala Asn Lys Leu Val Lys Asp Phe 580 585 590		
Leu Ser Ser Asn Lys Glu Leu Val Gly Lys Ala Leu Asn Phe Asn Lys 595 600 605		
Ala Val Ala Glu Ala Lys Asn Thr Gly Asn Tyr Asp Glu Val Lys Gln 610 615 620		
Ala Gln Lys Asp Leu Glu Lys Ser Leu Lys Lys Arg Glu Arg Leu Glu 625 630 635 640		
Lys Asp Val Ala Lys Asn Leu Glu Ser Lys Ser Gly Asn Lys Asn Lys 645 650 655		
Met Glu Ala Lys Ser Gln Ala Asn Ser Gln Lys Asp Glu Ile Phe Ala 660 665 670		
Leu Ile Asn Lys Glu Ala Asn Arg Asp Ala Arg Ala Ile Ala Tyr Ala 675 680 685		
Gln Asn Leu Lys Gly Ile Lys Arg Glu Leu Ser Asp Lys Leu Glu Asn 690 695 700		
Ile Asn Lys Asp Leu Lys Asp Phe Ser Lys Ser Phe Asp Glu Phe Lys 705 710 715 720		
Asn Gly Lys Asn Lys Asp Phe Ser Lys Ala Glu Glu Thr Leu Lys Ala 725 730 735		
Leu Lys Gly Ser Val Lys Asp Leu Gly Ile Asn Pro Glu Trp Ile Ser 740 745 750		

Lys	Val	Glu	Asn	Leu	Asn	Ala	Ala	Leu	Asn	Glu	Phe	Lys	Asn	Gly	Lys		
		755						760					765				
Asn	Lys	Asp	Phe	Ser	Lys	Val	Thr	Gln	Ala	Lys	Ser	Asp	Leu	Glu	Asn		
		770						775				780					
Ser	Ile	Lys	Asp	Val	Ile	Ile	Asn	Gln	Lys	Ile	Thr	Asp	Lys	Val	Asp		
		785					790				795				800		
Asn	Leu	Asn	Gln	Ala	Val	Ser	Val	Ala	Lys	Ala	Thr	Gly	Asp	Phe	Ser		
					805					810					815		
Gly	Val	Glu	Gln	Ala	Leu	Ala	Asp	Leu	Lys	Asn	Phe	Ser	Lys	Glu	Gln		
			820						825					830			
Leu	Ala	Gln	Gln	Ala	Gln	Lys	Asn	Glu	Asp	Phe	Asn	Thr	Gly	Lys	Asn		
			835						840				845				
Ser	Ala	Leu	Tyr	Gln	Ser	Val	Lys	Asn	Gly	Val	Asn	Gly	Thr	Leu	Val		
		850					855				860						
Gly	Asn	Gly	Leu	Ser	Lys	Ala	Glu	Ala	Thr	Thr	Leu	Ser	Lys	Asn	Phe		
		865				870				875					880		
Ser	Asp	Ile	Lys	Lys	Glu	Leu	Asn	Ala	Lys	Leu	Gly	Asn	Phe	Asn	Asn		
				885					890					895			
Asn	Asn	Asn	Asn	Gly	Leu	Glu	Asn	Ser	Thr	Glu	Pro	Ile	Tyr	Thr	Gln		
			900					905					910				
Val	Ala	Lys	Lys	Val	Lys	Ala	Lys	Ile	Asp	Arg	Leu	Asp	Gln	Ile	Ala		
		915						920					925				
Ser	Gly	Leu	Gly	Asp	Val	Gly	Gln	Ala	Ala	Ser	Phe	Leu	Leu	Lys	Arg		
		930					935				940						
His	Asp	Lys	Val	Asp	Asp	Leu	Ser	Lys	Val	Gly	Leu	Ser	Ala	Asn	His		
		945				950				955					960		
Glu	Pro	Ile	Tyr	Ala	Thr	Ile	Asp	Asp	Leu	Gly	Gly	Pro	Phe	Pro	Leu		
				965					970					975			
Lys	Arg	His	Asp	Lys	Val	Asp	Asp	Leu	Ser	Lys	Val	Gly	Leu	Ser	Arg		
			980					985					990				
Glu	Gln	Lys	Leu	Thr	Gln	Lys	Ile	Asp	Asn	Leu	Asn	Gln	Ala	Val	Ser		
		995						1000					1005				
Glu	Ala	Lys	Ala	Ser	His	Phe	Asp	Asn	Leu	Asp	Gln	Met	Ile	Asp	Lys		
		1010					1015					1020					
Leu	Lys	Asp	Ser	Thr	Lys	Lys	Asn	Val	Val	Asn	Leu	Tyr	Val	Glu	Ser		
		1025				1030				1035					1040		
Ala	Lys	Lys	Val	Pro	Thr	Ser	Leu	Ser	Ala	Lys	Leu	Asp	Asn	Tyr	Ala		
				1045					1050					1055			

Thr Asn Ser His Thr Arg Ile Asn Ser Asn Val Lys Asn Gly Thr Ile
 1060 1065 1070
 Asn Glu Lys Ala Thr Gly Met Leu Thr Gln Lys Asn Ser Glu Trp Leu
 1075 1080 1085
 Lys Leu Val Asn Asp Lys Ile Val Ala His Asn Val Gly Ser Ala Pro
 1090 1095 1100
 Leu Ser Ala Tyr Asp Lys Ile Gly Phe Asn Gln Lys Asn Met Lys Asp
 1105 1110 1115 1120
 Tyr Ser Asp Ser Phe Lys Phe Ser Thr Arg Leu Ser Asn Ala Val Lys
 1125 1130 1135
 Asp Ile Lys Ser Gly Phe Val Gln Phe Leu Thr Asn Ile Phe Ser Met
 1140 1145 1150
 Gly Ser Tyr Ser Leu Met Lys Ala Ser Val Glu His Gly Val Lys Asn
 1155 1160 1165
 Thr Asn Thr Lys Gly Gly Phe Gln Lys Ser
 1170 1175

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

Met Lys Ala Pro Ser Gln Xaa Asp Leu Lys Lys Ile Leu Gly Ile Glu
 1 5 10 15
 Glu Val Ile Xaa Xaa Ser Thr Ser Pro Met Glu Leu Arg Leu Ala Asn
 20 25 30
 Gln Lys Leu Gly Asn Arg Phe Ile Lys Thr Leu Gln Ala Met Asn Glu
 35 40 45
 Leu Asp Met Gly Ala Phe Phe Asn Ala Tyr Ala Gln Thr Thr Lys Asp
 50 55 60
 Pro Thr His Ala Thr Ser Tyr Gly Val Phe Ala Ala Ser Leu Asn Met
 65 70 75 80
 Glu Leu Lys Lys Ala Leu Arg His Tyr Leu Tyr Ala Gln Thr Ser Asn
 85 90 95

Met Val Ile Asn Cys Val Lys Ser Val Pro Leu Ser Gln Asn Asp Gly
100 105 110

Gln Lys Ile Leu Leu Ser Leu Gln Ser Pro Phe Asn Gln Leu Ile Glu
115 120 125

Lys Thr Leu Glu Leu Asp Glu Ser His Leu Cys Ala Ala Ser Val Gln
130 135 140

Asn Asp Ile Lys Ala Met Gln His Glu Ser Leu Tyr Ser Arg Leu Tyr
145 150 155 160

Met Ser

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 466 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

Met Lys Ala Leu Lys Thr Phe Leu Lys Lys Ser Leu Ile Leu Leu Leu
1 5 10 15

Ala Ile Ala Leu Asn His Leu Asn Ala Val Ala Met Ile Val Asp Asn
20 25 30

Pro Thr Gln Asn Ala Trp Asn Gly Ala Lys Arg Ala Trp Asp Glu Ser
35 40 45

Lys Trp Ala Lys His Leu Ala Thr Ile Thr Glu Arg Ile Lys Leu Ala
50 55 60

Gln Asp Thr Leu Asp Arg Ala Asn Gln Thr Leu Asn Ser Ile Asn Lys
65 70 75 80

Val Asn Asp Val Leu Asn Lys Thr Asn Gln Phe Leu Thr Gly Ser Ile
85 90 95

Leu Ser Ile Pro Asn Pro Met Gln Tyr Val Glu Lys Ile Gln Ser Phe
100 105 110

Ala Lys Gln Val Gln Ala Asn Thr Glu Arg Ile Lys Glu Asn Ala Gln
115 120 125

Asn Tyr Asp Ile Arg Asn Gln Ile Ala Ala Lys Arg Ile Ser Glu Lys
130 135 140

Cys	Pro	Glu	Leu	Asn	Trp	Asp	Val	Ser	Gln	Asp	Ala	Ser	Pro	Thr	Glu	
145					150					155					160	
Lys	Asn	Leu	His	Gln	Phe	Phe	Thr	Ser	Lys	Gly	Lys	Glu	Ser	Ala	Asn	
				165					170						175	
Thr	Lys	Ala	Leu	Lys	Asp	Phe	Ala	Asn	Ala	Ile	Gly	Asn	Thr	Gln	Ile	
			180					185					190			
Ser	Thr	Ala	Asn	Asp	Leu	Gly	Ala	Gly	Leu	Arg	Gly	Arg	Ala	Leu	Leu	
		195					200					205				
Glu	Tyr	Ile	Cys	Ile	Gln	Lys	Gly	Asn	Leu	Glu	Ala	Ala	Lys	Lys	Ile	
	210					215					220					
Gln	Leu	Leu	Asp	Ser	Gln	Met	Thr	Leu	Ala	Leu	Leu	Asn	Asn	Asp	Tyr	
225					230					235					240	
Thr	Ala	Tyr	Glu	Lys	Leu	Arg	Ala	Glu	Lys	Glu	Glu	Leu	Lys	Arg	Gln	
				245					250						255	
Ile	Ala	Ser	Asn	Val	Tyr	Ala	Lys	Val	Lys	Gln	Leu	Val	Val	Ala	Ser	
			260					265						270		
Gln	Asp	Arg	Ala	Phe	Ser	Gln	Met	Asp	Asn	Glu	Leu	Gly	Val	Lys	Thr	
		275					280					285				
Phe	Gly	Phe	Asn	Asp	Glu	Asn	Val	Lys	Lys	Gly	Tyr	Cys	Lys	Lys	Glu	
	290					295					300					
Asn	Arg	Asn	Gly	Lys	Ser	Glu	Cys	Ile	Pro	Asn	Met	Leu	Asn	Val	Asn	
305					310					315					320	
Arg	Leu	Lys	Ala	Gln	Phe	Asp	Glu	Leu	Asn	Leu	Asp	Tyr	Ser	Arg	Asp	
				325					330						335	
Ile	Ala	Gly	Lys	Lys	Gly	Glu	Ala	Ala	Ala	Lys	Val	Phe	Asn	Asp	Tyr	
			340					345						350		
Lys	His	Arg	Phe	Gln	Gln	Leu	Ser	Val	Glu	Thr	Ala	Leu	Glu	Ile	Ala	
		355					360					365				
Gln	Asn	Leu	Ser	Phe	Met	Asn	Lys	Thr	Leu	Gly	Leu	Met	Val	Gln	Met	
	370					375					380					
Gln	Ser	Tyr	Ala	Phe	Lys	Gln	Gln	Met	Gly	Tyr	Phe	Glu	Asp	Ile	Ile	
385					390					395					400	
Pro	Ala	Asp	Ala	Leu	Lys	Asp	Asp	Lys	Glu	His	Gln	Glu	Asn	Leu	Glu	
				405					410					415		
Gln	Lys	Gln	Gln	Glu	Ile	Glu	Lys	Val	Tyr	Arg	Ala	Lys	Leu	Asp	Ala	
			420					425					430			
Tyr	Gly	Phe	Pro	Asn	Gly	Ser	Val	Gly	Lys	Ala	Ser	Gly	Val	Asn	Ser	
		435					440					445				

Asn Ser Asn Asn Glu Ala Pro Ser Ser Asp Asn Ile Gln Ser Phe Asn
 450 455 460

Pro Tyr
 465

(2) INFORMATION FOR SEQ ID NO:476:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

Met Ala Phe Ile Leu Thr Thr Asn Leu Phe Ile Lys Ser Phe Thr Asn
 1 5 10 15
 Ser Ile Arg Ile Thr Gly Cys Ile Ile Ser Pro Asn Val Phe Phe Ala
 20 25 30
 Tyr Glu Phe Cys Ala Leu Gly Phe Arg Lys Gly Gly Leu Ile Leu Asp
 35 40 45
 Asn Phe Ser Lys Phe Val Ser His Arg Leu Gln
 50 55

(2) INFORMATION FOR SEQ ID NO:477:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 248 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

Val Arg Phe Phe Ile Phe Leu Ile Leu Ile Cys Pro Leu Ile Cys Pro
 1 5 10 15
 Leu Met Ser Ala Asp Ser Ala Leu Pro Ser Val Asn Leu Ser Leu Asn
 20 25 30

Ala	Pro	Ser	Asp	Pro	Lys	Gln	Leu	Val	Thr	Thr	Leu	Asn	Val	Ile	Ala	35	40	45	
Leu	Leu	Thr	Leu	Leu	Val	Leu	Ala	Pro	Ser	Leu	Ile	Leu	Val	Met	Thr	50	55	60	
Ser	Phe	Thr	Arg	Leu	Ile	Val	Val	Phe	Ser	Phe	Leu	Arg	Thr	Ala	Leu	65	70	75	80
Gly	Thr	Gln	Gln	Thr	Pro	Pro	Thr	Gln	Ile	Leu	Val	Ser	Leu	Ser	Leu	85	90	95	
Ile	Leu	Thr	Phe	Phe	Ile	Met	Glu	Pro	Ser	Leu	Lys	Lys	Ala	Tyr	Asp	100	105	110	
Thr	Gly	Ile	Lys	Pro	Tyr	Met	Asp	Lys	Lys	Ile	Ser	Tyr	Thr	Glu	Ala	115	120	125	
Phe	Glu	Lys	Ser	Thr	Leu	Pro	Phe	Lys	Glu	Phe	Met	Leu	Lys	Asn	Thr	130	135	140	
Arg	Glu	Lys	Asp	Leu	Ala	Leu	Phe	Phe	Arg	Ile	Arg	Asn	Leu	Pro	Asn	145	150	155	160
Pro	Lys	Thr	Pro	Asp	Asp	Val	Ser	Leu	Ser	Val	Leu	Ile	Pro	Ala	Phe	165	170	175	
Met	Ile	Ser	Glu	Leu	Lys	Thr	Ala	Phe	Gln	Ile	Gly	Phe	Leu	Leu	Tyr	180	185	190	
Leu	Pro	Phe	Leu	Val	Ile	Asp	Met	Val	Ile	Ser	Ser	Ile	Leu	Met	Ala	195	200	205	
Met	Gly	Met	Met	Met	Leu	Pro	Pro	Val	Met	Ile	Ser	Leu	Pro	Phe	Lys	210	215	220	
Ile	Leu	Val	Phe	Ile	Leu	Val	Asp	Gly	Phe	Asn	Leu	Leu	Thr	Glu	Asn	225	230	235	240
Leu	Val	Ala	Ser	Phe	Lys	Met	Val									245			

(2) INFORMATION FOR SEQ ID NO:478:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION: 1...44
 (D) OTHER INFORMATION: /note= "D-alanyl-D-alanine
 carboxypeptidase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

Val	Met	Asp	Ala	Glu	Asn	Gly	Glu	Leu	Leu	Val	Ala	Gly	Ser	Tyr	Pro
1				5				10						15	
Glu	Tyr	Asn	Leu	Asn	Asp	Phe	Val	Gly	Gly	Ile	Ser	Gln	Asp	Lys	Trp
		20						25					30		
Gln	Lys	Leu	Gln	Asp	Asp	Ile	Tyr	Asn	Pro	Leu	Leu				
		35					40								

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 421 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

Met	Asn	Phe	Phe	Asp	Thr	Leu	Met	Gly	Met	Phe	Val	Glu	Pro	Ser	Gln
1				5				10						15	
Lys	Val	Ala	Lys	Ser	Leu	Ala	Glu	His	Val	Gly	Ser	Phe	Phe	His	Ala
		20						25					30		
Gln	Leu	Ile	Leu	Asn	Thr	Ile	Ile	Thr	Ile	Leu	Phe	Met	Ile	Trp	Ala
	35						40					45			
Tyr	Lys	Arg	Val	Lys	Glu	Gly	Asp	Met	Phe	Glu	Phe	Lys	Thr	Ala	Met
	50					55				60					
Gly	Val	Val	Val	Phe	Ile	Ala	Phe	Val	Gly	Phe	Ile	Asn	Trp	Gly	Ile
65				70					75					80	
Lys	Asn	Pro	Asn	Asp	Phe	Asn	Thr	Tyr	Phe	Ile	Asn	Thr	Ile	Phe	Tyr
			85					90						95	
Pro	Ser	Glu	Lys	Leu	Ala	Ile	Leu	Ile	Ala	Gln	Ser	Leu	Asn	Asp	Gly
		100					105						110		
Leu	Glu	Ile	Pro	Thr	Asn	Thr	Asn	Leu	Ser	Pro	Ser	Glu	Ile	Phe	Ser
	115						120					125			
Ile	Gly	Asn	Leu	Ala	Ser	Ser	Ala	Tyr	Ala	Met	Ile	Val	Asn	Leu	Trp

130	135	140
Asp Asn Ala Phe Asp Gly Ile Asn Met Phe Asn Trp Leu Thr Met Ile 145 150 155 160		
Pro Lys Ile Ile Met Phe Phe Leu Val Ile Leu Gly Glu Leu Leu Phe 165 170 175		
Leu Gly Leu Leu Leu Ile Ile Val Leu Leu Val Thr Ala Glu Ile Phe 180 185 190		
Met Trp Ser Ala Leu Gly Leu Ile Val Leu Pro Leu Gly Leu Ile Pro 195 200 205		
Gln Thr Lys Gly Met Leu Phe Ser Tyr Leu Lys Lys Leu Ile Ser Leu 210 215 220		
Thr Leu Tyr Lys Pro Cys Met Met Leu Val Ala Phe Phe Asn Tyr Gly 225 230 235 240		
Ile Ile Tyr Lys Val Asn Thr Leu Ile Pro Thr Lys His Glu Val Thr 245 250 255		
Gln Gly Phe Tyr Gly Asn Ala Asp Lys Met Ala Asn Glu Gly Lys Ile 260 265 270		
Ile Asp Val Phe Gly Asn Val Leu Glu Gly Asp Trp Asn Ser Tyr Ile 275 280 285		
Ala His Ser Ser Ile Val Gly Phe Leu Thr Ile Ile Val Leu Gly Ser 290 295 300		
Val Ile Cys Phe Phe Leu Val Lys Arg Val Pro Asp Phe Ile Asn Asn 305 310 315 320		
Ile Phe Gly Thr Ser Gly Gly Val Gly Ala Val Thr Glu Met Met Gln 325 330 335		
Lys Ile Gly Met Thr Ile Gly Gly Ala Val Phe Gly Gly Ser Ala Val 340 345 350		
Met Val Ala Asn Gln Val Lys Gln Ala Tyr Gln Ser Ala Gly Gly Gly 355 360 365		
Leu Ala Gly Leu Gln Ala Gly Ala Lys Ala Phe Gly Leu Gly Ala Ile 370 375 380		
Ser Gly Gly Ala Ser Ala Met Ala Asn His Arg Ser Val Lys Ala Gly 385 390 395 400		
Val Lys His Phe Val Ala Ser Val Lys Ser Gly Phe Gly Phe Asp Asn 405 410 415		
Asp Lys Asn Asn Lys 420		

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

Leu	Leu	Val	Thr	Phe	Leu	Asn	Gly	Phe	Asp	Pro	Lys	Ile	Ala	Asn	Leu	
1				5				10						15		
Arg	Lys	Ala	Cys	Asn	Val	Tyr	Ser	Val	Gly	Val	Ile	Tyr	Ile	Val	Thr	
			20					25					30			
Thr	Asn	Thr	Leu	Asn	Ile	Leu	Ser	Cys	Glu	Ser	Phe	Glu	Ile	Leu	Glu	
			35				40					45				
Lys	Arg	Glu	Leu	Asp	Thr	Ser	Gly	Val	Thr	Lys	Thr	Ser	Thr	Pro	Phe	
	50					55					60					
Phe	Ser	Arg	Val	Glu	Gly	Ile	Asp	Ala	Gly	Thr	Leu	Gly	Lys	Leu	Phe	
65					70				75					80		
Ser	Gly	Ser	Gln	Ser	Lys	Asn	Tyr	Phe	Ala	Tyr	Tyr	Asp	Ala	Leu	Val	
				85					90					95		
Lys	Lys	Glu	Lys	Arg	Lys	Glu	Val	Arg	Ile	Glu	Lys	Lys	Glu	Glu	Arg	
			100					105					110			
Ile	Asp	Ala	Arg	Glu	Asn	Lys	Arg	Glu	Ile	Lys	Gln	Glu	Ala	Ile	Lys	
		115					120					125				
Glu	Pro	Lys	Lys	Ala	Asn	Gln	Gly	Thr	Glu	Asn	Ala	Pro	Thr	Leu	Glu	
		130				135					140					
Glu	Lys	Xaa	Tyr	Gln	Lys	Ala	Glu	Arg	Lys	Phe	Asp	Ala	Lys	Xaa	Xaa	
145					150					155					160	
Arg	Arg	Ser	Phe	Lys	Xaa											
				165												

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...89

(D) OTHER INFORMATION: /note= "ARGININE TRANSPORT ATP-BINDING
[E.coli] & homology to Myco.
leprae U00013_12 abc2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

```
Met Asp Glu Pro Glu Thr Ser Leu Glu Gln Asn Ala Leu Ile Arg Leu
1          5          10          15
Ser Asn Leu Ile Ser Leu Arg Asn Thr Gln Gln Leu Thr Ser Ile Ile
          20          25          30
Ala Thr His Asp Pro Ile Val Leu Asp Ser Cys Glu Trp Val Leu Leu
          35          40          45
Leu Lys Asn Gly Asn Ile Ala Gln Tyr Lys Pro Leu Asn Ser Ile Leu
          50          55          60
Lys Ser Val Ala Lys Thr Phe Asn Phe Lys Glu Lys Pro Thr Thr Lys
65          70          75          80
Asp Leu Leu Ala Leu Leu Lys Asp Ile
          85
```

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...237

(D) OTHER INFORMATION: /note= "proline/betaine transport protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

```
Val Lys Thr Leu Gly Leu Ser Ser Leu Gly Gly Thr Leu Glu Phe Tyr
1          5          10          15
Asp Phe Ile Ile Phe Val Phe Phe Thr Ser Ile Ile Ala Lys His Phe
```

20					25					30					
Phe	Pro	Asn	Thr	Leu	Ser	Pro	Ile	Trp	Ser	Glu	Ile	Asn	Thr	Tyr	Gly
		35					40					45			
Ile	Phe	Ala	Ala	Gly	Tyr	Leu	Ala	Arg	Pro	Leu	Gly	Gly	Ile	Val	Met
	50					55					60				
Ala	His	Phe	Gly	Asp	Lys	Phe	Gly	Arg	Lys	Asn	Met	Phe	Met	Leu	Ser
65						70					75				80
Ile	Leu	Leu	Met	Val	Ile	Pro	Thr	Phe	Ala	Leu	Ala	Leu	Met	Pro	Thr
			85					90					95		
Phe	Asn	Asp	Leu	Val	Gly	Phe	Gly	Val	Asp	Ser	Met	Gly	Leu	Thr	Pro
			100					105					110		
Lys	Asn	Ala	His	Tyr	Leu	Gly	Tyr	Ile	Ala	Pro	Val	Phe	Leu	Val	Leu
	115					120						125			
Val	Arg	Ile	Cys	Gln	Gly	Val	Ala	Val	Gly	Gly	Glu	Leu	Pro	Gly	Ala
	130					135					140				
Trp	Val	Phe	Val	His	Glu	His	Ala	Pro	Gln	Gly	Gln	Lys	Asn	Thr	Tyr
145						150					155				160
Ile	Gly	Phe	Leu	Thr	Ala	Ser	Val	Val	Ser	Gly	Ile	Leu	Leu	Gly	Ser
			165						170					175	
Leu	Val	Tyr	Ile	Gly	Ile	Tyr	Met	Val	Phe	Asp	Lys	Pro	Val	Val	Glu
		180						185					190		
Asp	Trp	Ala	Trp	Arg	Val	Ala	Phe	Gly	Leu	Gly	Gly	Ile	Phe	Gly	Ile
	195						200					205			
Ile	Ser	Val	Tyr	Leu	Arg	Arg	Phe	Leu	Glu	Glu	Thr	Pro	Val	Phe	Gln
	210					215					220				
Gln	Met	Lys	Gln	Gly	Arg	Cys	Leu	Ser	Gln	Ile	Pro	Ala			
225						230					235				

(2) INFORMATION FOR SEQ ID NO:483:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

Met	Arg	Lys	Phe	Leu	Asp	Gly	Ala	Lys	Ser	Glu	Val	Leu	Lys	Tyr	Asp		
1				5					10					15			
Val	Ile	Ser	Phe	Asp	Ile	Phe	Asp	Thr	Leu	Leu	Leu	Arg	Pro	Phe	Ile		
			20					25					30				
Lys	Pro	Thr	Asp	Leu	Phe	Leu	Tyr	Ile	Glu	Thr	Lys	Tyr	Asn	Ile	Lys		
		35					40					45					
Gly	Phe	His	Gln	Ala	Arg	Ile	Leu	Ala	Glu	Met	Gln	Ser	Arg	Lys	Leu		
	50					55					60						
Ser	Lys	Arg	Gln	Asp	Ile	Thr	Leu	Asp	Glu	Ile	Tyr	His	Gln	Ile	Pro		
65					70					75					80		
Lys	Glu	Phe	His	Ser	Tyr	Lys	Gly	Val	Glu	Ile	Ala	Thr	Glu	Lys	Glu		
				85					90					95			
Val	Leu	Val	Pro	Asn	Leu	Glu	Met	Leu	Glu	Leu	Tyr	Arg	Phe	Ala	Lys		
			100					105					110				
Glu	Asn	Asn	Lys	Arg	Val	Ile	Ile	Val	Ser	Asp	Met	Tyr	Leu	Pro	Leu		
		115					120					125					
Glu	Val	Leu	Glu	Asp	Ile	Leu	Ile	Ser	Lys	Gly	Phe	Asp	Gly	Tyr	Thr		
	130					135						140					
Asn	Phe	Tyr	Leu	Ser	Asn	His	Ile	Met	Leu	Thr	Lys	His	Ser	Lys	Asp		
145					150					155					160		
Leu	Phe	Lys	His	Val	Leu	Lys	Gln	Glu	Asn	Ile	Thr	Asn	Thr	Gln	Ile		
				165					170					175			
Leu	His	Ile	Gly	Asp	Asn	Ser	Trp	Ala	Asp	Asp	Ala	Met	Pro	Lys	Ser		
			180					185					190				
Leu	Gly	Ile	Ala	Thr	Leu	Phe	Arg	Lys	Ser	Val	Leu	Lys	Gln	Leu	Glu		
		195					200					205					
Glu	Val	Phe	Pro	Lys	Tyr	Lys	Thr	Phe	Asn	Pro	Thr	Ser	Val	Ala	Gln		
	210					215					220						
Ser	Phe	Ile	Leu	Gly	Ser	Leu	Cys	Val	Phe	Tyr	Lys	Asn	Tyr	Ile	Gln		
225					230					235					240		
Lys	His	Glu	Lys	Phe	Asp	Tyr	Trp	Phe	Leu	Leu	Gly	Ala	Met	Gln	Ala		
				245					250					255			
Gly	Ile	Ala	Ala	Val	Ala	Tyr	Cys	Gln	Phe	Ile	Tyr	Lys	Glu	Ile	His		
		260					265						270				
Lys	Arg	Asn	Ile	Asp	Thr	Leu	Val	Phe	Val	Ala	Arg	Asp	Gly	Tyr	Leu		
		275					280					285					
Leu	Gln	Lys	Ile	Phe	Asn	Ile	Leu	Tyr	Pro	Asn	Ser	Tyr	Lys	Thr	Thr		
	290					295					300						
Tyr	Val	Tyr	Ala	Pro	Arg	Ile	Leu	Lys	Lys	Ala	Val	Phe	Leu	Glu	Val		

305		310		315		320									
Val	Glu	Gly	Glu	Ser	Leu	Glu	Ile	Leu	Arg	Ile	Leu	Glu	Gly	Glu	Glu
				325					330					335	
Glu	Val	Lys	Lys	Lys	Gln	Ile	Thr	Thr	Asn	Gln	Gln	Ala	Tyr	Val	Tyr
			340					345					350		
Leu	Tyr	Ser	Asn	Phe	Glu	His	Cys	Arg	His	Leu	Ala	Leu	Lys	Cys	Leu
		355					360					365			
Asp	Asn	Tyr	Arg	Lys	Tyr	Leu	Phe	Ser	Ser	Asn	Leu	Glu	Gly	Asn	Ile
	370					375					380				
Ala	Ile	Val	Asp	Thr	Ile	Thr	Leu	Gly	Tyr	Ser	Ser	Gln	Gly	Leu	Ile
385					390					395					400
Gln	Lys	Ala	Leu	Asn	Lys	Glu	Val	Phe	Gly	Cys	Tyr	Val	Asp	Leu	Leu
			405						410					415	
Arg	Ile	Leu	Asn	Tyr	Asp	Cys	Val	Ser	Phe	Leu	Pro	Phe	Ser	His	Pro
			420					425					430		
Lys	Pro	Val	Tyr	Phe	His	Asn	Trp	Asp	Phe	Met	Glu	Phe	Leu	Leu	Thr
		435					440					445			
Ser	Pro	Glu	Tyr	Pro	Ile	Leu	Asn	Val	Glu	Asn	Gly	Val	Pro	Ile	Leu
	450					455					460				
Ser	Lys	Arg	Arg	Phe	Ile	Leu									
465					470										

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...123
- (D) OTHER INFORMATION: /note= "GLUTATHIONE-REGULATED POTASSIUM-EFFLUX SYSTEM PROTEIN"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

Val	Leu	Lys	Phe	Phe	Glu	Asp	Ser	Lys	Gln	Leu	Ser	Thr	Pro	Met	Gly
1				5					10					15	

Lys Ser Ala Val Gly Ile Leu Ile Phe Gln Asp Ile Ala Ala Ile Pro
 20 25 30
 Met Leu Leu Ile Leu Thr Ile Leu Gly Ser Lys Asp Ser His Val Asn
 35 40 45
 Leu Leu Ile Leu Lys Thr Leu Ile Ser Ala Gly Ile Ile Leu Ile Leu
 50 55 60
 Leu Leu Leu Pro Gly Lys Lys Gly Ala Asn Leu Ile Leu Glu Gln Ala
 65 70 75 80
 Lys Asp Thr Arg Leu Pro Glu Ile Phe Ile Gly Thr Asp Phe Ser Asp
 85 90 95
 Cys Leu Gln Arg Gly Gly Val Glu Pro Phe Phe Trp Val Phe Tyr Val
 100 105 110
 Phe Gly Gly Val His Cys Gly His Gly Asp Phe
 115 120

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

Met Glu Asn Ser Thr Leu Tyr Ile Val Ile Ala Gly Leu Trp Leu Ala
 1 5 10 15
 Val Gly Phe Gly Ile Phe Leu Lys Lys Leu Asp Met Pro Val Ile Ile
 20 25 30
 Gly Tyr Ile Cys Thr Gly Thr Val Leu Ala Ala Phe Phe Lys Ile Asn
 35 40 45
 Asp Phe Asn Leu Leu Ser Asp Ile Gly Glu Phe Gly Ile Val Phe Leu
 50 55 60
 Met Phe Met Ile Gly Ile Glu Phe Asn Phe Asp Lys Leu Lys Ser Ile
 65 70 75 80
 Lys Gln Glu Val Leu Val Phe Gly Leu Leu Gln Val Val Leu Cys Ala
 85 90 95
 Leu Ile Ala Phe Leu Leu Gly Tyr Phe Val Leu Gly Leu Ser Pro Ile
 100 105 110

Phe	Ser	Leu	Val	Leu	Gly	Met	Gly	Leu	Ser	Leu	Ser	Ser	Thr	Ala
		115					120					125		

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...259
- (D) OTHER INFORMATION: /note= "VIRULENCE FACTOR MVIN"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

Met	Ile	Leu	Ala	Leu	Leu	Ile	Ser	Lys	Glu	Lys	Thr	His	Leu	Glu	Ala
1				5					10					15	
Leu	Tyr	Tyr	Leu	Ser	Tyr	Gly	Val	Leu	Leu	Gly	Gly	Val	Ala	Gln	Ile
			20					25					30		
Leu	Leu	His	Phe	Tyr	Pro	Leu	Val	Lys	Leu	Gly	Leu	Trp	Asp	Leu	Leu
		35					40					45			
Phe	Lys	Gly	Leu	Leu	Gly	Phe	Lys	Thr	Lys	Asn	Thr	Asn	Lys	Lys	Glu
	50					55					60				
Tyr	Arg	Leu	Asn	Arg	Ala	Lys	Lys	Asp	Leu	Lys	Ala	Phe	Phe	Lys	Gln
65				70					75					80	
Phe	Phe	Pro	Ser	Val	Leu	Gly	Asn	Ser	Ser	Ala	Gln	Ile	Ala	Ser	Phe
			85					90						95	
Leu	Asp	Thr	Thr	Ile	Ala	Ser	Phe	Leu	Ala	Ser	Gly	Ser	Val	Ser	Tyr
			100					105					110		
Leu	Tyr	Tyr	Ala	Asn	Arg	Val	Phe	Gln	Leu	Pro	Leu	Ala	Leu	Phe	Ala
		115					120					125			
Ile	Ala	Ile	Ser	Thr	Ala	Leu	Phe	Pro	Ser	Ile	Ala	Ile	Ala	Leu	Lys
	130					135					140				
Asn	Asn	Gln	Gln	Asp	Leu	Ile	Leu	Gln	Arg	Leu	Gln	Lys	Ala	Trp	Phe
145					150				155					160	
Phe	Leu	Val	Gly	Val	Leu	Leu	Leu	Cys	Ser	Ile	Gly	Gly	Ile	Met	Leu
			165						170					175	

Ser Lys Glu Ile Thr Glu Leu Leu Phe Glu Arg Gly Gln Phe Ser Pro
180 185 190

Lys Asp Thr Leu Ile Thr Ser Gln Val Phe Ser Leu Tyr Leu Leu Gly
195 200 205

Leu Leu Pro Phe Gly Leu Thr Lys Leu Phe Ser Leu Trp Leu Tyr Ala
210 215 220

Lys Leu Glu Gln Lys Lys Ala Ala Lys Ile Ser Leu Ile Ser Leu Phe
225 230 235 240

Leu Gly Leu Ala Ala Ser Leu Ser Leu Met Pro Leu Leu Gly Val Leu
245 250 255

Gly Leu Arg

(2) INFORMATION FOR SEQ ID NO:487:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

Leu Leu Leu Met Leu Asn Lys Pro Lys Pro Leu Phe Leu Xaa Leu Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:488:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

Val Leu Lys Tyr Pro Thr Met Phe Met Cys Ala Asp Ala Val Ile Ile
1 5 10 15

Ser Lys Ala Asp Met Ile Glu Val Phe Asn Phe Arg Val Ser Gln Val
20 25 30

Lys Glu Asp Met Gln Lys Leu Lys Pro Glu Ala Pro Ile Phe Leu Met
35 40 45

Ser Ser Lys Asp Pro Lys Ser Leu Glu Asp Phe Lys Asn Phe Leu Leu
50 55 60

Glu Lys Lys Arg Glu Asn Tyr Gln Ser Thr His Ser Phe
65 70 75

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

Met Leu Leu Cys Ala Gly Arg Asn Glu Thr Leu Lys Lys Ala Val Pro
1 5 10 15

Ile Gly Val Gly Leu Ile Glu Ser Ala Ile Asn Leu Thr Arg Met Cys
20 25 30

Leu Lys Asn Pro Asp Thr Glu Ser Leu Ile Phe Ile Gly Ser Ala Gly
35 40 45

Ser Tyr Ser Pro Glu Thr Glu Ile Leu Ser Val Phe Glu Ser Ile Glu
50 55 60

Gly Tyr Gln Ile Glu Glu Ser Phe Ser His Leu Asn Ser Tyr Thr Pro
65 70 75 80

Leu Asp Asn Phe Ile His Ile Glu Thr Lys Glu Gln Ala Leu Phe Glu
85 90 95

Arg Val Arg Val Asn Ser Ser Asn Tyr Ile His Thr Ser Glu Met Phe
100 105 110

Ala Lys Lys Met Val Gln Lys Gly Val Leu Leu Glu Asn Met Glu Phe
115 120 125

Phe Ser Val Leu Ser Val Ala Lys Ile Phe Ser Leu Lys Ala Lys Gly
130 135 140

Ile Phe Cys Val Ser Asn His Val Gly Leu Asn Ala His Lys Glu Phe

145	150	155	160
Lys Glu Asn His	Ala Lys Val Lys Gln Ile	Leu Glu Asn Ile	Ile Asp
	165	170	175
Ser Leu Ile Val			
	180		

(2) INFORMATION FOR SEQ ID NO:490:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...213
 - (D) OTHER INFORMATION: /note= "FLAGELLAR M-RING PROTEIN"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

Val Tyr Glu Glu Arg Ile Thr Leu Ala Ser Gln Gly Ile Pro Lys Thr			
1	5	10	15
Ser Lys Val Gly Phe Glu Ile Phe Asp Thr Lys Asp Phe Gly Ala Thr			
	20	25	30
Asp Phe Asp Gln Asn Ile Lys Leu Ile Arg Ala Ile Glu Gly Glu Leu			
	35	40	45
Ser Arg Thr Ile Glu Ser Leu Asn Pro Ile Leu Lys Ala Asn Val His			
	50	55	60
Ile Ala Ile Pro Lys Asp Ser Val Phe Val Ala Lys Glu Val Pro Pro			
65	70	75	80
Ser Ala Ser Val Met Leu Lys Leu Lys Pro Asp Met Lys Leu Ser Pro			
	85	90	95
Thr Gln Ile Leu Gly Ile Lys Asn Leu Ile Ala Ala Ala Val Pro Lys			
	100	105	110
Leu Thr Ile Glu Asn Val Lys Ile Val Asn Glu Asn Gly Glu Ser Ile			
	115	120	125
Gly Glu Gly Asp Ile Leu Glu Asn Ser Lys Glu Leu Ala Leu Glu Gln			
	130	135	140
Leu Arg Tyr Lys Gln Asn Phe Glu Asn Ile Leu Glu Asn Lys Ile Val			

145		150		155		160
Asn Ile Leu Ala	Pro Ile Val Gly Xaa	Lys Asn Xaa Val	Val Xaa Xaa			
	165	170	175			
Val Asn Xaa Glu Phe	Xaa Phe Xaa Gln	Lys Lys Ser Thr	Lys Glu Thr			
	180	185	190			
Phe Asp Pro Asn Asn	Val Gly Lys Glu Arg	Ala Lys Phe Arg	Arg Lys			
	195	200	205			
Lys Arg Arg Arg Ser						
210						

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

Val Ile Lys Lys Gly Tyr Ile Arg Gly Asp Leu Met Arg Ile Val Arg		
1	5	10 15
Asn Leu Phe Leu Val Ser Phe Val Ala Tyr Ser Ser Ala Phe Ala Ala		
	20	25 30
Asp Leu Glu Thr Gly Thr Lys Asn Asp Lys Lys Ser Gly Lys Lys Phe		
	35	40 45
Tyr Lys Leu His Lys Asn His Gly Ser Glu Thr Glu Thr Lys Asn Asp		
	50	55 60
Lys Lys Leu Tyr Asp Phe Thr Lys Asn Ser Gly Leu Glu Gly Val Asp		
	65	70 75 80
Leu Glu Lys Ser Pro Asn Leu Lys Ser His Lys Lys Ser Asp Lys Lys		
	85	90 95
Phe Tyr Lys Gln Leu Ala Lys Asn Asn Ile Ala Glu Gly Val Ser Met		
	100	105 110
Pro Ile Val Asn Phe Asn Lys Ala Leu Ser Phe Gly Pro Tyr Phe Glu		
	115	120 125
Arg Thr Lys Ser Lys Lys Thr Gln Tyr Met Asp Gly Gly Leu Met Met		
	130	135 140

His Ile Arg Phe
145

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...281
- (D) OTHER INFORMATION: /note= "spoIIIE gene product"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

Val	Met	Ile	Asp	Pro	Lys	Met	Val	Glu	Phe	Ser	Ile	Tyr	Ala	Asp	Ile	
1				5					10					15		
Pro	His	Leu	Leu	Thr	Pro	Ile	Ile	Thr	Asp	Pro	Lys	Lys	Ala	Ile	Gly	
			20					25					30			
Ala	Leu	Gln	Ser	Val	Ala	Lys	Glu	Met	Glu	Arg	Arg	Tyr	Ser	Leu	Met	
		35					40					45				
Ser	Glu	Tyr	Lys	Val	Lys	Thr	Ile	Asp	Ser	Tyr	Asn	Glu	Gln	Ala	Gln	
	50					55					60					
Ser	Asn	Asp	Val	Glu	Ala	Phe	Pro	Tyr	Leu	Ile	Val	Val	Ile	Asp	Glu	
65				70					75					80		
Leu	Ala	Asp	Leu	Met	Met	Thr	Gly	Gly	Lys	Glu	Ala	Glu	Phe	Pro	Ile	
			85					90						95		
Ala	Arg	Ile	Ala	Gln	Met	Gly	Arg	Ala	Ser	Gly	Leu	His	Leu	Ile	Val	
		100						105					110			
Ala	Thr	Gln	Arg	Pro	Ser	Val	Asp	Val	Val	Thr	Gly	Leu	Ile	Lys	Thr	
		115					120					125				
Asn	Leu	Pro	Ser	Arg	Val	Ser	Phe	Arg	Val	Gly	Thr	Lys	Ile	Asp	Ser	
	130					135					140					
Lys	Val	Ile	Leu	Asp	Thr	Asp	Gly	Ala	Gln	Ser	Leu	Leu	Gly	Arg	Gly	
145				150					155					160		
Asp	Met	Leu	Phe	Thr	Pro	Pro	Gly	Thr	Asn	Gly	Leu	Val	Arg	Leu	His	
			165					170						175		

Ala Pro Phe Ala Thr Glu Asp Glu Ile Lys Lys Ile Val Asp Phe Ile
180 185 190

Lys Ala Gln Lys Glu Val Glu Tyr Asp Lys Asp Phe Leu Leu Glu Glu
195 200 205

Ser Arg Met Pro Leu Asp Thr Pro Asn Tyr Gln Gly Asp Asp Ile Leu
210 215 220

Glu Arg Ala Lys Ala Val Ile Leu Glu Lys Lys Ile Thr Ser Thr Ser
225 230 235 240

Phe Leu Gln Arg Gln Leu Lys Ile Gly Tyr Asn Gln Ala Ala Thr Ile
245 250 255

Thr Asp Glu Leu Glu Ala Gln Gly Phe Leu Ser Pro Arg Asn Ala Lys
260 265 270

Gly Asn Arg Glu Ile Leu Gln Asn Phe
275 280

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

Met Asn Phe Phe Lys Ile Leu Leu Met Glu Leu Arg Ala Ile Val Ser
1 5 10 15

His Lys Gly Val Leu Leu Ile Leu Ile Gly Ala Pro Leu Ile Tyr Gly
20 25 30

Leu Leu Tyr Pro Leu Pro Tyr Leu Lys Asp Ile Val Thr Gln Gln Lys
35 40 45

Ile Ala Leu Val Asp Glu Asp Asn Ser Phe Leu Ser Arg Gln Leu Ala
50 55 60

Phe Met Val Gln Ser Ser Asn Glu Leu Glu Ile Ala Phe Phe Ser Pro
65 70 75 80

Ser Met Leu Glu Ala Lys Lys Leu Leu Lys Glu Glu Lys Ile Tyr Gly
85 90 95

Ile Leu His Ile Pro Ser His Phe Glu Ala Asn Ile Tyr Lys Gln Ser
100 105 110

Ala Cys Asn Asp Arg Phe Leu Cys Glu Arg Gln Leu Leu Phe Asp Leu
115 120 125

Trp Cys Val Ser Glu Cys Gly Gly Gly Glu His Gln Arg Leu Lys Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:494:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

Val Gly Gly Leu Ala Met Leu Gly Phe Phe Tyr Asn Ile Glu Lys Ile
1 5 10 15

Ser Leu Ala Thr Ala Thr Ala Phe Ser Gln Cys Ala Pro Xaa Tyr Thr
20 25 30

Val Leu Leu Ser Pro Leu Leu Leu Lys Glu Lys Leu Lys Arg Ser Ala
35 40 45

Leu Ile Ser Ala Cys Ile Gly Leu Val Gly Val Val Leu Ile Ser Asp
50 55 60

Pro Ser Val Glu Asn Val Gly Pro Ser
65 70

(2) INFORMATION FOR SEQ ID NO:495:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 311 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...311
 - (D) OTHER INFORMATION: /note= "SODIUM/PROLINE SYMPORTER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

Val	Cys	Trp	Thr	Asp	Leu	Ile	Gln	Gly	Leu	Leu	Met	Met	Ser	Ala	Leu	
1				5					10					15		
Ile	Val	Val	Pro	Ile	Val	Met	Ile	Ile	His	Leu	Gly	Gly	Ile	Gly	Glu	
			20					25					30			
Gly	Ile	Lys	Ile	Ile	Arg	Glu	Ile	Lys	Pro	Glu	Asn	Leu	Ser	Phe	Xaa	
		35					40					45				
Gln	Gly	Ser	Ser	Val	Val	Ala	Ile	Ile	Ser	Ser	Leu	Ala	Trp	Gly	Leu	
	50					55					60					
Gly	Tyr	Phe	Gly	Gln	Pro	His	Ile	Leu	Val	Arg	Phe	Met	Ser	Ile	Arg	
65					70					75					80	
Ser	Ile	Arg	Asp	Val	Pro	Lys	Ala	Thr	Thr	Ile	Gly	Ile	Ser	Trp	Met	
				85					90					95		
Val	Ile	Ser	Leu	Ile	Gly	Ala	Cys	Val	Met	Gly	Leu	Leu	Gly	Val	Ala	
			100					105					110			
Tyr	Val	His	Lys	Xaa	Asp	Leu	Ser	Leu	Glu	Asp	Pro	Glu	Lys	Ile	Phe	
		115					120					125				
Ile	Val	Met	Ser	Gln	Leu	Leu	Phe	Asn	Pro	Trp	Ile	Thr	Gly	Ile	Leu	
	130					135					140					
Leu	Ser	Ala	Ile	Leu	Ala	Ala	Val	Met	Ser	Thr	Ala	Ser	Ser	Gln	Leu	
145					150					155					160	
Leu	Val	Ser	Ser	Ser	Thr	Ile	Ala	Glu	Asp	Phe	Tyr	Ala	Thr	Ile	Phe	
				165					170					175		
Asn	Lys	Asn	Ala	Pro	Gln	Lys	Leu	Val	Met	Thr	Ile	Ser	Arg	Leu	Ser	
			180					185					190			
Val	Leu	Gly	Val	Ala	Cys	Ile	Ala	Phe	Phe	Ile	Ser	Thr	Asp	Lys	Asn	
		195					200					205				
Ala	Ser	Ile	Leu	Ser	Ile	Val	Ser	Tyr	Ala	Trp	Ala	Gly	Phe	Gly	Ala	
	210					215					220					
Ser	Phe	Gly	Ser	Val	Ile	Leu	Phe	Ser	Leu	Phe	Trp	Ser	Arg	Met	Thr	
225					230					235					240	
Arg	Ile	Gly	Ala	Ile	Ala	Gly	Met	Leu	Ser	Gly	Ala	Ser	Thr	Val	Ile	
			245					250						255		
Leu	Tyr	Asp	Lys	Phe	Gly	Lys	Ser	Phe	Leu	Asp	Ile	Tyr	Glu	Ile	Val	
		260						265					270			
Pro	Gly	Phe	Ile	Val	Ala	Ser	Val	Ala	Ile	Val	Ala	Phe	Ser	Leu	Phe	
		275					280					285				
Ser	Ser	Val	Arg	Ser	Gly	Thr	Lys	Glu	Ala	Phe	Glu	Thr	Met	Leu	Lys	

290

295

300

Glu Ile Glu Ser Leu Lys His
305 310

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

Val	Gly	Leu	Phe	Ile	Val	Leu	Phe	Leu	Ile	Ile	Met	Lys	His	Gln	Thr	1	5	10	15
Ser	Pro	Tyr	Ala	Phe	Thr	His	Asn	Gln	Ala	Leu	Val	Thr	Gln	Thr	Pro	20	25	30	
Pro	Tyr	Phe	Thr	Gln	Leu	Thr	Ile	Pro	Lys	Pro	Asn	Asp	Ala	Leu	Ser	35	40	45	
Ala	His	Ala	Ser	Ser	Leu	Ile	Ser	Leu	Pro	Asn	Asp	Asn	Leu	Leu	Ser	50	55	60	
Ala	Tyr	Phe	Ser	Gly	Thr	Lys	Glu	Gly	Ala	Arg	Asp	Val	Lys	Ile	Ser	65	70	75	80
Ala	Asn	Leu	Phe	Asp	Ser	Lys	Thr	Asn	Arg	Trp	Ser	Glu	Ala	Phe	Ile	85	90	95	
Leu	Leu	Thr	Lys	Glu	Glu	Leu	Ser	His	His	Ser	His	Glu	Tyr	Ile	Lys	100	105	110	
Lys	Ile	Arg														115			

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...200

(D) OTHER INFORMATION: /note= "flagellar biosynthesis protein
flhF"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

```
Met Leu Val Gly Pro Thr Gly Val Gly Lys Thr Thr Thr Leu Ala Lys
1           5           10           15

Leu Ala Ala Arg Tyr Ser Arg Met Leu Ala Lys Lys Tyr Lys Val Gly
20           25           30

Ile Ile Thr Leu Asp Asn Tyr Arg Ile Gly Ala Leu Glu Gln Leu Ser
35           40           45

Trp Tyr Ala Asn Lys Met Lys Met Ser Ile Glu Ala Val Ile Asp Ala
50           55           60

Lys Asp Phe Ala Lys Glu Ile Glu Ala Leu Glu Tyr Cys Asp Phe Ile
65           70           75           80

Leu Val Asp Thr Thr Gly His Ser Gln Tyr Asp Lys Glu Lys Ile Ala
85           90           95

Gly Leu Lys Glu Phe Ile Asp Gly Gly Tyr Asn Ile Asp Val Ser Leu
100          105          110

Val Leu Ser Val Thr Thr Lys Tyr Glu Asp Met Lys Asp Ile Tyr Asp
115          120          125

Ser Phe Gly Val Leu Gly Ile Asp Thr Leu Ile Phe Thr Lys Leu Asp
130          135          140

Glu Ser Arg Gly Leu Gly Asn Leu Phe Ser Leu Val His Glu Ser Gln
145          150          155          160

Lys Pro Ile Ser Tyr Leu Ser Val Gly Gln Glu Val Pro Met Asp Leu
165          170          175

Lys Val Ala Thr Asn Glu Tyr Leu Val Asp Cys Met Leu Asp Gly Phe
180          185          190

Ser Asn Pro Asn Lys Glu Gln Ala
195          200
```

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...264
 (D) OTHER INFORMATION: /note= "vacuolating cytotoxin Hpylori"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

Val	Gly	Gly	Ala	Ser	Phe	Ile	Ser	Gly	Gly	Asn	Gly	Thr	Leu	Tyr	Gly	1	5	10	15
Leu	Asn	Val	Gly	Tyr	Asp	Arg	Leu	Val	Lys	Ser	Val	Ile	Leu	Gly	Gly	20	25	30	
Tyr	Val	Ala	Tyr	Gly	Tyr	Ser	Gly	Phe	Asn	Gly	Asn	Ile	Met	His	Ser	35	40	45	
Leu	Ala	Asn	Asn	Val	Asp	Val	Gly	Met	Tyr	Ala	Arg	Ala	Phe	Leu	Lys	50	55	60	
Arg	Asn	Glu	Phe	Thr	Leu	Ser	Ala	Asn	Glu	Thr	Tyr	Gly	Gly	Asn	Ala	65	70	75	80
Ser	His	Ile	Asn	Ser	Ser	Asn	Ser	Leu	Leu	Ser	Val	Leu	Asn	Gln	Arg	85	90	95	
Tyr	Asn	Tyr	Asn	Thr	Trp	Thr	Thr	Ser	Val	Asn	Gly	Asn	Tyr	Gly	Tyr	100	105	110	
Asp	Phe	Met	Phe	Lys	Gln	Lys	Ser	Val	Val	Leu	Lys	Pro	Gln	Val	Gly	115	120	125	
Leu	Ser	Tyr	His	Phe	Ile	Gly	Leu	Ser	Gly	Met	Lys	Gly	Lys	Met	Gln	130	135	140	
Asn	Pro	Ala	Tyr	Gln	Gln	Phe	Val	Met	His	Ser	Asn	Pro	Ser	Asn	Glu	145	150	155	160
Ser	Val	Leu	Thr	Leu	Asn	Met	Gly	Leu	Glu	Ser	Arg	Lys	Tyr	Phe	Gly	165	170	175	
Lys	Asn	Ser	Tyr	Tyr	Phe	Val	Thr	Ala	Arg	Leu	Gly	Arg	Asp	Leu	Leu	180	185	190	
Ile	Lys	Ala	Lys	Gly	Asp	Asn	Val	Val	Arg	Phe	Val	Gly	Glu	Asn	Thr	195	200	205	
Leu	Leu	Tyr	Arg	Lys	Gly	Glu	Ile	Phe	Asn	Thr	Phe	Ala	Ser	Val	Ile	210	215	220	
Thr	Gly	Gly	Glu	Met	His	Leu	Trp	Arg	Leu	Met	Tyr	Val	Asn	Ala	Gly	225	230	235	240

Val Gly Leu Lys Met Gly Leu Gln Tyr Gln Asp Leu Asn Ile Thr Gly
245 250 255

Asn Val Gly Met Arg Val Ala Phe
260

(2) INFORMATION FOR SEQ ID NO:499:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

Met	Asp	Gly	Tyr	Gly	Phe	Lys	Met	Gln	Asp	Leu	Gly	Gln	Lys	Thr	Gln	1	5	10	15
Val	Ile	Gln	His	Ile	Phe	Ala	Gly	Asp	Asp	Val	Ser	Ala	Leu	Glu	Val	20	25	30	
Lys	Glu	Asn	Glu	Cys	Val	Lys	Ile	Met	Thr	Gly	Ala	Met	Val	Pro	Lys	35	40	45	
Gly	Ile	Glu	Thr	Ile	Val	Pro	Ile	Glu	Cys	Met	Leu	Glu	Ser	His	Lys	50	55	60	
Asp	Phe	Ala	Leu	Ala	Pro	Lys	Asp	Phe	Lys	Ile	His	Ala	Asn	Ile	Arg	65	70	75	80
Gln	Lys	Gly	Glu	Asn	Ala	Ser	Leu	Asn	Ser	Val	Leu	Val	Pro	Lys	Asn	85	90	95	
Thr	Arg	Leu	Asn	Tyr	Gly	His	Ile	Ala	Leu	Ile	Ala	Ser	Gln	Gly	Phe	100	105	110	
Lys	Glu	Ile	Lys	Ala	Phe	Arg	Lys	Leu	Lys	Ile	Ala	Leu	Phe	Ser	Ser	115	120	125	
Gly	Asp	Glu	Leu	Val	Pro	Leu	Gly	Gln	Asn	Ala	Leu	Glu	Cys	Gln	Val	130	135	140	
Tyr	Asp	Val	Asn	Ser	Val	Gly	Val	Phe	Asn	Met	Leu	Lys	Asn	Tyr	Asn	145	150	155	160
Thr	His	Phe	Leu	Gly	Val	Leu	Lys	Asp	Asp	Lys	Asn	Leu	Gln	Leu	Lys	165	170	175	
Ile	Leu	Glu	Leu	Gln	Gly	Tyr	Asp	Val	Ile	Leu	Ser	Ser	Ala	Gly	Val				

180					185					190					
Ser	Val	Gly	Asp	Lys	Asp	Phe	Phe	Lys	Asp	Ala	Leu	Lys	Glu	Arg	Asn
		195					200					205			
Ala	Leu	Phe	Tyr	Tyr	Glu	Lys	Val	Asn	Leu	Lys	Pro	Gly	Lys	Pro	Val
	210					215					220				
Thr	Leu	Ala	Gln	Leu	Asn	Gln	Ser	Ile	Ile	Ile	Gly	Leu	Pro	Gly	Asn
225				230					235					240	
Pro	Leu	Ser	Cys	Leu	Leu	Val	Leu	Arg	Val	Leu	Ile	Leu	Pro	Leu	Leu
			245					250					255		
Glu	Arg	Leu	Ser	Leu	Asn	Lys	Asp	Phe	Lys	Leu	Lys	Pro	Phe	Lys	Ala
		260					265						270		
Gln	Ile	Asn	Ala	Pro	Leu	Lys	Leu	Asn	Asn	Lys	Arg	Thr	His	Leu	Ile
	275						280					285			
Leu	Gly	Asn	Tyr	Ser	Asn	His	Gln	Phe	Ile	Pro	Tyr	Asn	Asn	Arg	Tyr
	290					295					300				
Glu	Ser	Gly	Ala	Ile	Gln	Ala	Leu	Ala	Gln	Val	Asp	Ser	Ile	Thr	Leu
305				310					315					320	
Ile	Asp	Glu	Gly	Val	Gly	Leu	Val	Gln	Gly	Glu	Ile	Glu	Ile	Leu	Arg
			325					330						335	
Phe	Glu	Asn													

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

Met	Pro	Tyr	Ala	Leu	Arg	Lys	Arg	Phe	Phe	Lys	Arg	Leu	Leu	Leu	Phe
1				5				10					15		
Phe	Leu	Ile	Val	Cys	Met	Ile	Asn	Leu	His	Ala	Lys	Ser	Tyr	Leu	Phe
	20						25					30			
Ser	Pro	Leu	Pro	Pro	Ala	His	Gln	Gln	Ile	Ile	Lys	Thr	Glu	Pro	Cys
	35					40					45				

Ser Leu Glu Cys Leu Lys Asp Leu Met Leu Gln Asn Gln Ile Phe Ser
 50 55 60
 Phe Val Ser Gln Tyr Asp Asp Asn Asn Gln Asp Glu Ser Leu Lys Thr
 65 70 75 80
 Tyr Tyr Lys Asp Ile Leu Asn Lys Leu Asn Pro Val Phe Ile Ala Ser
 85 90 95
 Gln Thr Pro Ala Lys Glu Ser Tyr Glu Pro Lys Ile Glu Leu Ala Ile
 100 105 110
 Leu Leu Pro Lys Lys Val Val Gly Arg Tyr Ala Ile Leu Val Met Asn
 115 120 125
 Thr Leu Leu Ala Tyr Phe Glu His Gln Lys Gln Arg Phe Gln Tyr Pro
 130 135 140
 Ser Leu
 145

(2) INFORMATION FOR SEQ ID NO:501:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

Met Pro Ile Asn Pro Leu Tyr Leu Phe Pro Asn Leu Phe Thr Ala Ser
 1 5 10 15
 Ser Ile Phe Leu Gly Met Met Ser Ile Phe Tyr Ala Ser Ser Tyr Gln
 20 25 30
 Phe Val Met Ala Cys Trp Leu Val Val Ala Ser Leu Ile Leu Asp Gly
 35 40 45
 Leu Asp Gly Arg Val Ala Arg Leu Thr Lys His His
 50 55 60

(2) INFORMATION FOR SEQ ID NO:502:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 350 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

Met	Ala	Leu	Arg	Val	Leu	Leu	Phe	Phe	Cys	Phe	Leu	Phe	Leu	Gln	Ala	
1				5					10					15		
Glu	Asp	Lys	Ser	Gln	Glu	Leu	Ser	Ser	Ile	Gln	Lys	Gln	Met	Ala	Leu	
			20					25					30			
Val	Asp	Lys	Lys	Leu	Ala	Lys	Asp	Asp	Asn	Val	Trp	Leu	Lys	Lys	Phe	
			35				40					45				
Glu	Asn	Tyr	Lys	Ile	Tyr	Asn	Gln	Ile	Tyr	Thr	Glu	Lys	Glu	Ser	Val	
	50					55					60					
Arg	Gln	Glu	Leu	Arg	Arg	Leu	Lys	Asn	Lys	Lys	Ser	Lys	Asp	Leu	Leu	
65					70					75					80	
Lys	Ile	Ser	Thr	Leu	Glu	His	Thr	Leu	Lys	Ala	Leu	Glu	Ser	Gln	Gln	
				85					90					95		
Lys	Met	Phe	Glu	Ser	Tyr	Gly	Val	Asn	Pro	Phe	Lys	Asp	Leu	Ile	Glu	
			100					105					110			
Arg	Pro	Asn	Ile	Pro	Asn	Ile	Pro	Asn	Ile	Ala	Asn	Pro	Ile	Ala	Ile	
		115					120					125				
Ile	Asp	Gly	Ile	Ser	Phe	Ile	Lys	Ser	Met	Arg	Leu	Lys	His	Glu	Asn	
	130					135					140					
Leu	Lys	Asn	Asn	Gln	Thr	Ser	Leu	Gly	Glu	Val	Leu	Lys	Leu	Leu	Asp	
145					150					155					160	
Gln	Lys	His	Gln	Leu	Leu	Asn	Gln	Trp	His	Ala	Leu	Asp	Lys	Ser	Ala	
				165					170					175		
Lys	Leu	Ser	Asp	Glu	Ile	Tyr	Gln	Thr	Gln	Ala	Lys	Arg	Leu	Glu	Leu	
			180					185					190			
Gln	Gly	Ala	Gln	Asn	Ile	Leu	Lys	Thr	Thr	Ile	Gly	Ile	Phe	Gln	Lys	
		195					200					205				
Asp	Ser	Asp	Glu	Ala	Ile	Ser	Ile	Val	Lys	Ser	Gln	Val	Lys	Asn	Gln	
	210					215					220					
Leu	Phe	Lys	Leu	Val	Tyr	Val	Phe	Leu	Ala	Ala	Leu	Leu	Ser	Val	Val	
225					230					235					240	
Phe	Ala	Trp	Ile	Leu	Lys	Ile	Ile	Ser	Ser	Lys	Tyr	Ile	Glu	Asn	Asn	
				245					250					255		
Glu	Arg	Val	Tyr	Thr	Val	Asn	Lys	Ala	Ile	Asn	Phe	Val	Asn	Val	Ser	

260	265	270
Val Ile Xaa Xaa Ile Xaa Leu Phe Ser Tyr Leu Glu Asn Val Thr Tyr		
275	280	285
Leu Val Thr Val Leu Gly Phe Ala Ser Ala Gly Leu Ala Ile Xaa Met		
290	295	300
Lys Asp Leu Phe Met Ser Leu Leu Gly Trp Phe Ile Ile Leu Ile Gly		
305	310	315
Gly Ser Val His Val Gly Asp Arg Val Arg Ile Ala Lys Gly Thr Asp		
325	330	335
Ile Phe Ile Gly Asp Val Leu Asp Thr Ser Asn Val Val His		
340	345	350

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

Met	Leu	Ser	Ala	Leu	Leu	Ser	Lys	Met	Gly	Thr	Tyr	Ala	Leu	Leu	Arg
1				5					10					15	
Phe	Leu	Leu	Pro	Leu	Phe	Pro	Glu	Leu	Ser	Glu	Ile	Tyr	Leu	Thr	Pro
			20					25					30		
Ile	Ala	Ile	Val	Ala	Leu	Cys	Met	Ile	Ile	Tyr	Gly	Gly	Phe	Leu	Ala
		35					40					45			
Tyr	Ala	Gln	Lys	Asp	Leu	Lys	Thr	Leu	Ile	Ala	Tyr	Ser	Ser	Phe	Ser
	50					55					60				
His	Met	Gly	Val	Val	Val	Leu	Gly	Val	Phe	Ser	Phe	Asn	Val	Glu	Gly
65					70				75					80	
Val	Ser	Gly	Ala	Val	Phe	Met	Met	Phe	Ala	His	Gly	Val	Ile	Val	Met
				85				90					95		
Gly	Leu	Phe	Leu	Leu	Ala	Gly	Ile	Leu	Glu	Glu	Arg	Ala	Ser	Ser	Leu
			100				105					110			
Glu	Ile	Ala	Arg	Phe	Gly	Ser	Ile	Ala	Lys	Ser	Ala	Pro	Val	Phe	Ala
		115					120					125			

Ala Phe Phe Met Ile Val Leu Met Ala Asn Val Gly Met Pro Leu Ser
130 135 140

Ile Gly Phe Val Gly Glu Phe Leu Asn Leu Leu Gly Phe Phe Ala Thr
145 150 155 160

Tyr Pro Leu Leu Ala Ile Ile Ala Gly Thr Ser Leu Ile Leu Ser Ala
165 170 175

Val Tyr Ile Leu Thr Ser Tyr Lys Asp Val Phe Phe Gly Asn Leu Lys
180 185 190

Thr Gly Asn Asn Gln Ile Ser Val Phe Glu Asp Leu Asn Ala Arg Glu
195 200 205

Val Gly Val Leu Ser Val Ile Leu Ala Phe Asp Leu Asn Phe Arg Asp
210 215 220

Leu Tyr Lys Ser Ala Phe Lys Thr Asp
225 230

(2) INFORMATION FOR SEQ ID NO:504:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

Val Glu Leu Ile Ser Asn Asn Pro Asn Ala Ser Gln Gln Ser Ile Val
1 5 10 15

Ile Pro Leu Glu Thr Phe Ala Leu Ala Arg Ala Leu Lys Gly Ile Phe
20 25 30

(2) INFORMATION FOR SEQ ID NO:505:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 171 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...171
- (D) OTHER INFORMATION: /note= "UREASE OPERON UREC PROTEIN"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

Met Lys Ile Phe Gly Thr Asp Gly Val Arg Gly Lys Ala Gly Val Lys
1 5 10 15
Leu Thr Pro Met Phe Val Met Arg Leu Gly Ile Ala Ala Gly Leu Tyr
 20 25 30
Phe Lys Lys His Ser Gln Thr Asn Lys Ile Leu Ile Gly Lys Asp Thr
 35 40 45
Arg Lys Ser Gly Tyr Met Val Glu Asn Ala Leu Val Ser Ala Leu Thr
 50 55 60
Ser Ile Gly Tyr Asn Val Ile Gln Ile Gly Pro Met Pro Thr Pro Ala
65 70 75 80
Ile Ala Phe Leu Thr Glu Asp Met Arg Cys Asp Ala Gly Ile Met Ile
 85 90 95
Ser Ala Ser His Asn Pro Phe Glu Asp Asn Gly Ile Lys Phe Phe Asn
 100 105 110
Ser Tyr Gly Tyr Lys Leu Lys Glu Glu Glu Glu Arg Ala Ile Glu Glu
 115 120 125
Ile Phe His Asp Glu Glu Leu Leu His Ser Ser Tyr Lys Val Gly Glu
 130 135 140
Ser Val Gly Ser Ala Lys Arg Ile Asp Asp Val Ile Gly Pro Leu Tyr
145 150 155 160
Arg Ala Phe Glu Ala Leu Tyr Thr Gln Thr Phe
 165 170

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

Val Arg Ala Val Phe Val Phe Gly Leu Lys Ala Ala Phe Cys Ile Gly
 1 5 10 15
 Ile Phe Phe Tyr Gly Ala Tyr Tyr Phe Leu Asp Glu Phe Leu Ile Lys
 20 25 30
 Leu

(2) INFORMATION FOR SEQ ID NO:507:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

Met Lys Glu Gln Glu Trp Asp Leu Ser Ala Leu Phe Glu Asn Lys Glu
 1 5 10 15
 Ser Ala Glu Glu Phe Leu Lys Thr Leu Gln Thr Glu Val Gln Glu Phe
 20 25 30
 Glu Asn Ala Tyr Gln Asn Asn Leu Lys Asn Leu Asp Ala Ala Lys Phe
 35 40 45
 Ala Asn Thr Leu Lys His Tyr Glu Asn Leu Ser Glu Lys Ile Ser Arg
 50 55 60
 Ala Met Ala Tyr Ala Asn Tyr Phe Leu Pro Arg Thr Leu Lys Lys Arg
 65 70 75 80
 Ser Phe Ile Arg Asn Ala Asn Gly Leu Cys Lys Tyr Pro Thr Thr Pro
 85 90 95
 Phe Ile Leu

(2) INFORMATION FOR SEQ ID NO:508:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

```
Leu Arg Val Gly Met Tyr Glu Val Cys Asn His Lys Asp Gly Thr Ala
1          5          10          15
Tyr His Ser Thr Arg Gly Ser Lys Val Thr Leu Ala Cys Lys Thr Gly
          20          25          30
Thr Ala Gln Val Val Glu Ile Ala Gln Asn Ile Val Asn Arg Met Lys
          35          40          45
Glu Lys Asp Met Glu Tyr Phe His Xaa Ser His Xaa Trp Ile Thr Xaa
          50          55          60
Tyr Leu Xaa Pro Met Lys Asn Pro Asn Thr Leu Ser Leu Phe
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

```
Val Arg Ser Gly Lys Arg Leu Gly Tyr Thr Asn Gln Val Ile Thr Asp
1          5          10          15
Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Ala Leu Met Val
          20          25          30
Cys Thr Ala Leu Lys Arg Tyr Gly His Pro Arg Leu Lys Met His Phe
          35          40          45
Val Ser Asn Val Glu Trp His Ala Asp Phe Arg Arg Phe Gly Lys Asn
          50          55          60
Gln Pro Gly Gln Arg Ala
65          70
```

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

Leu	Gly	Leu	Val	Xaa	Gly	Ile	Ser	Leu	Leu	His	Leu	Ser	Leu	Glu	Gln
1				5				10					15		
Lys	Ile	Ser	Val	Phe	Leu	Gly	Xaa	Asn	Leu	Met	Leu	Tyr	Pro	Val	Xaa
			20					25					30		
Glu	Val	Leu	Phe	Ser	Ile	Leu	Arg	Arg	Lys	Ile	Lys	Arg	Gln	Lys	Ala
			35				40					45			
Thr	His	Ala	Gly												
			50												

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

Leu	Gly	Leu	Val	Xaa	Gly	Ile	Ser	Leu	Leu	His	Leu	Ser	Leu	Glu	Gln
1				5				10					15		
Lys	Ile	Ser	Val	Phe	Leu	Gly	Xaa	Asn	Leu	Met	Leu	Tyr	Pro	Val	Xaa
			20					25					30		
Glu	Val	Leu	Phe	Ser	Ile	Leu	Arg	Arg	Lys	Ile	Lys	Arg	Gln	Lys	Ala
			35				40					45			
Thr	His	Ala	Gly												
			50												

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

Met	Leu	Glu	Lys	Leu	Ile	Glu	Arg	Val	Leu	Phe	Ala	Thr	Arg	Trp	Leu	
1				5				10						15		
Leu	Ala	Pro	Leu	Cys	Ile	Ala	Met	Ser	Leu	Val	Leu	Val	Val	Leu	Gly	
			20					25						30		
Tyr	Val	Phe	Met	Lys	Glu	Leu	Trp	His	Met	Leu	Ser	His	Leu	Asn	Thr	
			35					40						45		
Ile	Ser	Glu	Thr	Asp	Leu	Val	Leu	Ser	Ala	Leu	Gly	Leu	Val	Asp	Leu	
			50					55						60		
Leu	Val	His	Gly	Arg	Ala	Cys	Phe	Asp	Gly	Ala	Ala	Arg	Gln	Leu		
65							70						75			

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

Met	His	Tyr	Gln	Leu	Thr	Ser	Phe	Asn	Ile	Ile	Gln	Asp	Leu	Phe	Ile	
1				5					10					15		
Thr	Cys	His	Val	Leu	Arg	Ile	Lys	Met	Arg	Val	Phe	Val	Cys	Phe	Leu	
			20					25						30		
Gly	Val	Phe	Val	Ser	Asn	Gly	Leu	Ala	Arg	Phe	Gly	Tyr	Val	Val	Leu	
			35					40						45		
Ile	Pro	Leu	Leu	Ile	Leu	Ser	Gly	Ser	Leu	Thr	Pro	His	Gln	Ser	Phe	
			50					55						60		
Gln	Leu	Gly	Ile	Ala	Val	Leu	Met	Gly	Tyr	Val	Phe	Gly	Ser	Phe	Leu	
65							70							75		80

Ile Gln Phe Leu Ser Pro Leu Met Ser Leu Lys Ser Ile Ala Lys Ile
85 90 95
Ser Phe Lys Leu Thr Leu
100

(2) INFORMATION FOR SEQ ID NO:514:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...15
 - (D) OTHER INFORMATION: /note= "vacuolating cytotoxin of Hpylori"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

Val Asp Met Lys Asp Ala Val Gly Thr Tyr Lys Leu Xaa Arg Ala
1 5 10 15
6

(2) INFORMATION FOR SEQ ID NO:515:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

Leu Ala Gln Pro Val Gln Val Arg Thr Val Phe Met Ser Met Thr Leu
1 5 10 15
Asn Ala Met Gly Gln Phe Ala Tyr Asn Phe Pro Ala Asn Ile Ser Lys
20 25 30
Asp Lys Gln Lys Leu Thr Met Val Tyr Met Asp Lys Asp Tyr Gly Ala
35 40 45
Tyr Gly Asn Ile Val Ala Met Gly Gly Glu Tyr Val Lys Ile Glu Leu

50					55					60					
Gly 65	Thr	Asp	Thr	Gly	Leu 70	Asn	Pro	Phe	Ala	Trp 75	Ala	Ala	Cys	Val	Gln 80
Lys	Thr	Asn	Ala	Thr 85	Met	Glu	Gln	Lys	Gln 90	Thr	Ala	Ile	Ser	Val 95	Val
Lys	Glu	Leu	Val 100	Lys	Asn	Leu	Ala	Thr 105	Lys	Ser	Asp	Glu	Lys	Asp 110	Glu
Asn	Gly	Asn	Ser 115	Ile	Ser	Phe	Ser	Leu 120	Ala	Asp	Ser	Asn 125	Thr	Leu	Ala
Ala 130	Ala	Val	Thr	Asn	Leu	Ile 135	Thr	Gly	Asp	Met	Asn 140	Leu	Asp	Tyr	Pro
Ile 145	Thr	Gln	Leu	Ile	Asn 150	Ala	Phe	Gly	Lys	Asp 155	His	Asn	Asp	Pro	Asn 160
Gly	Leu	Val	Ala	Arg 165	Leu	Ala	Pro	Phe	Cys 170	Lys	Ser	Thr	Asn	Gly 175	Glu
Phe	Gln	Trp	Leu 180	Phe	Asp	Asn	Lys	Ala 185	Thr	Asp	Arg	Leu	Asp 190	Phe	Ser
Lys	Thr	Ile 195	Ile	Gly	Val	Asp	Gly 200	Ser	Ser	Phe	Leu	Asp 205	Asn	Asn	Asp
Val 210	Ser	Pro	Phe	Ile	Cys	Phe 215	Tyr	Leu	Phe	Ala	Arg 220	Ile	Gln	Glu	Ala
Met 225	Asp	Gly	Arg	Arg	Phe 230	Val	Leu	Asp	Ile	Asp 235	Glu	Ala	Trp	Lys	Tyr 240
Leu	Gly	Asp	Pro	Lys 245	Val	Ala	Tyr	Phe	Val 250	Arg	Asp	Met	Leu	Lys 255	Thr
Ala	Arg	Lys	Arg 260	Asn	Ala	Ile	Val	Arg 265	Leu	Ala	Thr	Gln	Ser	Ile 270	Thr
Asp	Leu	Leu	Ala 275	Cys	Pro	Ile	Ala 280	Asp	Thr	Ile	Arg	Glu	Gln	Cys	Pro 285
Thr 290	Lys	Ile	Phe	Leu	Arg	Asn 295	Asp	Gly	Gly	Asn 300	Leu	Ser	Asp	Tyr	Gln
Arg 305	Leu	Ala	Asn	Val	Thr 310	Glu	Lys	Glu	Phe	Glu 315	Ile	Ile	Thr	Lys	Gly 320
Leu	Asp	Arg	Lys 325	Ile	Leu	Tyr	Lys	Gln	Asp 330	Gly	Ser	Pro	Ser	Val 335	Ile
Ala	Ser	Phe	Asn 340	Leu	Arg	Gly	Ile	Pro 345	Lys	Glu	Tyr	Leu	Lys	Ile 350	Leu
Ser	Thr	Asp	Thr 355	Val	Phe	Val	Lys 360	Glu	Ile	Asp	Lys	Ile 365	Ile	Gln	Asn

His Ser Ile Ile Asp Lys Tyr Gln Pro
 370 375

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...1027
- (D) OTHER INFORMATION: /note= "mature-parasite-infected erythrocyte surface antigen"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

Val	Cys	Leu	Asp	His	Gln	Val	Gly	Ala	Gly	Lys	Thr	Leu	Cys	Ala	Ile	1	5	10	15
Ala	Ser	Cys	Met	Glu	Gln	Lys	Arg	Met	Gly	Leu	Val	Asn	Lys	Thr	Leu	20	25	30	
Ile	Ala	Val	Pro	Asn	His	Leu	Thr	Lys	Gln	Trp	Gly	Asp	Glu	Phe	Tyr	35	40	45	
Lys	Ala	Tyr	Pro	Asn	Ala	Asn	Val	Leu	Val	Val	Asp	Ser	Lys	Asp	Thr	50	55	60	
Thr	Glu	Lys	Glu	Arg	Glu	Leu	Leu	Phe	Asn	Gln	Ile	Ala	Asn	Asn	Asn	65	70	75	80
Tyr	Asp	Ala	Val	Val	Ile	Ala	His	Thr	His	Leu	Glu	Leu	Leu	Ser	Asn	85	90	95	
Pro	Arg	Gly	Ile	Ile	Glu	Glu	Leu	Lys	Glu	Glu	Glu	Leu	Val	Asn	Ala	100	105	110	
Glu	Lys	Asn	Phe	Glu	Arg	Gln	Glu	Leu	Ala	Tyr	Lys	Asn	Asn	Pro	Arg	115	120	125	
Glu	Thr	Lys	Lys	Pro	Asn	Glu	Arg	Ala	Phe	Lys	Asn	Lys	Leu	Asp	Lys	130	135	140	
Ile	Arg	Ala	Lys	Tyr	Asp	Ala	Ile	Leu	Glu	Lys	Gln	Gly	Ser	His	Ile	145	150	155	160
Asp	Ile	Ser	Gln	Met	Gly	Ile	Asp	Asn	Leu	Ile	Val	Asp	Glu	Ala	His				

				165					170					175			
Leu	Phe	Lys	Asn	Leu	Ala	Phe	Glu	Thr	Ser	Met	Glu	Lys	Ile	Ala	Gly		
			180					185					190				
Leu	Gly	Asn	Gln	Gln	Gly	Ser	Asn	Arg	Ala	Arg	Asp	Leu	Phe	Ile	Lys		
		195					200					205					
Thr	Arg	Tyr	Leu	His	Gln	Asn	Asp	Lys	Lys	Ile	Met	Phe	Leu	Thr	Gly		
	210					215					220						
Thr	Pro	Ile	Ala	Asn	Ser	Leu	Ser	Glu	Met	Tyr	His	Leu	Gln	Arg	Tyr		
225					230					235					240		
Leu	Thr	Pro	Asp	Val	Leu	Lys	Glu	Arg	Gly	Leu	Glu	Phe	Phe	Asp	Asp		
				245					250					255			
Trp	Ala	Lys	Thr	Tyr	Gly	Glu	Val	Val	Asn	Asp	Phe	Glu	Leu	Asp	Thr		
			260					265					270				
Ser	Ala	Gln	Ser	Tyr	Lys	Met	Val	Asn	Arg	Phe	Ser	Lys	Phe	Ser	Asp		
		275					280					285					
Val	Gln	Gly	Leu	Ser	Thr	Met	Tyr	Arg	Ala	Phe	Ala	Asp	Ile	Val	Ser		
	290					295					300						
Asn	Asp	Asp	Ile	Leu	Lys	His	Asn	Pro	His	Phe	Val	Pro	Lys	Val	Tyr		
305					310					315					320		
Gly	Asp	Lys	Pro	Ile	Asn	Val	Val	Val	Lys	Arg	Ser	Glu	Glu	Val	Ala		
				325					330					335			
Gln	Phe	Ile	Gly	Val	Ala	Leu	Glu	Asn	Gly	Lys	Tyr	Asn	Glu	Gly	Ser		
			340					345					350				
Ile	Ile	Asp	Arg	Met	Gln	Lys	Cys	Glu	Gly	Lys	Lys	Ser	Gln	Lys	Gly		
		355					360					365					
Gln	Asp	Asn	Ile	Leu	Ser	Cys	Thr	Thr	Asp	Ala	Arg	Lys	Val	Ala	Leu		
	370					375					380						
Asp	Tyr	Arg	Leu	Ile	Asp	Pro	Asn	Ala	Lys	Val	Glu	Lys	Glu	Phe	Ser		
385					390					395					400		
Lys	Ser	Tyr	Ala	Met	Ala	Lys	Asn	Ile	Tyr	Glu	Asn	Tyr	Leu	Glu	Thr		
				405					410					415			
His	Ala	Thr	Lys	Gly	Thr	Gln	Leu	Gly	Phe	Ile	Gly	Leu	Ser	Thr	Pro		
			420					425					430				
Lys	Thr	His	Ser	Gln	Lys	Val	Ser	Leu	Glu	Ala	Leu	Asp	Asn	Ala	His		
		435					440					445					
Glu	Thr	Glu	Asn	Lys	Asn	Pro	Leu	Asp	Lys	Ala	Gln	Glu	Leu	Leu	Glu		
	450					455					460						
Ser	Leu	Ser	Ser	Tyr	Asp	Glu	Lys	Gly	Asn	Leu	Ile	Ala	Pro	Ser	Lys		
465					470					475					480		

Lys	Glu	Leu	Glu	Asn	Glu	Leu	Lys	Glu	Lys	Glu	Ala	Lys	Ser	Val	Asn	
				485					490						495	
Leu	Asp	Glu	Glu	Ile	Ala	Lys	Gly	Cys	Ser	Phe	Asp	Val	Tyr	Ser	Asp	
			500					505					510			
Val	Leu	Arg	His	Leu	Val	Gln	Met	Gly	Ile	Pro	Gln	Asn	Glu	Ile	Ala	
		515					520					525				
Phe	Ile	His	Asp	Ala	Lys	Thr	Glu	Glu	Gln	Lys	Gln	Asp	Leu	Phe	Lys	
	530					535					540					
Lys	Leu	Asn	Arg	Gly	Gly	Val	Arg	Val	Leu	Leu	Gly	Ser	Pro	Ala	Lys	
545					550					555					560	
Met	Gly	Val	Gly	Thr	Asn	Val	Gln	Glu	Arg	Leu	Val	Ala	Met	His	Glu	
				565					570					575		
Leu	Asp	Cys	Pro	Trp	Arg	Pro	Asp	Glu	Leu	Leu	Gln	Met	Glu	Gly	Arg	
			580					585					590			
Gly	Ile	Arg	Gln	Gly	Asn	Ile	Leu	His	Gln	Asn	Asp	Pro	Glu	Asn	Phe	
		595					600					605				
Arg	Met	Lys	Ile	Tyr	Arg	Tyr	Ala	Thr	Glu	Lys	Thr	Tyr	Asp	Ser	Arg	
	610					615					620					
Met	Trp	Gln	Ile	Ile	Glu	Thr	Lys	Ser	Lys	Gly	Ile	Glu	Gln	Phe	Arg	
625					630					635					640	
Asn	Ala	His	Lys	Leu	Gly	Leu	Asn	Glu	Leu	Glu	Asp	Phe	Asn	Met	Gly	
				645					650					655		
Ser	Ser	Asn	Ala	Ser	Glu	Met	Lys	Ala	Glu	Ala	Thr	Gly	Asn	Pro	Leu	
			660					665					670			
Ile	Ile	Glu	Glu	Val	Lys	Leu	Arg	Ala	Glu	Ile	Lys	Ser	Glu	Glu	Ser	
		675					680					685				
Lys	Tyr	Lys	Ala	Phe	Asn	Lys	Glu	His	Tyr	Phe	Asn	Glu	Glu	Ser	Leu	
	690					695					700					
Lys	Asn	Asn	Ala	Ser	Lys	Leu	Asp	Tyr	Leu	Lys	Gln	Glu	Leu	Lys	Asp	
705					710					715					720	
Leu	Glu	Thr	Leu	Gln	Arg	Ser	Val	Ile	Ile	Pro	Thr	His	Thr	Glu	Ile	
				725					730					735		
Lys	Leu	Tyr	Asp	Leu	Lys	Asn	Glu	Glu	Ser	Lys	Asp	Tyr	Glu	Leu	Ile	
			740					745					750			
Lys	Val	Lys	Glu	Val	Glu	Pro	Leu	Lys	Glu	Asn	Ala	Ser	Met	Ser	Glu	
		755					760					765				
Glu	Leu	Thr	His	Lys	Lys	Leu	Lys	Glu	Gln	Asn	Lys	Gln	Ile	Ala	Glu	
	770					775					780					

Gln	Asn	Lys	Glu	Lys	Leu	Asp	Ala	Ile	Lys	Lys	Gln	Phe	Ala	Ser	Asn	
785					790					795					800	
Leu	Asn	Thr	Leu	Phe	Val	Asn	Glu	Glu	Glu	Asp	Tyr	Lys	Leu	Leu	Glu	
				805					810					815		
Tyr	Lys	Gly	Phe	Val	Val	Asn	Ala	Tyr	Lys	Thr	Lys	Tyr	Gln	Val	Glu	
			820					825					830			
Phe	Ser	Leu	Ser	Pro	Lys	Asp	Asn	Pro	Asn	Ile	Ala	Tyr	Ser	Pro	Ser	
		835					840					845				
Asn	Met	Val	Tyr	Lys	Asn	Asp	Thr	Ile	Asn	Met	Phe	Ser	Ser	Tyr	Asn	
	850					855					860					
Phe	Cys	Ala	Glu	Ile	Lys	Phe	Asp	Gly	Phe	Leu	Lys	Arg	Leu	Asp	Asn	
865					870					875					880	
Ala	Ile	Thr	Lys	Leu	Pro	Glu	Lys	Ile	Lys	Glu	Leu	Glu	Asn	Ser	Ile	
				885					890					895		
Glu	Ile	Thr	Lys	Lys	Asn	Ile	Ala	Lys	Tyr	Thr	Arg	Leu	Val	Glu	Gln	
			900					905					910			
Lys	Pro	Ser	Tyr	Pro	Arg	Leu	Glu	Tyr	Leu	Gln	Ala	Leu	Lys	Trp	Asp	
		915					920					925				
His	Lys	Thr	Leu	Ile	Asp	Asp	Leu	Ala	Lys	Met	Ser	Lys	Asp	Arg	Asn	
	930					935					940					
Tyr	Lys	Pro	Ala	Phe	Asn	Pro	Lys	Ser	Lys	Glu	Val	Leu	Lys	Asn	Leu	
945					950					955					960	
Asn	Ala	Glu	Lys	Arg	Ala	Ser	Leu	Glu	Asn	Glu	Arg	Glu	Glu	Gln	Gly	
				965					970					975		
Val	Lys	Gly	Asn	Thr	Lys	Ser	His	Asp	Glu	Ile	Glu	Pro	Ala	Thr	Glu	
			980					985					990			
Gln	Val	Ile	Glu	Lys	Glu	Ile	Glu	Lys	Gly	Asp	Glu	Ile	Ala	Asn	Asn	
	995						1000					1005				
Val	Asp	Tyr	Tyr	Glu	Asn	Glu	Gln	Glu	Val	Glu	Ile	Thr	Lys	Ser	Met	
	1010					1015					1020					
Gly	Arg	Arg														
1025																

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

Met	Lys	Leu	Val	Ser	Leu	Ile	Val	Ala	Leu	Val	Phe	Cys	Cys	Phe	Leu
1				5					10					15	
Gly	Ala	Val	Glu	Leu	Pro	Gly	Val	Tyr	Gln	Thr	Gln	Glu	Phe	Leu	Tyr
			20					25					30		
Met	Lys	Ser	Ser	Phe	Val	Glu	Phe	Phe	Glu	His	Asn	Gly	Lys	Phe	Tyr
		35					40					45			
Ala	Tyr	Gly	Ile	Ser	Asp	Val	Xaa	Xaa	Ser	Lys	Ala	Lys	Lys	Asp	Lys
	50					55					60				
Leu	Asn	Pro	Asn	Pro	Lys	Leu	Arg	Asn	Arg	Ser	Asp	Lys	Gly	Val	Val
65					70				75					80	
Phe	Leu	Ser	Asp	Leu	Ile	Lys	Val	Gly	Glu	Gln	Ser	Tyr	Lys	Gly	Gly
				85					90					95	
Lys	Ala	Xaa	Asn	Phe	Xaa	Asp	Gly	Lys	Thr	Xaa	His	Val	Arg	Val	Thr
			100					105					110		
Gln	Xaa	Ser	Asn	Gly	Asp	Leu	Xaa	Phe	Thr	Ser	Ser	Tyr	Xaa	Lys	Trp
		115					120					125			
Gly	Tyr	Val	Gly	Lys	Thr	Phe	Thr	Trp	Lys	Arg	Leu	Ser	Asp	Glu	Glu
	130					135					140				
Ile	Lys	Asn	Leu	Lys	Leu	Lys	Arg	Phe	Asn						
145					150										

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

Met	Ala	Glu	Glu	Glu	Lys	Thr	Glu	Leu	Pro	Ser	Ala	Lys	Lys	Ile	Gln
1					5				10					15	
Lys	Ala	Arg	Glu	Glu	Gly	Asn	Val	Pro	Lys	Ser	Met	Glu	Val	Val	Gly

	20		25		30										
Val	Phe	Arg	Val	Ile	Gly	Trp	Ala	Asn	Glu	Tyr	Phe	Cys	Phe	Phe	Tyr
	35						40					45			
Met	Val	Gly	Gly	Met	Ala	Leu	Ala	Arg	Cys	Ile	Ala	Met	Cys		
	50					55						60			

(2) INFORMATION FOR SEQ ID NO:519:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

Met	Lys	Thr	Leu	Val	Lys	Asn	Thr	Ile	Tyr	Ser	Phe	Leu	Leu	Leu	Ser
1				5					10				15		
Val	Leu	Met	Ala	Glu	Asp	Ile	Thr	Ser	Gly	Leu	Lys	Gln	Leu	Asp	Asn
			20					25					30		
Thr	Tyr	Gln	Glu	Thr	Asn	Gln	Gln	Val	Leu	Lys	Asn	Leu	Asp	Glu	Ile
		35					40					45			
Phe	Ser	Thr	Thr	Ser	Pro	Ser	Ala	Asn	Asn	Lys	Ile	Gly	Gln	Glu	Asp
	50					55					60				
Ala	Leu	Asn	Ile	Lys	Lys	Ala	Ala	Ile	Ala	Leu	Arg	Gly	Asp	Leu	Ala
65				70					75					80	
Leu	Leu	Lys	Ala	Asn	Phe	Glu	Ala	Asn	Glu	Leu	Phe	Phe	Ile	Ser	Glu
			85					90						95	
Asp	Val	Ile	Phe	Lys	Thr	Tyr	Met	Ser	Ser	Pro	Glu	Leu	Leu	Leu	Thr
			100					105					110		
Tyr	Met	Lys	Ile	Asn	Pro	Leu	Asp	Gln	Lys	Thr	Ala	Glu	Gln	Gln	Cys
	115						120					125			
Gly	Ile	Ser	Asp	Lys	Val	Leu	Val	Leu	Tyr	Cys	Glu	Gly	Lys	Leu	Lys
	130					135					140				
Ile	Glu	Gln	Glu	Lys	Gln	Asn	Ile	Arg	Glu	Arg	Leu	Glu	Thr	Ser	Leu
145					150				155						160
Lys	Ala	Tyr	Gln	Ser	Asn	Ile	Gly	Gly	Thr	Ala	Ser	Leu	Ile	Thr	Ala
				165					170					175	

Ser Gln Thr Leu Val Glu Ser Leu Lys Asn Lys Asn Phe Ile Lys Gly
180 185 190

Ile Lys Lys Leu Met Leu Ala His Asn Lys Val Phe Leu Asn Tyr Leu
195 200 205

Glu Glu Leu Asp Ala Leu Glu Arg Ser Leu Glu Gln Ser Lys Arg Gln
210 215 220

Tyr Leu Gln Glu Arg Gln Ser Ser Lys Ile Ile Val Lys
225 230 235

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

Val Ser Glu Lys Asp Arg Ala Phe Leu Leu Ala Ser Leu Ser Cys Val
1 5 10 15

Asp Tyr Val Val Val Phe Gly Glu Asp Thr Pro Ile Lys Leu Ile Gln
20 25 30

Ala Leu Lys Pro Asp Ile Leu Val Lys Gly Ala Asp Tyr Leu Asn Lys
35 40 45

Glu Val Ile Gly Ser Glu Leu Ala Lys Glu Thr Arg Leu Ile Glu Phe
50 55 60

Glu Glu Gly Tyr Ser Thr Ser Ala Ile Ile Glu Lys Ile Lys Arg Thr
65 70 75 80

His Asn Asp

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

Leu Glu Thr Leu Phe Leu Val
1 5

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

Val Tyr Asp Lys Ser Leu Cys Lys Thr Met Ala Leu Ala Leu Lys Ala
1 5 10 15
Leu Gly Val Lys Arg Ala Met Val Val Asn Gly Gly Gly Thr Gly Glu
20 25 30
Ile Val Leu His Asp Ile Thr His Ala Cys Glu Leu Lys Asn Asn Glu
35 40 45
Ile Leu Glu Tyr Asp Leu Ser Ala Lys Asp Phe Asp Leu Pro Pro Ser
50 55 60

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1...228
(D) OTHER INFORMATION: /note= "D-XYLOSE TRANSPORT ATP-BINDING
PROTEIN"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

Met	Leu	Val	Glu	Ile	Glu	Asn	Leu	Thr	Lys	Thr	Tyr	Gly	Ser	Leu	Lys	
1				5					10					15		
Ala	Leu	Asp	Asn	Ile	Ser	Leu	Lys	Leu	Pro	Lys	Gln	Gln	Phe	Ile	Gly	
			20					25					30			
Leu	Leu	Gly	Pro	Asn	Gly	Ala	Gly	Lys	Thr	Thr	Leu	Leu	Lys	Ile	Leu	
		35					40					45				
Ala	Gly	Leu	Asn	Leu	Asn	Tyr	Gln	Gly	Glu	Val	Lys	Ile	Leu	Asn	Gln	
	50					55					60					
Lys	Ile	Gly	Ile	Glu	Thr	Lys	Lys	Ser	Val	Ala	Phe	Leu	Ser	Asp	Gly	
65					70					75					80	
Asp	Phe	Leu	Asp	Pro	Lys	Leu	Thr	Pro	Leu	Lys	Ala	Ile	Ala	Phe	Tyr	
				85					90					95		
Lys	Asp	Phe	Phe	Ser	Asp	Phe	Asp	Glu	Ser	Lys	Ala	Leu	Asn	Leu	Leu	
			100					105					110			
Lys	Arg	Phe	Ser	Val	Pro	Leu	Lys	Arg	Glu	Phe	Lys	Ala	Leu	Ser	Lys	
	115						120					125				
Gly	Met	Arg	Glu	Lys	Leu	Gln	Leu	Ile	Leu	Thr	Leu	Ser	Arg	Asn	Ala	
	130					135					140					
Ser	Leu	Tyr	Leu	Phe	Asp	Glu	Pro	Val	Ala	Gly	Ile	Asp	Pro	Ile	Ala	
145					150					155					160	
Arg	Glu	Glu	Ile	Phe	Glu	Leu	Ile	Ala	Lys	Glu	Phe	Ser	Gln	Asn	Ala	
				165					170					175		
Ser	Leu	Leu	Val	Ser	Thr	His	Leu	Val	Val	Asp	Val	Glu	Lys	Tyr	Leu	
			180					185					190			
Asp	Ser	Ala	Ile	Phe	Leu	Lys	Glu	Ala	Lys	Val	Val	Ala	Phe	Gly	Asp	
	195						200					205				
Val	Gly	Glu	Leu	Lys	Lys	Gly	Tyr	Ser	Ser	Leu	Glu	Ala	Ala	Tyr	Lys	
	210					215					220					
Glu	Arg	Leu	Lys													
225																

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

Met	Asn	Lys	Leu	Phe	Leu	Ala	Phe	Ile	Val	Gly	Gly	Met	Leu	Leu	Ser	
1			5					10					15			
Ala	Asp	Ala	Leu	Asn	Asp	Lys	Ile	Glu	Asn	Leu	Met	Gly	Glu	Arg	Ser	
			20				25					30				
Tyr	His	Met	Asn	Lys	Leu	Phe	Leu	Glu	Arg	Leu	Phe	Lys	Asn	Arg	Lys	
		35				40					45					
Asp	Phe	Tyr	Glu	Met	Gly	Arg	Leu	Asp	Ser	Leu	Lys	Leu	Leu	Asn	Thr	
	50					55					60					
Leu	Lys	Glu	Asn	Gly	Leu	Leu	Ser	Phe	Asn	Phe	Asp	Lys	Pro	Ser	Val	
65				70					75						80	
Leu	Lys	Ile	Thr	Phe	Lys	Ala	Ser	Ser	Asn	Pro	Leu	Ala	Phe	Ala	Lys	
				85					90					95		
Ser	Ile	Asn	Asn	Ser	Leu	Asn	Met	Met	Gly	Tyr	Ser	Tyr	Val	Leu	Pro	
			100					105					110			
Ile	Arg	Met	Gln	Ser	Ser	Ser	Gly	Glu	Asn	Val	Phe	Ser	Tyr	Glu	Leu	
		115					120					125				
Lys	Thr	Glu	Tyr	Val	Leu	Asp	Pro	Asn	Ile	Leu	Ile	Glu	Thr	Met	Lys	
	130					135					140					
Arg	His	Gly	Phe	Asp	Phe	Met	Asp	Ile	Arg	Arg	Val	Ser	Leu	Lys	Glu	
145					150					155					160	
Trp	Glu	Tyr	Asp	Phe	Ala	Leu	Gln	Lys	Ile	Lys	Leu	Pro	Asn	Ala	Arg	
				165					170					175		
Ala	Leu	Val	Leu	Ser	Ser	Asp	Pro	Val	Glu	Phe	Lys	Glu	Ala	Ser	Gly	
			180					185					190			
Lys	Tyr	Trp	Leu	Ser	Val	Asn	Gln	Asn	Ala	Tyr	Leu	Lys	Ile	Ser	Ser	
		195					200					205				
Asn	Asn	Pro	Leu	Trp	Gln	Pro	Lys	Ile	Ile	Phe	Tyr	Asp	Glu	Asn	Leu	
	210					215					220					
Lys	Ile	Ile	Gln	Ile	Ile	Ala	Lys	Glu	Asn	Arg	Gln	Gln	Glu	Ile	Ala	
225					230					235					240	
Leu	Asn	Leu	Leu	Asp	Gly	Val	Arg	Phe	Ile	His	Ile	Thr	Asp	Ala	Lys	
				245					250					255		
Asn	Pro	Ile	Ile	Leu	Lys	Asn	Gly	Ile	Ser	Val	Val	Phe	Asp	Ala	Met	
			260					265					270			

Pro

(2) INFORMATION FOR SEQ ID NO:525:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...15
 - (D) OTHER INFORMATION: /note= "H.influenzae lic-1 operon licA-licD genes"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

Val	Ser	Arg	Pro	Phe	Lys	Thr	Ile	Lys	Lys	Pro	Pro	Gln	Pro	Pro
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:526:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

Met	Xaa	Thr	His	Asp	Arg	Arg	Lys	Leu	Arg	Ile	Xaa	Leu	Thr	Gln	Thr
1				5				10						15	
Thr	Thr	Leu	Val	Ala	Thr	Ile	Gly	Ser	Asn	Ala	Pro	Tyr	Ile	Gly	Leu
			20					25					30		
Leu	Gly	Thr	Val	Met	Gly	Ile	Met	Leu	Thr	Phe	Met	Asp	Leu	Gly	Ser
			35				40					45			
Ala	Ser	Gly	Ile	Asp	Thr	Lys	Ala	Ile	Met	Thr	Asn	Leu	Ala	Leu	Ala
			50				55				60				

Leu Lys Ala Thr Gly Met Gly Leu Leu Val Ala Ile Pro Ala Ile Val
 65 70 75 80
 Ile Tyr Asn Leu Leu Val Arg Lys Ser Glu Ile Leu Val Thr Lys Trp
 85 90 95
 Asp Ile Phe His His Pro Val Asp Thr Gln Ser His Glu Val Tyr Ser
 100 105 110
 Lys Ala

(2) INFORMATION FOR SEQ ID NO:527:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...67
 - (D) OTHER INFORMATION: /note= "probable cadmium-transporting ATPase"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

Met Ile Ala Val Leu Pro Pro Leu Phe Ser Met Gly Ser Phe Asp Glu
 1 5 10 15
 Trp Ile Tyr Arg Gly Leu Val Ala Leu Met Val Ser Cys Pro Cys Ala
 20 25 30
 Leu Val Ile Ser Val Pro Leu Gly Tyr Phe Gly Gly Val Gly Ala Ala
 35 40 45
 Ser Arg Lys Gly Ile Leu Met Lys Gly Val His Val Leu Glu Gly Ala
 50 55 60
 Tyr Pro Asn
 65

(2) INFORMATION FOR SEQ ID NO:528:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 323 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

Val	Gln	His	Phe	Asn	Phe	Leu	Tyr	Lys	Asp	Ser	Leu	Phe	Ser	Ile	Ala	
1				5					10					15		
Leu	Phe	Thr	Phe	Ile	Ile	Ala	Leu	Val	Ile	Leu	Leu	Glu	Gln	Ala	Arg	
			20					25					30			
Ala	Tyr	Phe	Thr	Arg	Lys	Arg	Asn	Lys	Lys	Phe	Leu	Gln	Lys	Phe	Ala	
		35					40					45				
Gln	Asn	Gln	Asn	Ala	Tyr	Ala	Ser	Ser	Glu	Asn	Leu	Asp	Glu	Leu	Leu	
	50					55					60					
Lys	His	Ala	Lys	Ile	Ser	Ser	Leu	Met	Phe	Leu	Ala	Arg	Ala	Tyr	Ser	
65					70					75					80	
Lys	Ala	Asp	Val	Glu	Met	Ser	Ile	Glu	Ile	Leu	Lys	Gly	Leu	Leu	Asn	
				85					90					95		
Arg	Pro	Leu	Lys	Asp	Glu	Glu	Lys	Ile	Ala	Val	Leu	Asp	Leu	Leu	Ala	
			100					105					110			
Lys	Asn	Tyr	Phe	Ser	Val	Gly	Tyr	Leu	Gln	Lys	Thr	Lys	Asp	Thr	Val	
		115					120						125			
Lys	Glu	Ile	Leu	Arg	Phe	Ser	Pro	Arg	Asn	Val	Glu	Ala	Leu	Leu	Lys	
	130					135					140					
Leu	Leu	His	Ala	Tyr	Glu	Leu	Glu	Lys	Asp	Tyr	Ser	Lys	Ala	Leu	Glu	
145					150					155					160	
Thr	Leu	Glu	Cys	Leu	Glu	Glu	Leu	Glu	Val	Pro	Lys	Ile	Glu	Thr	Ile	
				165					170					175		
Lys	Asn	Tyr	Leu	Tyr	Leu	Met	His	Leu	Ile	Glu	Asn	Lys	Glu	Asp	Ala	
			180					185					190			
Ala	Lys	Ile	Leu	His	Val	Ser	Lys	Ala	Ser	Leu	Asp	Leu	Lys	Lys	Ile	
		195					200					205				
Ala	Leu	Asn	His	Leu	Lys	Ser	His	Asp	Glu	Asn	Leu	Phe	Trp	Gln	Glu	
	210					215					220					
Ile	Asp	Thr	Thr	Glu	Arg	Leu	Glu	Asn	Val	Ile	Asp	Leu	Leu	Trp	Asp	
225					230					235					240	
Met	Asn	Ile	Pro	Ala	Phe	Ile	Leu	Glu	Lys	His	Ala	Leu	Leu	Gln	Asp	
				245					250					255		
Ile	Ala	Arg	Ser	Gln	Gly	Leu	Leu	Leu	Asp	His	Lys	Pro	Cys	Gln	Ile	
			260					265						270		

Phe Glu Leu Glu Val Leu Arg Ala Leu Leu His Ser Pro Ile Lys Ala
 275 280 285
 Ser Leu Thr Phe Glu Tyr Arg Cys Lys His Cys Lys Gln Ile Phe Pro
 290 295 300
 Phe Glu Ser His Arg Cys Pro Val Cys Tyr Gln Leu Ala Phe Met Asp
 305 310 315 320
 Met Val Ala

(2) INFORMATION FOR SEQ ID NO:529:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

Met Glu His Leu Thr Arg Gly Ile Lys His
 1 5 10

(2) INFORMATION FOR SEQ ID NO:530:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...12
- (D) OTHER INFORMATION: /note= "penicillin-binding protein 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

Val Val Ile Leu Gly Ser His Gly Lys Glu Glu Tyr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

Met	Lys	Lys	Val	Ile	Val	Ala	Leu	Gly	Val	Leu	Ala	Phe	Ala	Asn	Val
1				5					10					15	
Leu	Met	Ala	Thr	Asp	Val	Lys	Ala	Leu	Val	Lys	Gly	Cys	Ala	Ala	Cys
			20					25					30		
His	Gly	Val	Lys	Phe	Glu	Lys	Lys	Ala	Leu	Gly	Lys	Ser	Lys	Ile	Val
		35					40					45			
Asn	Met	Met	Ser	Glu	Lys	Glu	Ile	Glu	Glu	Asp	Leu	Met	Ala	Phe	Lys
	50					55				60					
Ser	Gly	Ala	Asn	Lys	Asn	Pro	Val	Met	Thr	Arg	Lys	Leu	Lys	Asn	
65					70					75					

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...95
- (D) OTHER INFORMATION: /note= "influenzae type B
lipooligosaccharide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

Met	Gly	Ile	Ala	Thr	Ser	Leu	Ile	Ser	Glu	Val	Ser	Lys	Phe	Tyr	Tyr
1					5				10					15	

Ala	Leu	Lys	Tyr	His	Ala	Lys	Phe	Met	Ser	Leu	Gly	Glu	Leu	Gly	Cys
		20						25					30		
Tyr	Ala	Ser	His	Tyr	Ser	Leu	Trp	Gln	Lys	Cys	Ile	Glu	Leu	Asn	Glu
		35					40					45			
Ala	Ile	Cys	Ile	Leu	Glu	Asp	Asp	Ile	Thr	Leu	Lys	Glu	Asp	Phe	Lys
	50					55					60				
Glu	Gly	Leu	Asp	Phe	Leu	Glu	Lys	His	Ile	Gln	Glu	Leu	Gly	Tyr	Ala
65					70					75					80
Arg	Leu	Met	His	Leu	Leu	Tyr	Asp	Ala	Ser	Val	Lys	Ser	Glu	Pro	
				85					90					. 95	

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

Met	Gln	Asp	Leu	Asp	Asn	Asn	Met	Ser	Leu	Asp	Thr	Ala	His	Asn	Thr
1				5					10					15	
Leu	Ser	Ser	Asn	Gly	Lys	Asn	Ile	Thr	Ile	Ala	Gly	Val	Val	Lys	Ala
			20					25					30		
Leu	Gln	Lys	Ile	Gly	Val	Ser	Ala	Lys	Gly	Met	Val	Ser	Ile	Leu	Gln
		35					40					45			
Ala	Leu	Lys	Lys	Ser	Gly	Ala	Ile	Ser	Ala	Lys	Trp	Arg	Tyr	Tyr	Asp
	50					55					60				
Lys	Gln	Gln													
65															

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

Met Gln Asp Leu Asp Asn Asn Met Ser Leu Asp Thr Ala His Asn Thr
1 5 10 15
Leu Ser Ser Asn Gly Lys Asn Ile Thr Ile Ala Gly Val Val Lys Ala
20 25 30
Leu Gln Lys Ile Gly Val Ser Ala Lys Gly Met Val Ser Ile Leu Gln
35 40 45
Ala Leu Lys Lys Ser Gly Ala Ile Ser Ala Lys Trp Arg Tyr Tyr Asp
50 55 60
Lys Gln Gln
65

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

Val Gln Pro Met Lys Ser Lys Lys Leu Tyr Leu Ala Leu Ile Ile Gly
1 5 10 15
Val Leu Leu Ala Phe Leu Thr Leu Ser Ser Trp Leu Gly Asn Ser Gly
20 25 30
Leu Val Gly Arg Phe Gly Val Trp Phe Ala Ala Ile Asn Lys Lys Tyr
35 40 45
Phe Gly Tyr Leu Ser Leu Ile Asn Leu Pro Tyr Leu Ala Trp Val Leu
50 55 60
Phe Leu Leu Tyr Arg Ala Lys Asn Pro Phe Thr Glu Ile Val Leu Glu
65 70 75 80
Lys Thr Leu Gly His Leu Leu Gly Ile Leu Ser Leu Leu Phe Leu Gln
85 90 95
Ser Ser Leu Leu Asn Gln Gly Glu Ile Gly Asn Ser Ala Arg Leu Phe
100 105 110

Leu His Pro Phe Ile Gly Asp Phe Gly Leu Tyr Val Leu Ile Met Leu
 115 120 125
 Met Val Val Ile Ser Tyr Leu Ile Leu Phe Lys Leu Pro Pro Lys Ser
 130 135 140
 Val Phe Tyr Pro Tyr Met Asn Lys Thr Gln Ser Leu Leu Lys Glu Ile
 145 150 155 160
 Tyr Lys Gln Cys Leu Gln Ala Phe Ser Pro Asn Phe Ser Leu Lys Lys
 165 170 175
 Glu Gly Phe Glu Asn Thr Pro Ser Asp Ser Gln Lys Lys Glu Thr Asn
 180 185 190
 Asn Asp Lys Glu Lys Glu Asn Leu Lys Glu Asn Pro Ile Asp Glu Asn
 195 200 205
 His Asn Thr Pro Asn Glu Glu Ser Phe Leu Ala Ile Pro Thr Pro Tyr
 210 215 220
 Asn Thr Thr Leu Asn Asn Ser Glu Pro Gln Glu Gly Leu Val Gln Ile
 225 230 235 240
 Ser Pro His Pro Pro Thr His Tyr Thr Ile Tyr Pro Lys Arg Asn Arg
 245 250 255
 Phe Asp Asp Leu Thr Asn Pro Thr Leu Lys Glu Pro Lys Gln Glu Thr
 260 265 270
 Lys Glu Arg Glu Pro Thr Leu Lys Lys Glu Thr Pro Thr Thr Leu Lys
 275 280 285
 Pro Ile Met Pro Ile Ser Ala Ser Thr Gln Lys Ile Met Thr Lys Gln
 290 295 300
 Lys Thr Thr Lys Pro Leu Thr Thr Pro
 305 310

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

Val Met Leu Ser Arg Asp Ile Val Gln Tyr Ser Lys Ile Arg Thr Glu

1					5					10					15				
Leu	Tyr	Ala	Tyr	Leu	Thr	Tyr	Leu	Phe	Ser	His	Asn	Ile	Arg	Asn	His				
			20				25						30						
Leu	Pro	Glu	Ile	Thr	Leu	Asp	Tyr	Leu	Asn	Arg	Gln	Ile	Ser	Lys	Met				
			35				40						45						
Gln	Ala	Glu	Ile	Lys	Met	Ala	Lys	Ser	Phe	Phe	Val	Leu	Asp	Ala	Lys				
			50				55						60						
Gly	Met	Leu	Met	Leu	Lys	Pro	Ser	Gln	Phe	Lys	Glu	Gln	Gly	His	Lys				
			65				70						75			80			
Glu	Gly	Leu	Leu	Glu	His	Asp	Leu	Thr	Glu	Gly	Ile	Glu	Leu	Glu	Ser				
			85						90						95				
His	Val	Ser	Phe	Ser	Asp	Lys	Tyr	Tyr	Phe	Tyr	Gln	Ala	Val	Asn	Glu				
			100						105						110				
Lys	Arg	Cys	Ile	Leu	Thr	Asp	Pro	Tyr	Pro	Ser	Lys	Lys	Gly	Asn	His				
			115			120						125							
Leu	Val	Val	Ser	Ala	Ser	Tyr	Pro	Val	Tyr	Asp	Gln	Asn	Asn	Asp	Leu				
			130			135						140							
Ala	Phe	Val	Val	Cys	Leu	Gln	Ile	Pro	Leu	Arg	Val	Ala	Ile	Glu	Ile				
			145			150						155			160				
Ser	Ser	Pro	Ser	Lys	Tyr	Phe	Lys	Thr	Phe	Ser	Glu	Gly	Ser	Met	Val				
			165						170						175				
Met	Tyr	Phe	Met	Ile	Ser	Ile	Met	Leu	Thr	Leu	Val	Ser	Leu	Leu	Leu				
			180						185						190				
Phe	Val	Lys	Cys	Ile	Ser	Ser	Phe	Trp	Thr	Ala	Ile	Val	His	Phe	Ser				
			195			200						205							
Ser	Phe	Asp	Ile	Lys	Glu	Val	Phe	His	Pro	Ile	Val	Leu	Leu	Thr	Leu				
			210			215						220							
Ala	Leu	Ala	Thr	Phe	Asp	Leu	Val	Lys	Ala	Ile	Phe	Glu	Glu	Glu	Val				
			225			230						235			240				
Leu	Gly	Lys	Asn	Ser	Gly	Asp	Asn	His	His	Ala	Ile	His	Arg	Thr	Met				
			245						250						255				
Ile	Arg	Phe	Leu	Gly	Ser	Ile	Ile	Ile	Ala	Leu	Ala	Ile	Glu	Ala	Leu				
			260						265						270				
Met	Leu	Val	Phe	Lys	Phe	Ser	Val	Ser	Glu	Pro	Asp	Lys	Ile	Thr	Tyr				
			275			280						285							
Ala	Val	Tyr	Leu	Ala	Ile	Gly	Val	Ala	Val	Leu	Leu	Ile	Ser	Leu	Ala				
			290			295						300							
Ile	Tyr	Val	Lys	Phe	Ala	Tyr	Ser	Val	Leu	Pro	Lys	Arg	Glu	Arg					
			305			310						315							

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

Met	Val	Ile	His	Glu	Lys	Ile	Lys	Ser	Arg	Phe	Ser	Arg	Asn	Trp	Ser	
1				5					10					15		
Leu	Arg	Asn	Arg	Gly	Arg	His	Phe	Ala	Ser	Ser	Ser	Val	Tyr	Phe	Phe	
			20					25					30			
Ser	Leu	Leu	Val	Ile	Thr	Ala	Val	Asn	Arg	Ser	Ser	Ala	Val	Ala	Trp	
			35				40					45				
Leu	Leu	Met	Pro	Glu	His	Leu	Ile	Gly	Trp	Phe	Leu	Ile	Ser	Phe	Ser	
			50				55				60					
Gly	Glu	Phe	Val	Ala	Asp	Met	Ala	Phe	Gly	Lys	Lys	Ser	Lys	Ile	Phe	
65					70				75					80		
Lys	Thr	Arg	Phe	Gly	Ile	Ser	Ile	Val	Ser	Gly	Val	Ser	Leu	Leu	Leu	
				85				90						95		
Gly	Ala	Tyr	Gln	Arg	Phe	Tyr	Phe	Leu	Tyr	Gly	Leu	Ala	Leu	Leu	Ile	
			100					105					110			
Gly	Gly	Leu	Ser	Phe	Leu											
					115											

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

Leu His Pro Leu Ala Asp Val Phe Val Val Asn Asp Lys Arg Xaa Val
 1 5 10 15
 Leu Ala Met Val Xaa Met Leu Ile Xaa Ser Leu Ala Asn Ile Phe Phe
 20 25 30
 Asn Tyr Leu Phe Ile Phe Xaa Leu Glu Val Gly Val Gln Gly Xaa Ala
 35 40 45
 Ile Val Thr Val Ile Gly His Ala Ile Gly Gly Leu Val Leu Met Gln
 50 55 60
 His Phe Trp Arg Lys Lys Gly Glu Leu Tyr Phe Ile Lys Leu Ile Phe
 65 70 75 80
 Phe Ile Phe Ser His Phe Phe Ser
 85

(2) INFORMATION SEQ ID NO:539:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

Met Phe Lys Ser Arg Leu Asn Ser Trp Ile Leu Leu Gly Ile Leu Gly
 1 5 10 15
 Val Leu Val Val Val Phe Trp Asp Val Ile Lys Tyr Lys Ile Glu Asp
 20 25 30
 Leu Gln His Asp His Tyr Leu Ser Gln Val Lys Glu Arg Glu Glu Tyr
 35 40 45
 Tyr Lys Asn His Ile Glu Glu Ala Leu Lys Lys Asp Ser Glu Cys Phe
 50 55 60
 Glu Lys Gly Gly Asp Lys Val Asp Cys Ser Ala Ala Met Arg Ile Ala
 65 70 75 80
 Ala Gly Glu Arg Asn Arg Arg Met Leu Glu Ile Lys
 85 90

(2) INFORMATION FOR SEQ ID NO:540:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

Met	Val	Phe	Trp	Gly	Ala	Val	Phe	Phe	Leu	Trp	Asp	Arg	Thr	Ala	Trp	
1				5					10					15		
Lys	Arg	Leu	Met	Val	Phe	Leu	Asn	Ser	Leu	Xaa	Xaa	Met	Leu	Ala	Ala	
			20					25					30			
Leu	Ser	Leu	Gly	Ser	Phe	Leu	Gly	Ala	Trp	Ile	Lys	Asn	Glu	Ala	His	
		35					40					45				
Thr	Thr	Gln	Ile	Val	Leu	Ile	Ser	Ser	Leu	Pro	Leu	Ile	Phe	Met	Met	
	50					55					60					
Gly	Phe	Val	Trp	Pro	Phe	Glu	Ser	Leu	Pro	Ser	Tyr	Leu	Gln	Val	Phe	
65					70					75				80		
Val	Gln	Ile	Val	Pro	Ala	Tyr	His	Gly	Ile	Ser	Leu	Leu	Gly	Arg	Leu	
				85					90					95		
Asn	Gln	Met	His	Ala	Glu	Phe	Ile	Asp	Val	Ser	Ile	His	Phe	Tyr	Ala	
		100						105					110			
Leu	Ile	Ala	Ile	Phe	Ile	Val	Ser	Phe	Ile	Gly	Cys	Val	Phe	Lys	Leu	
		115					120					125				
Ser	Ser	Leu	Lys	Lys	Ala	Cys	Glu	Asn	Ala							
	130						135									

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

Met Leu Arg Lys Asn Ile Leu Ala Tyr Tyr Gly Ala Asn Phe Leu Leu

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

Met	His	Glu	Gln	Gly	Ser	Ile	Ser	Phe	Ile	Gly	Glu	Gln	Gly	Ala	Lys	
1				5					10					15		
Arg	Leu	Leu	Tyr	Ile	Leu	Tyr	Lys	Leu	Ala	Phe	Asn	Ala	Lys	Ser	Asn	
			20					25					30			
Lys	Ile	Ala	Leu	Asp	Arg	His	Tyr	Ala	Lys	Met	Phe	Leu	Gln	Val	Val	
		35					40					45				
Ala	Arg	Thr	Leu	Ile	Lys	Asn	Val	Asn	Ile	Leu	Glu	Glu	Gln	Gly	Phe	
	50					55					60					
Ile	Glu	Val	Ile	Lys	Gly	Lys	Gln	Arg	Tyr	Leu	Tyr	Val	Tyr	Leu	Lys	
65					70					75					80	
Asp	Tyr	Arg	Glu	Leu	Glu	Cys	Leu	Val	Lys	Ser	Lys	Met	Ala	Lys	Tyr	
				85					90					95		
Val	Met	Tyr	Leu	Arg	Gln	Phe	Phe	Asp	Tyr	Leu	Asp	Arg	Lys	Arg	Arg	
			100					105					110			
Tyr	Gly	Phe	Asp	Phe	Thr	Leu	Lys	Asn	Leu	Ala	Phe	Ala	Lys	Thr	Lys	
		115					120					125				
Glu	Ser	Leu	Pro	Arg	His	Leu	Asn	Asp	Lys	Asp	Leu	Lys	Ser	Phe	Leu	
		130				135					140					
Lys	Thr	Leu	Leu	Asp	Tyr	Lys	Pro	Ala	Thr	Ser	Phe	Glu	Lys	Arg	Asn	
145					150				155						160	
Lys	Cys	Ile	Leu	Leu	Ile	Val	Ile	Leu	Gly	Gly	Leu	Arg	Lys	Cys	Glu	
			165						170					175		
Val	Leu	Asn	Ile	Glu	Leu	Lys	His	Ile	Gln	Val	Glu	Glu	Gln	Asn	Tyr	
			180					185					190			
Ser	Ile	Leu	Ile	Gln	Gly	Lys	Gly	Arg	Lys	Glu	Arg	Lys	Ala	Tyr	Ile	
		195					200					205				
Lys	Lys	Ser	Leu	Leu	Glu	Pro	Ser	Leu	Asn	Ala	Trp	Ile	Ser	Asp	Asp	
		210				215					220					
Tyr	Arg	Leu	Lys	Tyr	Phe	Asn	Gly	Ala	Tyr	Leu	Phe	Lys	Lys	Asp	Lys	
225					230					235					240	
Gln	Lys	Ser	Gln	Asn	Ser	Leu	Thr	Leu	Tyr	Asn	Leu	Ser	Pro			

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...185
- (D) OTHER INFORMATION: /note= "weak homology to [Rhodo. capsulatus] membrane-associated c-type cytochrome"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

Val	Val	Phe	Lys	Ile	Leu	Ser	Leu	Trp	Leu	Gly	Val	Phe	Cys	Phe	Leu	1	5	10	15
Arg	Ala	Thr	His	Leu	Tyr	Leu	Gly	Glu	Glu	Pro	Lys	Tyr	Lys	Asp	Asn	20	25	30	
Phe	Thr	His	Phe	Glu	Tyr	Ala	Asn	Pro	Asn	Ala	Arg	Lys	Gly	Gly	Val	35	40	45	
Leu	Arg	Asn	Asp	Ala	Ile	Gly	Thr	Phe	Asp	Ser	Leu	Asn	Pro	Phe	Ala	50	55	60	
Leu	Lys	Gly	Thr	Lys	Ala	Glu	Gly	Leu	Asp	Leu	Ile	Tyr	Asp	Thr	Leu	65	70	75	80
Met	Val	Gln	Ser	Leu	Asp	Glu	Pro	Phe	Ala	Glu	Tyr	Pro	Leu	Ile	Ala	85	90	95	
Lys	Asp	Ala	Glu	Val	Ala	Lys	Asp	Asn	Ser	Tyr	Val	Ile	Phe	Thr	Leu	100	105	110	
Asp	Lys	Arg	Ala	Arg	Phe	Ser	Asn	Asn	Ala	Pro	Ile	Leu	Ala	Ser	Asp	115	120	125	
Val	Lys	Phe	Ser	Phe	Asp	Thr	Ile	Met	Lys	Leu	Gly	Ser	Pro	Leu	Tyr	130	135	140	
Arg	Gln	Tyr	Tyr	Gln	Asp	Val	Lys	Lys	Ala	Val	Ile	Leu	Asp	Lys	His	145	150	155	160
His	Val	Lys	Phe	Ile	Tyr	Lys	Thr	Thr	Glu	Asn	Lys	Glu	Leu	Pro	Leu	165	170	175	

Ile Leu Gly Gln Leu Gln Ile Phe Ser
 180 185

(2) INFORMATION FOR SEQ ID NO:544:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

Val Ala Met Ile Asp Cys Ala Ile Ile Gly Gly Gly Pro Ala Gly Leu
 1 5 10 15
 Ser Ala Gly Leu Tyr Ala Thr Arg Gly Gly Val Lys Asn Ala Val Leu
 20 25 30
 Phe Glu Lys Gly Met
 35

(2) INFORMATION FOR SEQ ID NO:545:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

Leu Tyr Pro Pro Gly Ser Val Val Lys Met Gly Val Gly Leu Ser Phe
 1 5 10 15
 Leu Glu Asn Leu His Ile Thr Glu Asn Thr Thr Ile Pro Thr Pro Pro
 20 25 30
 Phe Ile Glu Val Gly Lys Arg Lys Phe Arg Asp Trp Lys Lys Thr Gly
 35 40 45
 His Gly Asn Ser Asn Leu Tyr Lys Ala Ile Arg Glu Ser Val Asp Val
 50 55 60

Tyr Phe Tyr Lys Phe Gly Leu Glu Ile Ser Ile Glu Xaa Leu Ser Lys
 65 70 75 80

Xaa Phe Lys Xaa Ser Gly Leu Trp Gly Lys Asn Gly Arg
 85 90

(2) INFORMATION FOR SEQ ID NO:546:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 182 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

Val	Gly	Lys	Ser	Leu	Arg	Tyr	Ser	Leu	Asn	Leu	Asp	Leu	Asn	Gln	Lys	1	5	10	15
Ala	Asp	Leu	Phe	Phe	Thr	Glu	Leu	Glu	Pro	Thr	Gly	Leu	Thr	Leu	Ser	20	25	30	
Pro	Ile	Met	Lys	Arg	Phe	Thr	Ile	Lys	Gly	Asp	Phe	Asp	Ser	Gly	Leu	35	40	45	
Lys	Ser	Tyr	Asp	Met	Ser	Tyr	Met	Tyr	Ala	Ser	Leu	Gln	Ala	Ile	Ser	50	55	60	
Ala	Ile	Arg	Arg	Leu	Pro	Leu	Gly	Leu	Tyr	Asp	Gly	Val	His	Val	Tyr	65	70	75	80
Ser	Lys	Thr	Pro	Met	Lys	Asp	Ile	Glu	Lys	Leu	Arg	Asn	Ala	Leu	Lys	85	90	95	
Thr	Ile	Asn	His	His	Gly	Ile	Gly	Ile	Glu	Gly	Trp	Trp	Gln	Gln	Asn	100	105	110	
Gly	Asn	Phe	Phe	Ser	Ala	Met	Glu	Leu	Glu	Lys	Arg	Ala	Leu	Phe	Ile	115	120	125	
Val	Leu	Met	Leu	Ile	Ile	Leu	Met	Ala	Ser	Leu	Asn	Ile	Ile	Ser	Ser	130	135	140	
Leu	Leu	Met	Val	Val	Met	Asn	Arg	Arg	Lys	Glu	Ile	Ala	Leu	Leu	Phe	145	150	155	160
Ser	Met	Gly	Ser	Ser	Gln	Lys	Glu	Ile	Gln	Lys	Thr	Phe	Phe	Tyr	Leu	165	170	175	
Gly	Asn	Ile	Ile	Ser	Leu														

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

```

Met Lys Lys Thr Phe Leu Ile Ala Leu Ala Leu Thr Ala Ser Leu Ile
 1                               5              10              15

Gly Ala Glu Asn Thr Lys Trp Asp Tyr Lys Asn Lys Glu Asn Gly Pro
                20              25              30

His Arg Trp Asp Lys Leu His Lys Asp Phe Glu Val Cys Lys Ser Gly
        35              40              45

Lys Ser Gln Ser Pro Ile Asn Ile Glu His Tyr Tyr His Thr Gln Asp
 50              55              60

Lys Ala Asp Leu Gln Phe Lys Tyr Ala Ala Ser Lys Pro Lys Ala Val
65              70              75              80

Phe Phe Thr His His Thr Leu Lys Ala Ser Phe Glu Pro Thr Asn His
        85              90              95

Ile Asn Tyr Arg Gly His Asp Tyr Val Leu Asp Asn Val His Phe His
        100             105             110

Ala Pro Met Glu Phe Leu Ile Asn Asn Lys Thr Arg Pro Leu Ser Ala
        115             120             125

His Phe Val His Lys Asp Ala Lys Gly Arg Leu Leu Val Leu Ala Ile
        130             135             140

Gly Phe Glu Glu Gly Lys Glu Asn Pro Asn Leu Asp Pro Ile Leu Glu
145             150             155             160

Gly Ile Gln Lys Lys Gln Asn Leu Lys Glu Val Ala Leu Asp Ala Phe
        165             170             175

Leu Pro Lys Ser Ile Asn Tyr Tyr His Phe Asn Gly Ser Leu Thr Ala
        180             185             190

Pro Pro Cys Thr Glu Gly Val Ala Trp Phe Val Ile Glu Glu Pro Leu
        195             200             205

```

Glu Val Ser Ala Lys Gln Leu Ala Glu Ile Lys Lys Arg Met Lys Asn
 210 215 220
 Ser Pro Asn Gln Arg Pro Val Gln Pro Asp Tyr Asn Thr Val Ile Ile
 225 230 235 240
 Lys Ser Ser Ala Glu Thr Arg
 245

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...422
- (D) OTHER INFORMATION: /note= "UDP-N-ACETYLMURAMOYLALANINE--D-GLUTAMATELIGASE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

Met Lys Ile Ser Leu Leu Gly His Gly Lys Thr Thr Leu Ala Leu Gly
 1 5 10 15
 Arg Phe Phe Lys Lys Asn His Asn Glu Val Lys Phe Phe Asp Asp Lys
 20 25 30
 Phe Pro Ala Phe Phe Lys Asp Ser Glu Gly Phe Leu Cys Tyr Pro Ser
 35 40 45
 Lys Asp Phe Asn Pro Asn Asp Ser Gln Leu Glu Ile Val Ser Pro Gly
 50 55 60
 Ile Ser Phe Thr His Pro Leu Val Met Lys Ala Lys His Leu Met Ser
 65 70 75 80
 Glu Tyr Asp Tyr Ile Asp Ser Leu Phe Asp His Ser Phe Thr Pro Thr
 85 90 95
 Met Ile Ser Ile Ser Gly Thr Asn Gly Lys Thr Thr Thr Thr Glu Met
 100 105 110
 Leu Thr Thr Leu Leu Glu Asp Phe Lys Ala Val Ser Gly Gly Asn Ile
 115 120 125
 Gly Thr Pro Leu Ile Glu Leu Phe Glu Lys Arg Ser Pro Leu Trp Val
 130 135 140

Leu	Glu	Thr	Ser	Ser	Phe	Ser	Leu	His	Tyr	Thr	Asn	Lys	Ala	Tyr	Pro	145	150	155	160
Leu	Ile	Tyr	Leu	Leu	Ile	Asn	Val	Glu	Ala	Asp	His	Leu	Thr	Trp	His	165	170	175	
Cys	Asn	Phe	Glu	Asn	Tyr	Leu	Asn	Ala	Lys	Leu	Lys	Val	Leu	Thr	Leu	180	185	190	
Met	Pro	Lys	Thr	Ser	Leu	Ala	Ile	Leu	Pro	Leu	Lys	Phe	Lys	Glu	His	195	200	205	
Pro	Ile	Val	Gln	Asn	Ser	Gln	Ala	Gln	Lys	Ile	Phe	Phe	Asp	Lys	Ser	210	215	220	
Glu	Glu	Val	Leu	Glu	Cys	Leu	Lys	Ile	Pro	Ser	Asn	Ala	Leu	Phe	Phe	225	230	235	240
Lys	Gly	Ala	Phe	Leu	Leu	Asp	Ala	Ala	Leu	Ala	Leu	Leu	Val	Tyr	Glu	245	250	255	
Gln	Phe	Leu	Lys	Ile	Lys	Asn	Leu	Lys	Trp	Gln	Asp	Tyr	Arg	Glu	Asn	260	265	270	
Ala	Leu	Lys	Arg	Leu	Asn	Ala	Phe	Lys	Ile	Gly	Ser	His	Lys	Met	Glu	275	280	285	
Glu	Phe	Arg	Asp	Lys	Gln	Gly	Arg	Leu	Trp	Val	Asp	Asp	Ser	Lys	Ala	290	295	300	
Thr	Asn	Ile	Asp	Ala	Thr	Leu	Gln	Ala	Leu	Lys	Thr	Phe	Lys	Asn	Gln	305	310	315	320
Lys	Ile	His	Leu	Ile	Leu	Gly	Gly	Asp	Ile	Lys	Gly	Val	Asn	Leu	Thr	325	330	335	
Pro	Leu	Phe	Glu	Glu	Phe	Lys	Asn	Tyr	Lys	Ile	Ser	Leu	Tyr	Ala	Ile	340	345	350	
Gly	Ser	Ser	Ala	Ser	Ile	Ile	Gln	Ala	Leu	Ala	Leu	Glu	Phe	Asn	Val	355	360	365	
Ser	Cys	Gln	Val	Cys	Leu	Lys	Leu	Glu	Lys	Ala	Val	Gln	Glu	Ile	Lys	370	375	380	
Ser	Val	Leu	Leu	Gln	Asn	Glu	Val	Ala	Leu	Leu	Ser	Pro	Ser	Ala	Ala	385	390	395	400
Ser	Leu	Asp	Gln	Phe	Ser	Ser	Tyr	Lys	Glu	Arg	Gly	Glu	Lys	Phe	Lys	405	410	415	
Ala	Phe	Val	Leu	Lys	Asp											420			

(2) INFORMATION FOR SEQ ID NO:549:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

```
Met Ala His His Xaa Glu Gln His Gly Gly His His His His His His
1           5           10           15
His Thr His His His His Tyr His Gly Gly Glu His His His His His
20           25           30
His Ser Ser His His Glu Glu Gly Cys Cys Ser Thr Ser Asp Ser His
35           40           45
His Gln Glu Glu Gly Cys Cys His Gly Xaa His Glu
50           55           60
```

(2) INFORMATION FOR SEQ ID NO:550:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...54
 (D) OTHER INFORMATION: /note= "iron(II) transport system"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

```
Met Lys Glu Ile Ile Val Ala Leu Val Gly Gln Pro Asn Val Gly Lys
1           5           10           15
Ser Ser Leu Ile Asn Ala Leu Ser Asn Thr His Leu Lys Val Gly Asn
20           25           30
Phe Thr Glu Val Thr Val Asp Lys Met Glu Val Ser Leu Ile Gln Lys
35           40           45
Asp His Gln Ile Asn Ser
```


(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

```

Leu Val Lys Ile Arg Leu Phe Asp Phe Thr Ile Arg Leu Phe Lys Pro
1           5           10           15

Glu Phe His Ile Phe Asp Phe Leu Lys Gly Ile Arg Val Leu Met Ile
20           25           30

Glu Trp Met Gln Asn His Arg Lys Tyr Leu Val Val Thr Ile Trp Ile
35           40           45

Ser Thr Ile Ala Phe Ile Ala Ala Gly Met Ile Gly Trp Gly Gln Tyr
50           55           60

Ser Phe Ser Leu Asp Ser Asp Ser Ala Ala Lys Val Gly Gln Ile Lys
65           70           75           80

Ile Ser Gln Glu Glu Leu Ala Gln Glu Tyr Arg Arg Leu Lys Asp Ala
85           90           95

Tyr Ala Glu Ser Ile Pro Asp Phe Lys Glu Leu Thr Glu Asp Gln Ile
100          105          110

Lys Ala Met His Leu Glu Lys Ser Ala Leu Asp Ser Leu Ile Asn Gln
115          120          125

Ala Leu Leu Arg Asn Phe Ala Leu Asp Leu Gly Leu Gly Ala Thr Lys
130          135          140

Gln Glu Val Ala Lys Glu Ile Arg Lys Thr Asn Val Phe Gln Lys Asp
145          150          155          160

Gly Val Phe Asp Glu Glu Leu Tyr Lys Asn Ile Leu Lys Gln Ser His
165          170          175

Tyr Arg Pro Lys His Phe Glu Glu Ser Val Glu Arg Leu Leu Ile Leu
180          185          190

Gln Lys Ile Ser Ala Leu Phe Pro Lys Thr Thr Thr Pro Leu Glu Gln
195          200          205

```

Ser Ser Leu Ser Leu Trp Ala Lys Leu Gln Asp Lys Leu Asp Ile Leu
 210 215 220
 Ile Leu Asn Pro Asn Asp Val Lys Ile Ser Leu Asn Glu Glu Glu Met
 225 230 235 240
 Lys Lys Tyr Tyr Glu Asn His Arg Lys Asp Phe Lys Lys Pro Thr Ser
 245 250 255
 Phe Lys Thr Arg Ser Leu Tyr Phe Asp Ala Ser Leu Glu Lys Thr Asp
 260 265 270
 Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser Tyr Leu
 275 280 285
 Asp Xaa Xaa Gly Glu Ile Thr Gly Phe
 290 295

(2) INFORMATION FOR SEQ ID NO:552:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

Met Val Lys His Tyr Leu Phe Met Ala Val Ser Gln Val Phe Phe Ser
 1 5 10 15
 Phe Phe Leu Val Leu Phe Phe Ile Ser Ser Ile Val Leu Leu Ile Ser
 20 25 30
 Ile Ala Ser Val Thr Leu Val Ile Lys Val Ser Phe Leu Asp Leu Val
 35 40 45
 Gln Leu Phe Leu Tyr Ser Leu Pro Gly Thr Ile Phe Phe Ile Leu Pro
 50 55 60
 Ile Thr Phe Phe Ala Ala Xaa Arg Leu Gly Xaa Ser Arg Leu Ser Tyr
 65 70 75 80
 Asp His Glu Leu Leu Val Phe Phe Leu Xaa
 85 90

(2) INFORMATION FOR SEQ ID NO:553:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

Val	His	Arg	Phe	Ser	Arg	Asn	Pro	Cys	Ala	Ser	Cys	Asn	Arg	Ala	Arg
1				5				10						15	
Ser	Cys	Ser	Arg	Leu	Ser	Arg	Ser	Leu	Val	Ser	Ala	Val	Thr	Trp	Trp
			20					25					30		
Leu	Ser	Leu	Ser	Phe	Ser	Val	Val	Ser	Ala	Leu	Phe	Ser	Leu	Val	Ser
		35					40					45			
Ser	Val	Ile	Leu	Trp	Val	Ser	Ser	Val	Phe	Ser	Leu	Phe	Ser	Leu	Ser
	50					55					60				
Phe	Ser	Val	Val	Asn	Ser	Leu	Phe	Ser	Ser	Val	Ser	Arg	Ser	Leu	Ala
65				70					75					80	
Ala	Asn	Lys	Arg	Val	Phe	Ser	Leu	Ala	Lys	Met	Ser	Phe	Ser	Val	Phe
				85					90					95	
Ser	Ser	Ala	Phe	Ser	Leu	Val	Ser	Leu	Leu	Leu	Phe	Cys	His	Asn	
		100						105					110		

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

Met	Gln	Lys	Met	Gly	Val	Val	Ser	Tyr	Ser	Val	Phe	Gln	Ala	Phe	Glu
1				5				10						15	
Lys	Ala	Leu	Ser	Arg	Phe	Lys	Glu	Gly	Val	Val	Leu	Ile	Val	Asp	Ser
			20					25					30		
Leu	Arg	Arg	Leu	Ile	Met	Gly	Ser	Ala	Ser	Val	Lys	Glu	Leu	Ser	Gly
			35				40					45			

Val Ile Gly Ile Val Gly Ala Leu Ser His Ala Asn Ser Val Ser Met
50 55 60

Leu Leu Leu Phe Gly Ala Phe Leu Ser Ile Asn Leu Gly Ile Leu Asn
65 70 75 80

Leu Leu Pro Ile Pro Ala Leu Asp Gly Ala Gln Met Leu Gly Val Val
85 90 95

Phe Lys Asn Ile Phe His Ile Ala Leu Pro Thr Pro Ile Gln Asn Ala
100 105 110

Leu Trp Leu Val Gly Val Gly Phe Leu Val Phe Val Met Phe Leu Gly
115 120 125

Leu Phe Asn Asp Ile Thr Arg Leu Leu
130 135

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...124
- (D) OTHER INFORMATION: /note= "H⁺-transporting ATP synthase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

Val Met Ala Leu Leu Lys Ile Ser Val Val Val Pro Glu Gly Glu Val
1 5 10 15

Tyr Thr Gly Glu Val Lys Ser Val Val Leu Pro Gly Val Glu Gly Glu
20 25 30

Phe Gly Val Leu Tyr Gly His Ser Asn Met Ile Thr Leu Leu Gln Ala
35 40 45

Gly Val Val Glu Ile Glu Thr Glu Asn Gln Lys Glu His Ile Ala Ile
50 55 60

Asn Trp Gly Tyr Ala Glu Val Thr Asn Glu Arg Val Asp Ile Leu Ala
65 70 75 80

Asp Gly Ala Val Phe Ile Lys Lys Gly Ser Asp Asp Arg Asp Asp Ala
85 90 95

Ile Ser Arg Ala Lys Lys Leu Leu Glu Asp Ala Ser Ser Asp Arg Leu
100 105 110
Ala Val Ser Ser Val Leu Ala Lys Ile Glu Ser Leu
115 120

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...86
- (D) OTHER INFORMATION: /note= "UDP-N-ACETYLMURAMYL-TRYPEPTIDE SYNTHETASE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

Met Tyr Ser Leu Leu Leu Asp Leu Asn Lys Lys Thr Ala Leu Leu Gly
1 5 10 15
Thr Arg Gly Phe Phe Ile Asp Asp Lys His Ile Lys Glu Lys Gly Leu
20 25 30
Thr Thr Pro Thr Leu Leu Glu Leu Tyr Ser Asp Leu Glu Glu Ala Ile
35 40 45
Arg Leu Lys Cys Glu Tyr Phe Ile Met Glu Val Ser Ser His Ala Ile
50 55 60
Val Gln Asn Ala Ser Leu Gly Leu Ile Ser Leu Leu Lys Phe Ser Pro
65 70 75 80
Ile Ser Gln Ala Ile Ile
85

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

```
Met Ser Lys Arg Ala Ile Arg Phe Pro Asn Lys Leu Phe Ser Tyr Pro
1          5          10          15
Lys Pro Lys Ile Lys Ala Thr Asn Thr Ser His Thr Val Leu Phe Ala
          20          25          30
Tyr Pro Leu Lys Pro His Glu Met Ala Leu Leu Ala Leu Ala Thr Ser
          35          40          45
Leu Leu Ala Pro Ile Phe Asn Ala Ile His Ser Thr Asn Ala Leu Asn
          50          55          60
Ala Ile Lys Pro Asp Gly Thr Gly Ser Lys Ile Asn Pro Ile Ile Met
65          70          75          80
Pro Met Lys Ile Gln Lys
          85
```

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

```
Met Lys Thr Asn Phe Tyr Lys Ile Lys Leu Leu Phe Ala Trp Cys Leu
1          5          10          15
Ile Ile Gly Met Phe Asn Ala Pro Leu Asn Ala Asp Gln Asn Thr Asp
          20          25          30
Ile Lys Asp Ile Ser Pro Glu Asp Met Ala Leu Asn Ser Val Gly Leu
          35          40          45
Val Ser Arg Asp Gln Leu Lys Ile Glu Ile Pro Lys Glu Thr Leu Glu
          50          55          60
Gln Lys Val Thr Ile Leu Asn Asp Tyr Asn Asp Lys Asn Val Asn Ile
65          70          75          80
Lys Phe Asp Asp Ile Ser Leu Gly Ser Phe Gln Pro Asn Asp Asn Leu
```

95

105

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

10

20

15

60

84

95

11

12

14

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

Met	Ile	Asp	Asn	Leu	Asp	Gly	Ala	Lys	Asp	Ala	Gln	Leu	Ile	Lys	Lys	
1			5					10						15		
Ala	Tyr	Ala	Phe	Leu	Cys	Leu	Gly	Gly	Asp	Gly	Thr	Ile	Leu	Gly	Ala	
			20					25					30			
Leu	Arg	Met	Thr	His	Ala	His	Asn	Lys	Pro	Cys	Phe	Gly	Val	Arg	Ile	
		35					40					45				
Gly	Asn	Leu	Gly	Phe	Leu	Ser	Ala	Val	Glu	Leu	Asn	Gly	Leu	Lys	Asp	
	50					55					60					
Phe	Leu	Gln	Asp	Leu	Lys	Gln	Asn	Arg	Ile	Lys	Leu	Glu	Glu	His	Leu	
65				70					75						80	
Ala	Leu	Glu	Gly	Arg	Ile	Gly	Asn	Thr	Ser	Phe	Tyr	Ala	Ile	Asn	Glu	
				85					90					95		
Ile	Val	Ile	Ala	Lys	Lys	Lys	Ala	Leu	Gly	Val	Leu	Asp	Ile	Lys	Ala	
			100					105					110			
Cys	Ala	Gly	His	Thr	Pro	Phe	Asn	Thr	Tyr	Lys	Gly	Asp	Gly	Leu	Ile	
		115					120					125				
Ile	Ala	Thr	Pro	Leu	Gly	Ser	Thr	Ala	Tyr	Asn	Leu	Ser	Ala	His	Gly	
	130					135					140					
Pro	Ile	Val	His	Ala	Leu	Ser	Gln	Ser	Tyr	Ile	Leu	Thr	Pro	Leu	Cys	
145					150					155					160	
Asp	Phe	Ser	Leu	Thr	Gln	Arg	Pro	Leu	Val	Leu	Gly	Ala	Glu	Phe	Cys	
				165					170					175		
Leu	Ser	Phe	Cys	Ala	His	Glu	Asp	Ala	Leu	Val	Val	Ile	Asp	Gly	Gln	
			180					185					190			
Ala	Thr	Tyr	Asp	Leu	Lys	Ala	Asn	Gln	Pro	Leu	Tyr	Ile	Gln	Lys	Ser	
	195						200					205				
Pro	Thr	Thr	Thr	Lys	Leu	Leu	Gln	Lys	Asn	Ser	Arg	Asp	Tyr	Phe	Lys	
	210					215					220					
Val	Leu	Lys	Glu	Lys	Leu	Leu										
225					230											

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

Met	Xaa	Glu	Asn	Gly	Arg	Gly	Val	Pro	Lys	Asp	Tyr	Lys	Lys	Ala	Val	
1				5					10					15		
Glu	Tyr	Phe	Gln	Lys	Ala	Val	Asp	Asn	Asp	Ile	Pro	Arg	Gly	Tyr	Asn	
			20					25					30			
Asn	Leu	Gly	Val	Met	Tyr	Lys	Glu	Gly	Lys	Gly	Val	Pro	Lys	Asp	Glu	
		35					40					45				
Lys	Lys	Ala	Val	Glu	Tyr	Phe	Arg	Ile	Ala	Thr	Glu	Lys	Gly	Tyr	Thr	
	50					55					60					
Asn	Ala	Tyr	Ile	Asn	Leu	Gly	Ile	Met	Tyr	Met	Glu	Gly	Arg	Gly	Val	
65					70					75					80	
Pro	Ser	Asn	Tyr	Ala	Lys	Ala	Thr	Glu	Cys	Phe	Arg	Lys	Ala	Met	His	
				85					90					95		
Lys	Gly	Asn	Val	Xaa	Ala	Tyr	Ile	Leu	Leu	Gly	Asp	Ile	Tyr	Tyr	Ser	
		100						105					110			
Gly	Met	Ile	Asn	Trp	Val	Leu	Ser	Arg	Thr	Lys	Ile	Arg	Leu	Val	His	
	115					120						125				
Tyr	Lys	Met	Ala	Ala	Asp	Val	Ser	Ser	Ser	Arg	Ala	Tyr	Xaa	Gly	Leu	
	130					135					140					
Ser	Glu	Ser	Tyr	Xaa	Tyr	Gly	Leu	Gly	Val	Glu	Lys	Xaa	Xaa	Lys	Lys	
145					150					155					160	
Ala	Glu	Glu	Tyr	Met	Gln	Lys	Ala	Cys	Asp	Phe	Asp	Ile	Asp	Lys	Asn	
				165					170					175		
Cys	Lys	Lys	Lys	Asn	Thr	Ser	Ser	Arg								
			180					185								

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

Met	Ile	Val	Gly	Leu	Ile	Gly	Val	Val	Glu	Lys	Ile	Ser	Ala	Leu	Glu	
1			5						10					15		
Ala	His	Ile	Glu	Val	Gln	Gly	Val	Val	Tyr	Gly	Val	Gln	Val	Ser	Met	
			20					25					30			
Arg	Thr	Ala	Ala	Leu	Leu	Gln	Thr	Gly	Gln	Lys	Ala	Arg	Leu	Lys	Ile	
		35					40					45				
Leu	Gln	Val	Ile	Lys	Glu	Asp	Ala	His	Leu	Leu	Tyr	Gly	Phe	Leu	Glu	
	50					55					60					
Glu	Ser	Glu	Lys	Ile	Leu	Phe	Glu	Arg	Leu	Leu	Lys	Ile	Asn	Gly	Val	
65					70					75					80	
Gly	Gly	Arg	Ile	Ala	Leu	Ala	Ile	Leu	Ser	Ser	Phe	Ser	Pro	Asn	Glu	
				85					90					95		
Phe	Glu	Asn	Ile	Ile	Ala	Thr	Lys	Glu	Val	Lys	Arg	Leu	Gln	Gln	Val	
			100					105					110			
Pro	Gly	Ile	Gly	Lys	Lys	Leu	Ala	Asp	Lys	Ile	Met	Val	Asp	Leu	Ile	
		115					120					125				
Gly	Phe	Phe	Ile	Gln	Asp	Glu	Asn	Arg	Pro	Ala	Arg	Asn	Glu	Val	Phe	
	130					135					140					
Leu	Ala	Leu	Glu	Ser	Leu	Gly	Phe	Lys	Ser	Ala	Glu	Ile	Asn	Pro	Val	
145					150					155					160	
Leu	Lys	Thr	Leu	Lys	Pro	His	Leu	Ser	Ile	Glu	Ala	Ala	Ile	Lys	Glu	
				165					170					175		
Ala	Leu	Gln	Gln	Leu	Arg	Ser										
			180													

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

Val Gly Val Leu Leu Ala Leu Phe Phe Phe Tyr Ala Lys Asn Asn Leu
1 5 10 15
Leu Glu Asn Thr Gln Ile Arg Met Gln Tyr Thr Ala Asp Ala Ile Ala
20 25 30
Lys Ser Leu Leu Glu Leu Asn Asn Ala Ser Ser Leu Glu Pro Leu Lys
35 40 45
Ile Leu Glu Glu Arg Phe Lys Asn Thr Pro Phe Val Leu Leu Asp Ala
50 55 60
Asp Asn Arg Val Lys Phe Ser Asn Ile Gly Val Phe Val Ala Ser Phe
65 70 75 80
Lys Asn Asp Ala Leu Ile Lys Thr Pro Tyr Phe Ala Leu Lys Lys Gln
85 90 95
Gly Phe Tyr Leu Thr Asp Ser Ala Pro Thr Asn Arg Leu Gly Val Ser
100 105 110
Lys Ile Ile Ile Ala Glu Glu Glu Ile Gln Lys Ile Phe Ile Pro Leu
115 120 125
Tyr Lys Met Ile Gly Tyr Val Phe Leu Gly Ala Ser Leu Phe Val Ala
130 135 140
Leu Ile Ala Met Trp Leu Tyr Lys Ile Pro
145 150

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

Val Val Ile Met Ile Leu Val Cys Phe Leu Ala Cys Ser Gln Glu Ser
1 5 10 15
Phe Ile Lys Met Gln Lys Lys Ala Gln Glu Gln Glu Asn Asp Gly Ser
20 25 30
Lys Arg Pro Ser Tyr Val Asp Ser Asp Tyr Glu Val Phe Ser Glu Thr
35 40 45

Ile	Phe	Leu	Gln	Asn	Met	Val	Tyr	Gln	Pro	Ile	Glu	Glu	Arg	Asn	Ala	
50						55				60						
Phe	Phe	Gln	Leu	Thr	Lys	Asp	Glu	Asp	Asn	Ser	Phe	Asn	Pro	Glu	Asn	
65					70					75					80	
Ser	Val	Ile	Leu	Leu	Asn	Glu	Pro	Ser	Asp	Asn	Ser	Glu	Lys	Asn	Leu	
			85						90					95		
Leu	Ser	Tyr	Pro	Asn	Asp	Pro	Asn	Asn	Asn	Glu	Asp	Asn	Ala	Asn	Asn	
			100					105					110			
Ser	Gln	Lys	Asn	Pro	Phe	Leu	Tyr	Lys	Pro	Lys	Arg	Lys	Thr	Lys	Asn	
		115					120					125				
Pro	Lys	Leu	Ile	Glu	Tyr	Ser	Gln	Gln	Asp	Phe	Tyr	Pro	Leu	Lys	Asn	
	130					135					140					
Gly	Asp	Ile	Ile	Met	Ser	Lys	Glu	Gly	Asp	Gln	Trp	Leu	Ile	Glu	Ile	
145					150					155					160	
Gln	Ser	Lys	Ala	Leu	Lys	Arg	Phe	Leu	Lys	Asp	Gln	Asn	Asp	Lys	Asp	
			165						170					175		
Arg	Gln	Ile	Gln	Thr	Phe	Thr	Phe	Asn	Asp	Thr	Lys	Thr	Gln	Ile	Ala	
		180						185					190			
Gln	Ile	Lys	Gly	Lys	Ile	Ser	Ser	Tyr	Val	Tyr	Thr	Thr	Asn	Asn	Gly	
	195					200						205				
Ser	Leu	Ser	Leu	Arg	Pro	Phe	Tyr	Glu	Ser	Phe	Leu	Leu	Glu	Lys	Lys	
	210					215					220					
Ser	Asp	Asn	Val	Tyr	Thr	Ile	Glu	Asn	Lys	Ala	Leu	Asp	Thr	Met	Glu	
225					230					235					240	
Ile	Ser	Lys	Cys	Gln	Met	Val	Leu	Lys	Lys	His	Ser	Thr	Asp	Lys	Leu	
			245						250					255		
Asp	Ser	Gln	His	Lys	Ala	Ile	Ser	Ile	Asp	Leu	Asp	Phe	Lys	Lys	Glu	
		260						265				270				
Arg	Phe	Lys	Ser	Asp	Thr	Glu	Leu	Phe	Leu	Glu	Cys	Leu	Lys	Glu	Ser	
	275						280					285				

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

Met Ala Ala Pro Leu Leu Ala Leu Pro Phe Leu Ser Asn Pro Leu Val
1 5 10 15
Leu Gly Ala Leu Ala Val Ile Gly Val Gly Ala Tyr Leu Tyr Pro Asn
20 25 30
Lys Gln Asp Ser Leu Val Val Gln Ala Asp Gly Leu Tyr Ser Glu Ile
35 40 45
Leu Gly Phe Phe Ile Ser Phe Ser Ser Lys Ile Leu Lys Gly Ile Gly
50 55 60
Glu Pro Leu Ala Asn Val Ile Gln Pro Phe Gly Met Val Leu Gly Met
65 70 75 80
Leu Leu Ile Leu Leu Tyr Ser Phe Lys Arg Tyr Gln Asn Asn Asp Leu
85 90 95
Phe Glu Ile Lys Thr Phe Leu Met Leu Phe Val Phe Val Gly Tyr Leu
100 105 110
Ser Leu Tyr His Tyr Ala Phe Lys Ser Asp Gly Ser Ser Ser Gly Asn
115 120 125
Gly Arg Ser Ser Phe Ala Phe Gln Asn His Val Thr Glu Ile Phe Asp
130 135 140
Thr Pro Ala Asn Leu Leu Asn Ala Gly Ile Ser Asn Val Val Lys Glu
145 150 155 160
Tyr Gln Thr Asn Ser Ala Arg Glu His Lys Asn Ile Asp Thr His His
165 170 175
Ser Ile Thr Asn Ala Asn Ile Ser Phe His Val Arg Gln Ile Leu Thr
180 185 190
Ser Leu Asn Lys Leu Tyr Glu Asp Phe Lys Ile Asn Asn Gly Leu Ser
195 200 205
Leu Lys Thr Leu Ile Ala Ala Val Leu Leu Leu Val Ile Leu Gly Leu
210 215 220
Glu Leu Phe Leu Leu Phe Lys Val Phe Cys Tyr Val Phe Met Thr Tyr
225 230 235 240
Leu Glu Lys Ile Ile Tyr Leu Ser Leu Val Ile Phe Met Leu Leu Leu
245 250 255
Gly Phe Phe Gln Gln Thr Arg Gly Phe Leu Val Ser Tyr Val Lys Lys
260 265 270
Ile Ile Ser Leu Thr Phe Tyr Met Pro Leu Leu Leu Leu Leu Val Leu
275 280 285

Phe Asn Ser Phe Ala Leu Gln Tyr Ala Ile Lys Val Gly Gly Ser Asn
 290 295 300
 Glu Ile Val Ala Lys Phe Gly Ile Ile Val Ala Ile Gly Ile Ser Leu
 305 310 315 320
 Thr Phe Ile Gln Lys Val Pro Glu Met Ile Asn Ala Ile Phe Gly Thr
 325 330 335
 Gln Gly Gly Leu Thr Asp Ala Lys Ser Phe Ile Tyr Gln Gly Val Gln
 340 345 350
 Met Ala Ser Ala Gly Ala Gly Ala Ile Ala Gly Ser Leu Lys Ser Val
 355 360 365
 Gly Arg Ser Ala Phe Gly Arg Thr Leu Glu Ala Tyr Lys Asp Ala Lys
 370 375 380
 Ser Thr Ile Asn Ser Thr Thr Ala Asn Met Arg Asp Met Pro Gly His
 385 390 395 400
 Pro Gly Val Arg Val Gly Val Glu Thr Ile Glu Leu Pro Lys Ser His
 405 410 415
 Arg Ala Ser Lys
 420

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:

Val Leu Lys Phe Gln Lys Leu Pro Leu Leu Phe Val Ser Ile Leu Tyr
 1 5 10 15
 Asn Gln Ser Pro Leu Leu Ala Phe Asp Tyr Lys Phe Ser Gly Val Ala
 20 25 30
 Glu Ser Val Ser Lys Val Gly Phe Asn His Ser Lys Leu Asn Ser Lys
 35 40 45
 Glu Gly Ile Phe Pro Thr Ala Thr Phe Val Thr Ala Thr Ile Lys Leu
 50 55 60
 Gln Val Asn Tyr Lys Ser Ala Pro
 65 70

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...205
- (D) OTHER INFORMATION: /note= "serotonin transport protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

Met	Gly	Asn	His	Phe	Ser	Lys	Leu	Gly	Phe	Val	Leu	Ala	Ala	Leu	Gly	
1				5				10						15		
Ser	Ala	Ile	Gly	Leu	Gly	His	Ile	Trp	Arg	Phe	Pro	Tyr	Met	Thr	Gly	
		20						25					30			
Val	Ser	Gly	Gly	Gly	Ala	Phe	Val	Leu	Leu	Phe	Leu	Phe	Leu	Ser	Leu	
		35					40					45				
Ser	Val	Gly	Ala	Ala	Met	Phe	Ile	Ala	Glu	Met	Leu	Leu	Gly	Gln	Ser	
	50					55					60					
Thr	Gln	Lys	Asn	Val	Thr	Glu	Ala	Phe	Lys	Glu	Leu	Asp	Ile	Asn	Pro	
65				70					75					80		
Lys	Lys	Arg	Trp	Lys	Tyr	Ala	Gly	Ile	Met	Leu	Ile	Ser	Gly	Pro	Leu	
			85					90					95			
Ile	Leu	Thr	Phe	Tyr	Gly	Thr	Ile	Leu	Gly	Trp	Val	Leu	Tyr	Tyr	Leu	
			100					105					110			
Val	Ser	Ile	Ser	Phe	Asn	Leu	Pro	Ser	Ser	Ile	Gln	Glu	Ser	Glu	Gln	
		115					120					125				
Ile	Phe	Thr	Gln	Thr	Leu	Gln	Ser	Ile	Gly	Leu	Gln	Ser	Ile	Gly	Leu	
	130					135					140					
Phe	Ser	Val	Leu	Phe	Ile	Thr	Gly	Trp	Ile	Val	Ser	Arg	Gly	Ile	Lys	
145					150				155						160	
Glu	Gly	Ile	Glu	Lys	Leu	Asn	Leu	Val	Leu	Met	Pro	Leu	Leu	Phe	Ala	
			165					170						175		
Thr	Phe	Phe	Gly	Leu	Leu	Phe	Tyr	Ala	Met	Ser	Met	Asp	Ser	Phe	Ser	
			180					185					190			

Lys	Ala	Phe	His	Phe	Met	Leu	Ile	Ser	Ser	Gln	Lys	Ile
	195						200					205

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

Met	Glu	Lys	Val	Cys	Val	Ser	Ala	Trp	Gly	Leu	Pro	Lys	Ile	Leu	Glu
1			5						10					15	
Glu	Arg	Leu	Lys	Glu	Lys	Tyr	Gly	Asp	Asp	Trp	Glu	Lys	His	Val	Lys
		20						25					30		
Ala	Lys	Ala	Ile	Asn	Glu	Glu	Glu	Leu	Glu	Glu	Gln	Val	Lys	Ala	Lys
		35						40				45			
Ala	Lys	Glu	Gln	Gln	Lys	Thr	Gln	Arg	Glu	Lys	Thr	Leu	Asn	Gly	Phe
	50					55					60				
Leu	Lys	Lys	Val	Gly	Leu	Lys	Lys	Arg	Asp	Met	Leu	Gln	Ser	Thr	Met
65				70					75						80
Leu	Phe	Asp	Glu	Val	Lys	Glu	Ala	Asp	Val	Leu	Phe	Gln	Ala	Glu	Arg
			85						90					95	
Lys	Ile	Gly	Asp	Trp	Ile	Phe	Ser	Ser	Ala	Val	Phe	Phe	Phe	Ala	Leu
		100						105					110		
Ala	Leu	Ile	Glu	Ala	Ile	Ile	Ile	Val	Cys	Leu	Leu	Pro	Leu	Lys	Glu
		115						120					125		
Lys	Val	Pro	Tyr	Leu	Val	Thr	Phe	Ser	Asn	Ala	Thr	Gln	Asn	Phe	Ala
	130					135						140			
Ile	Val	Gln	Arg	Ala	Asp	Lys	Ser	Ile	Arg	Ala	Asn	Gln	Ala	Leu	Val
145				150						155					160
Arg	Gln	Leu	Val	Ala	Ser	Tyr	Val	Asn	Asn	Arg	Glu	Asn	Ile	Ser	Ser
			165						170					175	
Ile	Lys	Glu	Gln	Asn	Glu	Ile	Ala	His	Glu	Thr	Ile	Arg	Leu	Gln	Ser
		180						185						190	
Ala	Phe	Glu	Val	Trp	Asp	Phe	Phe	Glu	Lys	Leu	Val	Ser	Tyr	Glu	His

195	200	205
Ser Ile Tyr Thr Asn Ile	Asn Leu Thr Arg Lys Ile	Ser Ile Ile Asn
210	215	220
Ile Ala Leu Ile Ser Lys Thr Gln Ala Asn Ile Glu Ile Ser Ala Gln		
225	230	235 240
Leu Phe His Lys Glu Lys Leu Glu Ser Glu Lys Arg Tyr Arg Ile Ile		
	245	250 255
Met Thr Phe Glu Phe Glu Pro Ile Glu Ile Asp Thr Lys Ser Val Pro		
	260	265 270
Leu Asn Pro Thr Gly Phe Ile Val Thr Gly Tyr Asp Val Thr Glu Ile		
	275	280 285
Ala Ile Leu Lys Asp Leu Asp Glu Lys Asn Lys Val Lys Asp Asp Gly		
	290	295 300
Val Lys Ser Arg Ile Ile His Val Glu Lys Lys Asp Pro His Met Ser		
305	310	315 320
Gln Tyr Lys Asp Val Lys Glu Gln		
	325	

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

Leu Leu Asn Met Trp Asp Glu Ala Lys Lys Glu Gly Ile Asn Ile Asn
1 5 10 15
Thr Glu Lys Leu Ser Gln Glu Leu Gly Val Val Cys Val Pro Thr Ser
20 25 30
Ala Arg Xaa Lys Glu Asp Arg Leu Asn Thr Glu Leu Leu Leu Asp Glu
35 40 45
Ile Val Arg Leu Tyr Ser Gln Asn Thr Thr Asn Asn Glu Asn Ile Lys
50 55 60
Val Pro Ser Gln Ser Phe Lys Glu Ser Leu Lys Tyr Ser Gln Ser Ala
65 70 75 80

Gln Arg Ile Ala Lys Ser Val Ile Ser Glu Asn Lys Gln Asn Ala Ser
85 90 95

Phe Glu His Thr Tyr Lys Ile Asp Lys Ile Phe Asn Ala Pro Ala Leu
100 105 110

Trp Asp Phe His Phe Phe Xaa Val Tyr Val Tyr His Leu Phe Phe Glu
115 120 125

Leu Phe Asn Arg Arg Gly Ser Ala Lys Ser Pro
130 135

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

Met Leu His Lys Ala Lys Val Gly Ile Val Phe Gln Ala Leu Leu Gly
1 5 10 15

Ile Phe Cys Val Phe Leu Leu Leu Phe Tyr Leu Ser Ala Phe Leu Met
20 25 30

Val Ala Phe Lys Asp Thr Lys Arg Met Phe Ile Ser Val Leu Ile Gly
35 40 45

Ser Val Val Phe Leu Trp Ser Asp Leu Leu Val Phe Val Gly Phe Lys
50 55 60

Asn Ile Ser Phe Val Leu Asp Ile Gly Tyr Glu Ile
65 70 75

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

Met	Gln	Glu	Ala	Leu	Leu	Arg	Phe	Gln	Glu	Gly	Phe	Lys	Glu	Trp	Gly	
1				5					10					15		
Tyr	Leu	Ile	Leu	Phe	Leu	Tyr	Ser	Leu	Gly	Gly	Gly	Tyr	Val	Gly	Ile	
			20					25					30			
Val	Ile	Ala	Ser	Ile	Leu	Ser	Ala	Thr	Thr	His	Ala	Leu	Asp	Ile	Lys	
		35					40					45				
Ile	Thr	Ile	Leu	Val	Ala	Phe	Leu	Gly	Asn	Leu	Ile	Gly	Ser	Gly	Ala	
	50					55					60					
Leu	Val	Ile	Phe	Ala	Arg	Tyr	Gln	Lys	Arg	Glu	Phe	Leu	Lys	Tyr	Phe	
65					70					75					80	
Gln	Lys	His	Arg	Arg	Lys	Leu	Ala	Leu	Ala	Ser	Leu	Trp	Val	Lys	Arg	
				85					90					95		
Tyr	Ala	Leu	Leu	Met	Ile	Phe	Val	Asn	Lys	Tyr	Leu	Tyr	Gly	Ile	Lys	
			100					105					110			
Ser	Val	Val	Pro	Leu	Ala	Ile	Gly	Phe	Ser	Lys	Tyr	Pro	Leu	Lys	Lys	
		115					120					125				
Phe	Leu	Trp	Leu	Asn	Val	Phe	Ser	Ser	Phe	Leu	Trp	Ala	Leu	Ile	Val	
	130					135					140					
Gly	Ser	Val	Ser	Phe	Gln	Ala	Ser	Asp	Trp	Val	Lys	Thr	Leu	Tyr	Glu	
145					150					155					160	
Arg	Leu	Ser	His	Tyr	Thr	Ser	Phe	Phe	Val	Ile	Ser	Phe	Val	Leu	Ile	
				165					170					175		
Ala	Leu	Leu	Ile	Trp	Phe	Leu	Leu	Lys	Arg	Tyr	Ser	Arg	Lys	Met	Gly	
			180					185					190			

Phe

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

```

Met Pro Phe Leu Lys Asn Trp Ile Trp Ser Leu Lys Met Ala Leu Ser
1           5           10           15

Ala Ile Ser Gly Ala Ser Gly Val Gly Lys Ser Val Leu Ile Ala Ser
          20           25           30

Leu Leu Gly Ala Phe Gly Leu Lys Glu Ser Asn Ala Ser Asn Ile Glu
          35           40           45

Val Glu Leu Ile Ala Pro Phe Leu Asp Thr Glu Glu Tyr Gly Ile Phe
          50           55           60

Arg Glu Asp Glu His Glu Pro Leu Val Ile Ser Val Ile Lys Lys Glu
65           70           75           80

Lys Thr Arg Tyr Phe Leu Asn Gln Thr Ser Leu Ser Lys Asn Thr Leu
          85           90           95

Lys Ala Leu Leu Lys Gly Leu Ile Lys Arg Leu Ser Asn Asp Arg Phe
          100          105          110

Ser Gln Asn Glu Leu Asn Asp Ile Leu Met Leu Ser Leu Leu Asp Gly
          115          120          125

Tyr Ile Gln Asn Lys Asn Lys Arg Leu Ala Pro Phe
          130          135          140

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(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...308
- (D) OTHER INFORMATION: /note= "ToxR-activated (tagE) gene
[*Vibrio cholerae*] (inner membrane)"

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:573:

```

Met Pro Gln Asn Gln Leu Val Ile Thr Ile Ile Asp Glu Ser Gly Ser
1           5           10           15

Lys Gln Leu Lys Phe Ser Lys Asn Leu Lys Arg Asn Leu Ile Ile Ser
          20           25           30

Val Val Ile Leu Leu Leu Ile Val Gly Leu Gly Val Gly Phe Leu Lys

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35					40					45					
Phe	Leu	Ile	Ala	Lys	Met	Asp	Thr	Met	Thr	Ser	Glu	Arg	Asn	Ala	Val
50					55					60					
Leu	Arg	Asp	Phe	Arg	Gly	Leu	Tyr	Gln	Lys	Asn	Tyr	Ala	Leu	Ala	Lys
65					70					75					80
Glu	Ile	Lys	Asn	Lys	Arg	Glu	Glu	Leu	Phe	Ile	Val	Gly	Gln	Lys	Ile
			85						90					95	
Arg	Gly	Leu	Glu	Ser	Leu	Ile	Glu	Ile	Lys	Lys	Gly	Ala	Asn	Gly	Gly
		100					105						110		
Gly	His	Leu	Tyr	Asp	Glu	Val	Asp	Leu	Glu	Asn	Leu	Ser	Leu	Asn	Gln
	115						120					125			
Lys	His	Leu	Ala	Leu	Met	Leu	Ile	Pro	Asn	Gly	Met	Pro	Leu	Lys	Thr
	130					135					140				
Tyr	Ser	Ala	Ile	Lys	Pro	Thr	Lys	Glu	Arg	Asn	His	Pro	Ile	Lys	Lys
145					150					155					160
Ile	Lys	Gly	Val	Glu	Ser	Gly	Ile	Asp	Phe	Ile	Ala	Pro	Leu	Asn	Thr
			165					170						175	
Pro	Val	Tyr	Ala	Ser	Ala	Asp	Gly	Ile	Val	Asp	Phe	Val	Lys	Thr	Arg
		180					185						190		
Ser	Asn	Ala	Gly	Tyr	Gly	Asn	Leu	Val	Arg	Ile	Glu	His	Ala	Phe	Gly
	195					200					205				
Phe	Ser	Ser	Ile	Tyr	Thr	His	Leu	Asp	His	Val	Asn	Val	Gln	Pro	Lys
	210					215					220				
Ser	Phe	Ile	Gln	Lys	Gly	Gln	Leu	Ile	Gly	Tyr	Ser	Gly	Lys	Ser	Gly
225					230					235					240
Asn	Ser	Gly	Gly	Glu	Lys	Leu	His	Tyr	Glu	Val	Arg	Phe	Leu	Gly	Lys
			245						250					255	
Ile	Leu	Asp	Ala	Glu	Lys	Phe	Leu	Ala	Trp	Asp	Leu	Asp	His	Phe	Gln
		260						265					270		
Ser	Ala	Leu	Glu	Glu	Asn	Lys	Phe	Ile	Glu	Trp	Lys	Asn	Leu	Phe	Trp
	275						280					285			
Val	Leu	Glu	Asp	Ile	Val	Gln	Leu	Gln	Glu	His	Val	Asp	Lys	Asp	Thr
	290					295					300				
Leu	Lys	Gly	Gln												
305															

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...339

(D) OTHER INFORMATION: /note= "phosphomannomutase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

Met	Ile	Thr	Gly	Ser	His	Asn	Pro	Lys	Glu	Tyr	Asn	Gly	Phe	Lys	Ile	
1				5					10					15		
Thr	Leu	Asn	Gln	Asn	Pro	Phe	Tyr	Gly	Lys	Asp	Ile	Gln	Ala	Leu	Lys	
		20						25					30			
Asn	Thr	Leu	Leu	Asn	Ala	Lys	His	Glu	Ile	Lys	Pro	Leu	Lys	Glu	Thr	
		35					40					45				
Pro	Glu	Lys	Val	Asn	Ala	Leu	Glu	Ala	Tyr	His	Arg	Tyr	Leu	Ile	Lys	
	50					55					60					
Asp	Phe	Lys	His	Leu	Lys	Asn	Leu	Lys	Tyr	Lys	Ile	Ala	Leu	Asp	Phe	
65					70				75						80	
Gly	Asn	Gly	Val	Gly	Ala	Leu	Gly	Leu	Glu	Pro	Ile	Leu	Lys	Ala	Leu	
			85					90						95		
Asn	Ile	Asp	Phe	Ser	Ser	Leu	Tyr	Ser	Asp	Pro	Asp	Gly	Asp	Phe	Pro	
			100					105					110			
Asn	His	His	Pro	Asp	Pro	Ser	Glu	Ala	Lys	Asn	Leu	Lys	Asp	Leu	Glu	
		115					120					125				
Lys	His	Met	Arg	Glu	Asn	Ala	Ile	Leu	Ile	Gly	Phe	Ala	Phe	Asp	Gly	
	130					135					140					
Asp	Ala	Asp	Arg	Ile	Ala	Met	Leu	Ser	Ser	His	His	Ile	Tyr	Ala	Gly	
145					150					155					160	
Asp	Glu	Leu	Ala	Ile	Leu	Phe	Ala	Lys	Arg	Leu	His	Ala	Gln	Gly	Ile	
			165						170					175		
Thr	Pro	Phe	Val	Ile	Gly	Glu	Val	Lys	Cys	Ser	Gln	Val	Met	Tyr	Asn	
			180					185					190			
Ala	Ile	Asn	Thr	Phe	Gly	Lys	Thr	Leu	Met	Tyr	Lys	Thr	Gly	His	Ser	
		195					200					205				
Asn	Leu	Lys	Ile	Lys	Leu	Lys	Glu	Thr	Asn	Ala	His	Phe	Ala	Ala	Glu	
	210					215					220					

Met Ser Gly His Ile Phe Phe Lys Glu Arg Tyr Phe Gly Tyr Asp Asp
 225 230 235 240
 Ala Leu Tyr Ala Cys Leu Arg Ala Leu Glu Leu Leu Leu Glu Gln Ser
 245 250 255
 Pro Ser Asp Leu Glu Asn Thr Ile Lys Asn Leu Pro Tyr Ser Tyr Thr
 260 265 270
 Thr Pro Glu Glu Lys Ile Ala Val Ser Glu Glu Glu Lys Phe Glu Ile
 275 280 285
 Ile Arg Asn Leu Gln Glu Ala Leu Lys Asn Pro Pro Ser His Phe Pro
 290 295 300
 Thr Ile Lys Glu Ile Ile Ser Ile Asp Gly Val Arg Val Val Phe Glu
 305 310 315 320
 His Gly Phe Gly Leu Ile Arg Ala Ser Asn Thr His Pro Leu Phe Ser
 325 330 335
 Gln Pro Leu

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

Met Ser Lys Asn Leu Gln Lys Lys Asn Pro Lys Lys Ser Xaa Pro Gln
 1 5 10 15
 Ala Gln Lys Ala Ile Arg Glu Met Lys Met Phe Glu Thr Ile Ala Phe
 20 25 30
 Tyr Phe Phe Ala Ile Leu Thr Leu Ser Met Ala Leu Val Val Ile Thr
 35 40 45
 Thr Thr Asn Ile Leu Tyr Ala Ile Thr Ala Leu Ala Ser Ser Met Val
 50 55 60
 Phe Ile Ser Ala Phe Phe Phe Leu Leu Asp Ala Glu Phe Leu Gly Val
 65 70 75 80
 Val Gln Ile Thr Val Tyr Val Gly Ala Val Ile Val Met Tyr Ala Phe

Leu Ala Leu Ile Ala Ser Arg Leu Ile Val Val Ile Leu Tyr Ala Phe
 100 105 110
 Ile Phe Ile Val Leu Ser Phe Tyr Ala Leu Asn Ile Ile Thr Ile Leu
 115 120 125
 Asn Phe Lys Ala Leu Ile Leu Gly Phe Ile Ser Ile Phe Ser Ser Ala
 130 135 140
 Leu Phe Cys Phe Cys Leu Ala Ile Phe Val Ala Arg Ile Phe Gln Asn
 145 150 155 160
 Glu Gln Ser Ile Leu Gly Phe Cys Asn Ile Ile Asn Leu Tyr Ala Leu
 165 170 175
 Met Ser Cys Asn Val Phe Val Pro Leu Glu Tyr Leu Pro Asn Ile Gly
 180 185 190
 Gln Leu Phe Ile Lys Thr Ser Ile Phe Tyr Tyr Leu Asn Gln Leu Leu
 195 200 205
 Ile Lys Ala Phe Gln Gly Ile Asp Thr Ile Leu Val Leu Ala Thr Ser
 210 215 220
 Thr Phe Phe Ile Ile Gly Gly Ile Ile Leu Phe Leu Leu Ser Ala Asn
 225 230 235 240
 Arg Met Leu Leu Thr Pro Lys Glu Arg Met Arg
 245 250

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

Met Ala Gly Thr Gln Ala Ile Tyr Glu Ser Ser Ser Ala Gly Phe Leu
 1 5 10 15
 Ser Gln Val Ser Ser Ile Ile Ser Ser Thr Ser Gly Val Ala Gly Pro
 20 25 30
 Phe Ala Gly Ile Val Ala Gly Ala Met Thr Ala Ala Ile Ile Pro Ile
 35 40 45
 Val Val Gly Phe Thr Asn Pro Gln Met Thr Asp Ile Ile Asn Pro Ile
 50 55 60

Lys Ser Lys His Arg
65

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...112
- (D) OTHER INFORMATION: /note= "spoIIIE gene product"

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:578:

Val	Ser	Arg	Ile	Leu	Gly	Leu	Ser	Asp	Asp	Leu	Ala	Met	Thr	Leu	Cys
1				5				10						15	
Ala	Glu	Ser	Ile	Arg	Ile	Gln	Ala	Pro	Ile	Lys	Gly	Lys	Asp	Val	Val
			20				25						30		
Gly	Ile	Glu	Ile	Pro	Asn	Ser	Gln	Ser	Gln	Ile	Ile	Tyr	Leu	Arg	Glu
		35				40						45			
Ile	Leu	Glu	Ser	Glu	Leu	Phe	Gln	Lys	Ser	Ser	Ser	Pro	Leu	Thr	Leu
	50				55						60				
Ala	Leu	Gly	Lys	Asp	Ile	Val	Gly	Asn	Pro	Phe	Ile	Thr	Asp	Leu	Lys
65				70					75					80	
Lys	Leu	Pro	His	Leu	Leu	Ile	Ala	Gly	Thr	Thr	Gly	Ser	Gly	Lys	Ser
			85					90						95	
Val	Gly	Val	Asn	Ala	Met	Ile	Leu	Ser	Leu	Leu	Tyr	Lys	Lys	Pro	Pro
		100					105						110		

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

Met	Asp	Glu	Xaa	Leu	Val	Tyr	Gly	Val	Ile	Cys	Met	Pro	Ser	Gln	Val
1				5				10						15	
Phe	Ala	Asn	Thr	Gly	Thr	Asn	Val	Ser	Ile	Ile	Phe	Phe	Gln	Lys	Thr
			20					25					30		
Pro	Ser	Ala	Lys	Glu	Val	Ile	Leu	Ile	Asp	Ala	Ser	Lys	Leu	Gly	Glu
		35					40					45			
Glu	Tyr	Thr	Glu	Asn	Lys	Asn	Lys	Lys	Thr	Arg	Leu	Arg	Pro	Ser	Asp
	50					55					60				
Met	Asp	Leu	Ile	Leu	Glu	Thr	Phe	Gln	Asn	Lys	Ala	Pro	Lys	Ser	Asp
65					70					75					80
Phe	Cys	Ala	Leu	Val	Ser	Phe	Asp	Glu	Ile	Thr	Glu	Lys	Asn	Tyr	Ser
				85					90					95	
Leu	Asn	Pro	Gly	Gln	Tyr	Phe	Thr	Ile	Glu	Asp	Thr	Ser	Glu	Thr	Ile
			100					105					110		
Ser	Gln	Ala	Glu	Phe	Glu	Asn	Leu	Met	Gln	Gln	Tyr	Ser	Ser	Glu	Leu
		115					120					125			
Ala	Ser	Leu	Phe	Asp	Glu	Ser	Gln	Asn	Leu	Gln	Gln	Glu	Ile	Leu	Glu
	130						135				140				
Thr	Leu	Lys	Gly	Val	Arg	Phe	Glu								
145							150								

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

Met	Arg	Lys	Gly	Arg	Val	Met	Leu	Cys	Val	Phe	Asp	Ile	Glu	Thr	Ile
1					5				10					15	
Pro	Asn	Ile	Ser	Leu	Cys	Lys	Glu	His	Phe	Gln	Leu	Lys	Glu	Asp	Asp
			20					25					30		

Ala Leu Lys Ile Cys Glu Trp Ser Phe Glu Lys Gln Lys Glu Lys Ser
35 40 45

Gly Ser Glu Phe Leu Pro Leu Tyr Leu His Glu Ile Ile Ser Ile Ala
50 55 60

Ala Val Ile Gly Asp Asp Tyr Gly Gln Phe Ile Lys Val Gly Asn Phe
65 70 75 80

Gly Gln Lys His Glu Asn Lys Glu Asp Phe Ala Ser Glu Lys Glu Leu
85 90 95

Leu Glu Asp Phe Phe Lys Tyr Phe Asn Glu Lys Gln Pro Arg Leu Ile
100 105 110

Ser Phe Xaa Gly Arg Gly Phe Gly Tyr Ser Pro Thr His Ala Gln Ser
115 120 125

Pro

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...113
- (D) OTHER INFORMATION: /note= "chemotaxis protein cheY"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

Met Arg Arg Ile Ile Lys Asn Thr Leu Ser Arg Leu Gly Tyr Glu Asp
1 5 10 15

Val Leu Glu Ala Glu His Gly Val Glu Ala Trp Glu Lys Leu Asp Ala
20 25 30

Asn Ala Asp Thr Lys Val Leu Ile Thr Asp Trp Asn Met Pro Glu Met
35 40 45

Asn Gly Leu Asp Leu Val Lys Lys Val Arg Ala Asp Asn Arg Phe Lys
50 55 60

Glu Ile Pro Ile Ile Met Ile Thr Thr Glu Gly Gly Lys Ala Glu Val
65 70 75 80

Ile Thr Thr Leu Lys Ala Gly Val Asn Asn Tyr Ile Val Lys Pro Phe
85 90 95

Thr Pro Gln Val Leu Lys Glu Lys Leu Glu Val Val Leu Gly Thr Asn
100 105 110

Asp

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...174

(D) OTHER INFORMATION: /note= "component of flagellum"

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:582:

Met Ala Glu Glu Gln Glu Asn Thr Ala Gln Gln Pro Gln Lys Lys Ser
1 5 10 15

Lys Ala Leu Leu Phe Val Ile Ile Gly Ser Val Leu Val Met Leu Leu
20 25 30

Leu Val Gly Val Ile Ile Met Leu Leu Met Gly Asn Lys Glu Glu Ser
35 40 45

Lys Glu Asn Ala Ser Lys Asn Thr Gln Glu Val Gln Ala Asn Pro Met
50 55 60

Ala Asn Lys Asn Gln Glu Ala Lys Glu Gly Ser Asn Ile Gln Gln Tyr
65 70 75 80

Leu Val Leu Gly Pro Leu Tyr Ala Ile Asp Ala Pro Phe Ala Val Asn
85 90 95

Leu Val Ser Gln Asn Gly Arg Arg Tyr Leu Lys Ala Ser Ile Ser Leu
100 105 110

Glu Leu Ser Asn Glu Lys Leu Leu Asn Glu Val Lys Val Lys Asp Thr
115 120 125

Ala Ile Lys Asp Thr Ile Ile Glu Ile Leu Ser Ser Lys Ser Val Glu
130 135 140

Glu Val Val Thr Asn Lys Gly Lys Asn Lys Leu Lys Asp Glu Ile Lys

145	150	155	160
Ser His Leu Asn Ser Phe Leu Ile Asp Gly Phe Ile Lys Asn			
	165	170	

(2) INFORMATION FOR SEQ ID NO:583:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

Met	Gly	Cys	Phe	Ser	Thr	Ile	Cys	Cys	Lys	Gly	Leu	Thr	Leu	Ser	Val
1				5					10					15	
Gly	Gly	Phe	Leu	Val	Met	Met	Arg	Phe	Leu	Ile	Phe	Lys	Asp	Phe	Cys
			20				25						30		
Lys	Asp	Phe													
			35												

(2) INFORMATION FOR SEQ ID NO:584:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

Met	Ala	Lys	Lys	Lys	Ile	Ala	Ile	Ser	Cys	Gly	Asp	Ile	Gln	Gly	Val
1				5					10					15	
Gly	Leu	Glu	Leu	Ile	Leu	Lys	Ser	His	Lys	Glu	Val	Ser	Ala	Leu	Cys
			20				25						30		
Glu	Pro	Leu	Tyr	Leu	Val	His	Ser	Glu	Leu	Leu	Glu	Arg	Ala	Asn	Gln
		35				40					45				
Leu	Leu	Asp	Asn	Ala	Tyr	Glu	Thr	Lys	Thr	Leu	Asn	Ala	Ile	Ala	Ile

50	55	60
Asp Ala Pro Leu Pro Leu Leu Asn Ser Ser Thr Ile Gly Lys Val Ser		
65	70	75 80
Thr Gln Ser Gly Ala Tyr Ser Phe Glu Ser Phe Lys Lys Ala Cys Glu		
	85	90 95
Leu Ala Asp Ser Lys Glu Val Asp Gly Ile Cys Thr Leu Pro Ile Asn		
	100	105 110
Lys Leu Ala Trp Gln Gln Ala Gln Ile Pro Phe Val Gly His Thr Asp		
	115	120 125
Phe Leu Lys Gln Arg Tyr Lys Asp His Gln Ile Ile Met Met Leu Gly		
	130	135 140
Cys Ser Lys Leu Phe Val Gly Leu Phe Ser Asp His Val Pro Leu Ser		
	145	150 155 160
Ala Val Ser Gln Leu Ile Gln Val Lys Ala Leu Val Lys Phe Leu Leu		
	165	170 175
Ala Phe Gln Lys Ser Thr Gln Ala Lys Ile Val Gln Val Cys Gly Phe		
	180	185 190
Asn Pro His Ala Gly Glu Glu Gly Leu Phe Gly Glu Glu Asp Glu Lys		
	195	200 205
Ile Leu Lys Ala Ile Gln Glu Ser Asn Gln Thr Leu Gly Phe Glu Cys		
	210	215 220
Phe Leu Gly Pro Leu Pro Ala Asp Ser Ala Phe Ala Pro Asn Lys Arg		
	225	230 235 240
Lys Ile Thr Pro Phe Tyr Val Ser Met Ser His Asp Val Gly Leu Ala		
	245	250 255
Pro Leu Lys Ala Leu Tyr Phe Asp Glu Ser Ile Asn Val Ser Leu Asn		
	260	265 270
Ala Pro Ile Leu Arg Ala Ser Thr Asp His Gly Thr Ala Phe Asp Ile		
	275	280 285
Ala Tyr Gln Asn Lys Ala Asn His Lys Ser Tyr Leu Asn Ala Ile Lys		
	290	295 300
Tyr Leu Ala		
305		

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...702
 (D) OTHER INFORMATION: /note= "VirB4 homolog"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

Val	Ala	Arg	Leu	Val	Val	Lys	Arg	Arg	Lys	Ile	Asp	Tyr	Lys	Gln	Ser	1	5	10	15
Ile	Gln	Ser	Asp	Ser	Gln	Tyr	Leu	Gln	Ala	Xaa	Leu	Asn	Gln	Phe	Glu	20	25	30	
Asn	Lys	Glu	Val	Tyr	Glu	Asn	Gln	Tyr	Phe	Leu	Val	Leu	Glu	Ser	Thr	35	40	45	
His	Ser	Leu	His	Gly	Val	Leu	Glu	His	Lys	Lys	Lys	Ser	Phe	Met	His	50	55	60	
Ala	Asn	Arg	Glu	Asn	Phe	Lys	Asp	Ile	Leu	Ser	Tyr	Lys	Ala	His	Phe	65	70	75	80
Leu	Gln	Glu	Thr	Leu	Lys	Ser	Leu	Glu	Ile	Gln	Leu	Lys	Asn	Tyr	Ala	85	90	95	
Pro	Lys	Leu	Leu	Asn	Ser	Lys	Glu	Val	Leu	Asn	Phe	Tyr	Ala	Glu	Tyr	100	105	110	
Ile	Asn	Gly	Phe	Glu	Leu	Pro	Leu	Lys	Pro	Leu	Val	Gly	Gly	Tyr	Leu	115	120	125	
Ser	Asp	Ser	Tyr	Ile	Ala	Ser	Ser	Ile	Thr	Phe	Glu	Lys	Asp	Tyr	Phe	130	135	140	
Ile	Gln	Glu	Ser	Phe	Asn	Gln	Lys	Thr	Tyr	Asn	Arg	Leu	Ile	Gly	Ile	145	150	155	160
Lys	Ala	Tyr	Glu	Ser	Glu	Arg	Ile	Thr	Ser	Ile	Ala	Val	Gly	Ala	Leu	165	170	175	
Leu	Tyr	Gln	Glu	Thr	Pro	Leu	Asp	Ile	Ile	Phe	Ser	Ile	Glu	Pro	Met	180	185	190	
Ser	Val	Asn	Lys	Thr	Leu	Ser	Phe	Leu	Lys	Glu	Arg	Ala	Lys	Phe	Ser	195	200	205	
Met	Ser	Asn	Leu	Val	Lys	Asn	Glu	Leu	Leu	Glu	Tyr	Gln	Glu	Leu	Val	210	215	220	
Lys	Thr	Lys	Arg	Leu	Ser	Met	Gln	Lys	Phe	Ala	Leu	Asn	Val	Leu	Ile	225	230	235	240

Lys Ala Pro Ser Leu Glu Asp Leu Asp Ala Gln Thr Ser Leu Ile Leu
 245 250 255
 Gly Leu Leu Phe Lys Glu Asn Leu Val Gly Val Ile Glu Thr Phe Gly
 260 265 270
 Leu Lys Gly Gly Tyr Phe Ser Phe Phe Pro Glu Arg Ile His Leu Asn
 275 280 285
 His Arg Leu Arg Phe Leu Thr Ser Lys Ala Leu Ala Cys Leu Met Val
 290 295 300
 Phe Glu Arg Gln Asn Leu Gly Phe Lys Ala Asn Ser Trp Gly Asn Ser
 305 310 315 320
 Pro Leu Ser Val Phe Lys Asn Leu Asp Tyr Ser Pro Phe Leu Phe Asn
 325 330 335
 Phe His Asn Gln Glu Val Ser His Asn Asn Ala Lys Glu Ile Ala Arg
 340 345 350
 Val Asn Gly His Thr Leu Val Ile Gly Ala Thr Gly Ser Gly Lys Ser
 355 360 365
 Thr Leu Ile Ser Tyr Leu Met Met Ser Ala Leu Lys Tyr Gln Asn Met
 370 375 380
 Arg Leu Leu Ala Phe Asp Arg Met Gln Gly Leu Tyr Ser Phe Thr Glu
 385 390 395 400
 Phe Phe Lys Gly His Tyr His Asp Gly Gln Ser Phe Ser Ile Asn Pro
 405 410 415
 Phe Cys Leu Glu Pro Asn Leu Gln Asn Leu Glu Phe Leu Gln Ser Phe
 420 425 430
 Phe Leu Ser Met Leu Asp Leu Ala Pro Ser Arg Asp Lys Glu Ala Leu
 435 440 445
 Glu Asp Met Asn Ala Ile Ser Gly Ala Ile Lys Ser Leu Tyr Glu Thr
 450 455 460
 Leu Tyr Pro Lys Asp Phe Ser Leu Leu Asp Phe Lys Glu Thr Leu Lys
 465 470 475 480
 Arg Thr Ser Ser Asn Gln Leu Gly Leu Ser Leu Glu Pro Tyr Leu Asn
 485 490 495
 Asn Pro Leu Phe Asn Ala Leu Asn Asp Ala Phe Asn Ser Asn Ala Phe
 500 505 510
 Leu Asn Val Ile Asn Leu Asp Ala Ile Thr Gln Asn Pro Lys Asp Leu
 515 520 525
 Gly Leu Leu Ala Tyr Tyr Leu Phe Tyr Lys Ile Leu Glu Glu Ser Arg
 530 535 540

Lys Asn Asp Ser Gly Phe Leu Val Phe Leu Asp Glu Phe Lys Ser Tyr
 545 550 555 560
 Val Glu Asn Asp Leu Leu Asn Thr Lys Ile Asn Ala Leu Ile Thr Gln
 565 570 575
 Ala Arg Lys Ala Asn Gly Val Val Val Leu Ala Leu Gln Asp Ile Tyr
 580 585 590
 Gln Leu Ser Gly Val Lys Asn Ala His Ser Phe Leu Ser Asn Met Gly
 595 600 605
 Thr Leu Ile Leu Tyr Pro Gln Lys Asn Ala Arg Glu Leu Lys His Asn
 610 615 620
 Phe Asn Val Pro Leu Ser Glu Thr Glu Ile Ser Phe Leu Glu Asn Thr
 625 630 635 640
 Pro Leu Tyr Ala Arg Gln Val Leu Val Lys Asn Leu Gly Asn Gly Ser
 645 650 655
 Ser Asn Met Ile Asp Val Ser Leu Glu Gly Leu Gly Cys Tyr Leu Lys
 660 665 670
 Ile Phe Asn Ser Asp Ser Ser His Val Asn Lys Val Lys Ala Leu Gln
 675 680 685
 Lys Asp Tyr Pro Thr Glu Trp Arg Glu Lys Leu Leu Lys Ser
 690 695 700

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...293
- (D) OTHER INFORMATION: /note= "methyl-accepting chemotaxis protein;
transmembrane receptor"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

Met Gln Glu Asp Trp Gln Ala Val Gln Asp Thr Ile Lys Val Val Ser
 1 5 10 15
 Asp Val Lys Ala Gly Asn Phe Ala Val Arg Ile Thr Ala Glu Pro Ala
 20 25 30

Ser	Pro	Asp	Leu	Lys	Glu	Leu	Arg	Asp	Ala	Leu	Asn	Gly	Ile	Met	Xaa			
		35					40					45						
Tyr	Leu	Gln	Glu	Ser	Val	Gly	Thr	His	Met	Pro	Ser	Ile	Phe	Lys	Ile			
	50					55					60							
Phe	Glu	Ser	Tyr	Ser	Gly	Leu	Asp	Phe	Arg	Gly	Arg	Ile	Gln	Asn	Ala			
65					70					75					80			
Ser	Gly	Arg	Val	Glu	Leu	Val	Thr	Asn	Ala	Leu	Gly	Gln	Glu	Ile	Gln			
				85					90					95				
Lys	Met	Leu	Glu	Thr	Ser	Ser	Asn	Phe	Ala	Lys	Asp	Leu	Ala	Asn	Asp			
			100					105					110					
Ser	Ala	Asn	Leu	Lys	Glu	Cys	Val	Gln	Asn	Leu	Glu	Lys	Ala	Ser	Asn			
	115						120					125						
Ser	Gln	His	Lys	Ser	Leu	Met	Glu	Thr	Ser	Lys	Thr	Ile	Glu	Asn	Ile			
	130					135					140							
Thr	Thr	Ser	Ile	Gln	Gly	Val	Ser	Ser	Gln	Ser	Glu	Ala	Met	Ile	Glu			
145					150					155					160			
Gln	Gly	Lys	Asp	Ile	Lys	Ser	Ile	Val	Glu	Ile	Ile	Arg	Asp	Ile	Ala			
				165					170					175				
Asp	Gln	Thr	Asn	Leu	Leu	Ala	Leu	Asn	Ala	Ala	Ile	Glu	Ala	Ala	Arg			
			180					185					190					
Ala	Gly	Glu	His	Gly	Arg	Gly	Phe	Ala	Val	Val	Ala	Asp	Glu	Val	Arg			
	195						200					205						
Lys	Leu	Ala	Glu	Arg	Thr	Gln	Lys	Ser	Leu	Ser	Glu	Ile	Glu	Ala	Asn			
	210					215					220							
Ile	Asn	Ile	Leu	Val	Gln	Ser	Ile	Ser	Asp	Thr	Ser	Glu	Ser	Ile	Lys			
225					230				235					240				
Asn	Gln	Val	Lys	Glu	Val	Glu	Glu	Ile	Asn	Ala	Ser	Ile	Glu	Ala	Leu			
			245						250				255					
Arg	Ser	Val	Thr	Glu	Gly	Asn	Leu	Lys	Ile	Ala	Ser	Asp	Ser	Leu	Glu			
			260					265					270					
Ile	Ser	Gln	Glu	Ile	Asp	Lys	Val	Ser	Asn	Asp	Ile	Leu	Glu	Asp	Val			
	275						280					285						
Asn	Lys	Lys	Gln	Phe														
	290																	

(2) INFORMATION FOR SEQ ID NO:587:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...52
 - (D) OTHER INFORMATION: /note= "sodium/glutamate symport carrier protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

```

Met Pro Lys Ser Phe Thr Leu Pro Thr Phe Val Trp Cys Leu Phe Val
1           5                10                15

Gly Val Ile Leu Arg Asn Ala Leu Ser Phe Phe Lys Ile His Ser Val
          20                25                30

Phe Asp Arg Glu Val Ser Val Ile Gly Asn Val Ser Leu Ser Leu Phe
          35                40                45

Leu Ala Tyr Ala
50

```

(2) INFORMATION FOR SEQ ID NO:588:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 182 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...182
 - (D) OTHER INFORMATION: /note= "HYPOTHETICAL ABC TRANSPORTER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

```

Val Gly Leu Leu Asn Ser Lys Ala Phe Lys Pro Tyr Arg Lys Ile Leu
1           5                10                15

Gln Met Val Phe Gln Asp Pro Tyr Ala Ser Leu Asn Pro Arg Leu Ser
          20                25                30

Ile Gln Ser Ile Leu Ile Glu Ala Leu Arg Phe Ala Tyr Pro Lys Ala

```

35	40	45
Ser Gln Gln Glu Trp His His Leu Ala Glu Leu Cys Leu Glu Glu Val		
50	55	60
Cys Leu Asn Pro Glu Leu Leu Asn Phe Tyr Ala Tyr Glu Leu Ser Gly		
65	70	75
Gly Glu Arg Gln Arg Val Ala Ile Ala Arg Ala Ile Ala Leu Lys Pro		
85	90	95
Arg Ile Ile Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Lys Ser Ile		
100	105	110
Gln Lys Ser Val Leu Glu Leu Leu Leu Asn Leu Gln Glu Lys Gln Asp		
115	120	125
Leu Ser Tyr Leu Phe Ile Ser His Asp Leu Asp Val Ile Lys Ala Phe		
130	135	140
Cys Asp Arg Val Leu Val Val Ser Glu Gly Lys Ile Val Glu Thr Gly		
145	150	155
Ala Ile Glu Glu Val Phe Asp Asn Pro Lys His Ala Tyr Thr Lys Arg		
165	170	175
Leu Leu Glu Ser Arg Leu		
180		

(2) INFORMATION FOR SEQ ID NO:589:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 251 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

Val Ser Leu Ile Lys Val Ser Gly Asp Lys Lys Val Ile Glu Val Ser		
1	5	10
Ile Pro Leu Thr Ser Ile Ser Gly Lys Ala Arg Val Lys Ile Arg His		
20	25	30
Ala Phe Ser Asp Tyr Gly Ile Ser Thr Ala Thr Arg Lys Ile Pro Phe		
35	40	45
Ser Leu Lys His Tyr Val Glu Trp Gln Ile Gly Tyr Asp Val Pro Ile		
50	55	60

Lys	Asp	Lys	Glu	Lys	Phe	Glu	Leu	Thr	Thr	Leu	Lys	Asp	Glu	Lys	Tyr	65	70	75	80
His	Phe	Leu	Gly	Ala	Asn	Asn	Lys	Val	Lys	Thr	Leu	Tyr	Glu	Leu	Ser	85	90	95	
Glu	Met	Ile	Tyr	Tyr	Ala	Lys	Arg	Leu	Gly	Leu	Ile	Ser	Leu	Glu	Asn	100	105	110	
Leu	Glu	Asn	Thr	Leu	Lys	Phe	Leu	Glu	Lys	Gln	Lys	Gln	Phe	Ile	Glu	115	120	125	
Asp	Asn	Phe	Met	Ile	Thr	Arg	Glu	Arg	Phe	Arg	Ser	His	Gln	Phe	Gly	130	135	140	
Gly	Met	Asp	Phe	Glu	Leu	Ser	Arg	Ile	Ser	Tyr	Pro	Leu	Leu	Ile	His	145	150	155	160
Ser	Phe	Asp	Asp	Asn	Glu	Leu	Ser	Glu	Ile	Val	Ile	Lys	Glu	Gln	Gln	165	170	175	
Tyr	Gly	Ser	Lys	Thr	Gln	Ala	Met	Leu	Tyr	Phe	Cys	Phe	Ser	Ile	Leu	180	185	190	
Glu	Leu	Lys	Thr	Ala	Thr	Pro	Leu	Leu	Asn	Arg	Thr	Ala	Met	Pro	Lys	195	200	205	
Glu	His	Ala	Leu	Leu	Ile	Ile	His	Glu	Thr	Asn	Ala	Leu	Val	Phe	Leu	210	215	220	
Glu	Met	Leu	Lys	Ile	Phe	Gly	Leu	Leu	Ser	Gln	Val	His	His	Asn	Asp	225	230	235	240
Val	Leu	Lys	Ile	Leu	Glu	Lys	Ile	Leu	Gln	Asn						245	250		

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: /note= "major surface LPS-antigen"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

Val Ile Thr Ala Cys Phe Asn Arg Glu Lys Thr Ile Glu Asp Thr Ile
 1 5 10 15
 Leu Ser Val Leu Asn Gln Thr Tyr Lys Asn Ile Glu Tyr Ile Ile Ile
 20 25 30
 Asp Gly Ala Ser Ala Ile Ala Leu
 35 40

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

Val Phe Val Gly Leu Tyr His Gly Ala Ser Ile Phe Asp Leu Lys Phe
 1 5 10 15
 Glu Val Tyr Leu Thr Met Leu Ile Ser Leu Met Pro Phe Val Ala Thr
 20 25 30
 Ile Tyr Ile Asn Phe Pro Lys Thr Thr Glu Thr Ser His Gly Tyr Ala
 35 40 45
 Arg Trp Ala Asn Val Lys Asp Ile Glu Cys Phe Lys Ile Phe Ser Lys
 50 55 60
 Glu Gly Phe Cys Lys Val Val His Arg Leu Gly Val Gln Phe Asp Asn
 65 70 75 80
 Gly Phe Ile Leu Gly Lys Phe Gly Phe Pro Lys Leu Arg Asn Val Cys
 85 90 95
 Tyr Asp Lys Pro Leu Gly Thr Met Ile Val Ala Pro Pro Gly Ala Glu
 100 105 110
 Lys Leu His Val Trp Leu Cys Gln Ile Tyr
 115 120

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

Met Lys Arg Leu Ala Val Ala Leu Ile Leu Val Leu Gly Val Val Trp
1 5 10 15
Gly Lys Ser Leu Pro Lys Trp Ala Lys Asp Cys Ser Lys Glu Met Arg
 20 25 30
Ile Glu Lys Thr Gln Thr Lys Asp Glu Lys Ile Leu Val Cys Gly Met
 35 40 45
Ser Asp Ile Leu Leu Ser Asp Met Asp Tyr Ser Leu Ser Ser Ala Arg
 50 55 60
Gln Asn Ala Leu Glu Lys Val Met Glu Ala Phe Lys Gly Asp Arg Ile
65 70 75 80
Glu Ile Lys Ala Gly Glu Leu Lys Ala Thr Phe Ile Asp Thr Asp Lys
 85 90 95
Val Tyr Val Leu Leu Arg Ile Thr Lys Lys His Val Ala Leu Met Asn
 100 105 110
Glu

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...437

(D) OTHER INFORMATION: /note= "alpha-ketoglutarate permease"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

Met Asn Pro Gln Ile Gln Pro Ala Thr Lys Lys Pro Leu Lys Ser Leu
1 5 10 15

Leu	Ala	Ala	Ser	Ser	Gly	Asn	Leu	Val	Glu	Trp	Tyr	Asp	Phe	Tyr	Ala	
			20					25					30			
Tyr	Ala	Phe	Leu	Ala	Pro	Tyr	Phe	Ala	Lys	Glu	Phe	Thr	His	Thr	Asn	
		35					40					45				
Asp	Pro	Thr	Leu	Ala	Leu	Ile	Ser	Ala	Phe	Leu	Val	Phe	Met	Leu	Gly	
	50					55					60					
Phe	Phe	Met	Arg	Pro	Leu	Gly	Ser	Leu	Phe	Phe	Gly	Lys	Leu	Gly	Asp	
65					70					75					80	
Lys	Lys	Gly	Arg	Lys	Thr	Ser	Met	Val	Tyr	Ser	Ile	Ile	Leu	Met	Ala	
				85					90					95		
Leu	Gly	Ser	Phe	Met	Leu	Ala	Leu	Leu	Pro	Thr	Lys	Glu	Ile	Val	Gly	
			100					105					110			
Glu	Trp	Ala	Phe	Leu	Phe	Leu	Leu	Leu	Ala	Arg	Leu	Leu	Gln	Gly	Phe	
		115					120					125				
Ser	Val	Gly	Gly	Glu	Tyr	Gly	Val	Val	Ala	Thr	Tyr	Leu	Ser	Glu	Leu	
	130					135					140					
Gly	Lys	Asn	Gly	Lys	Lys	Gly	Phe	Tyr	Gly	Ser	Phe	Gln	Tyr	Val	Thr	
145					150					155					160	
Leu	Val	Gly	Gly	Gln	Leu	Leu	Ala	Ile	Phe	Ser	Leu	Phe	Ile	Val	Glu	
				165				170						175		
Asn	Val	Tyr	Thr	His	Glu	Gln	Ile	Ser	Ala	Phe	Ala	Trp	Arg	Tyr	Leu	
			180					185					190			
Phe	Ala	Leu	Glu	Gly	Ile	Leu	Ala	Leu	Leu	Ser	Leu	Phe	Leu	Arg	Asn	
		195					200					205				
Ile	Met	Glu	Glu	Thr	Met	Asp	Asn	Glu	Ala	Thr	Pro	Gln	Lys	Lys	Thr	
	210					215					220					
Asn	Val	Asn	Asn	Thr	Lys	Glu	Thr	His	Ile	Lys	Glu	Thr	Gln	Arg	Gly	
225					230					235					240	
Ser	Leu	Lys	Glu	Leu	Leu	Asn	His	Lys	Lys	Ala	Leu	Met	Ile	Val	Phe	
				245				250						255		
Gly	Leu	Thr	Met	Gly	Gly	Ser	Leu	Cys	Phe	Tyr	Thr	Phe	Thr	Val	Tyr	
			260					265					270			
Leu	Lys	Ile	Phe	Leu	Thr	Asn	Ser	Ser	Ser	Phe	Ser	Pro	Lys	Glu	Ser	
		275					280					285				
Ser	Phe	Ile	Met	Leu	Leu	Ala	Leu	Ser	Tyr	Phe	Ile	Phe	Leu	Gln	Pro	
	290					295					300					
Leu	Cys	Gly	Met	Leu	Ala	Asp	Lys	Ile	Lys	Arg	Thr	Gln	Met	Leu	Met	
305					310					315					320	
Val	Phe	Ala	Ile	Thr	Gly	Leu	Ile	Val	Thr	Pro	Ile	Val	Phe	Tyr	Gly	

	325		330		335
Ile Lys His Ala Thr Ser Val Tyr Glu Ala Leu Phe Tyr Glu Ile Leu					
	340		345		350
Ala Leu Ser Ser Met Ser Phe Tyr Thr Cys Ile Ala Gly Val Ile Lys					
	355		360		365
Ala Glu Leu Phe Pro Glu His Val Arg Ala Leu Gly Val Gly Leu Ala					
	370		375		380
Tyr Ala Ile Ala Asn Ala Leu Phe Gly Gly Ser Ala Ser Tyr Ile Ala					
385		390		395	400
Leu Glu Phe Lys Gln His Gly Phe Glu Glu Gly Phe Val Gly Tyr Val					
	405		410		415
Met Leu Ser Ile Val Ile Phe Met Val Met Val Ile Ile Phe Pro Lys					
	420		425		430
Lys Thr Tyr Leu Glu					
	435				

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

Met Ser Ser Gly Leu Ile Tyr Ile Ser Leu Glu Val Leu Val Xaa Cys			
1	5	10	15
Leu Ile Thr Ala Leu Ile Met Tyr Tyr Val Met Lys Lys Ile Tyr Tyr			
	20	25	30
Ala Arg Gly Gln Ala Ile Leu Lys Gly Ala Ser Ala Lys Ala Lys Leu			
	35	40	45
Met Glu Phe Gln Ala Lys Ser Phe Val Glu Ala Glu Glu Met Arg Met			
	50	55	60
Lys Ser Gln Glu Cys Lys Leu Gln Gln Gln Tyr Glu Asn Lys Asn Leu			
65	70	75	80
Gln Leu Gln Thr His Phe Asp Lys Lys Glu Ala His Leu Lys His Leu			
	85	90	95

Glu	Ala	Gln	His	Lys	Glu	Phe	Val	Arg	Asp	Glu	Lys	Arg	Tyr	Leu	Glu
			100					105					110		
Lys	Glu	Lys	Lys	Glu	Leu	Glu	Lys	Glu	Arg	Gln	Ile	Leu	Glu	Xaa	Glu
		115					120					125			
Arg	Glu	Asn	Phe	Xaa	Xaa	Gln	Arg	Ala	Phe	Val	Xaa	Xaa	Xaa	Xaa	Ala
	130					135					140				
Lys	Ala														
	145														

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

Met	Asn	Ile	Lys	Ile	Leu	Lys	Ile	Leu	Val	Gly	Gly	Leu	Phe	Phe	Leu
1			5					10						15	
Ser	Leu	Asn	Ala	His	Leu	Trp	Gly	Lys	Gln	Asp	Asn	Ser	Phe	Leu	Gly
		20					25					30			
Ile	Gly	Glu	Arg	Ala	Tyr	Lys	Ser	Gly	Asn	Tyr	Ser	Lys	Ala	Ala	Ser
	35					40					45				
Tyr	Phe	Lys	Lys	Ala	Cys	Asn	Asp	Gly	Val	Ser	Glu	Gly	Cys	Thr	Gln
	50				55					60					
Leu	Gly	Ile	Ile	Tyr	Glu	Asn	Gly	Gln	Gly	Thr	Arg	Ile	Asp	Tyr	Lys
65				70				75						80	
Lys	Ala	Leu	Glu	Tyr	Tyr	Lys	Thr	Ala	Cys	Gln	Ala	Asp	Asp	Arg	Glu
			85					90						95	
Gly	Cys	Phe	Gly	Leu	Gly	Gly	Leu	Tyr	Asp	Glu	Gly	Leu	Gly	Thr	Ala
		100					105					110			
Gln	Asn	Tyr	Gln	Glu	Ala	Xaa	Asp	Ala	Tyr	Ala	Arg	His	Ala	Phe	
	115						120					125			

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...95

(D) OTHER INFORMATION: /note= "phosphoglucomutase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

Met	Asp	Ile	Ser	Ile	Phe	Arg	Glu	Tyr	Asp	Ile	Arg	Gly	Ile	Tyr	Pro
1				5					10					15	
Thr	Thr	Leu	Asp	Glu	Asn	Thr	Ala	Phe	Ser	Ile	Gly	Val	Glu	Leu	Gly
			20					25					30		
Lys	Ile	Met	Arg	Glu	Tyr	Asp	Lys	Ser	Val	Phe	Val	Gly	His	Asp	Ala
		35					40					45			
Arg	Val	His	Gly	Arg	Phe	Leu	Phe	Glu	Val	Leu	Ser	Ala	Gly	Leu	Gln
		50				55					60				
Ser	Ser	Gly	Leu	Lys	Val	Tyr	Asp	Leu	Gly	Leu	Ile	Pro	Thr	Pro	Val
65				70					75						80
Ala	Tyr	Phe	Ala	Ala	Phe	Asn	Glu	Ile	Asp	Asn	Ile	Gln	Trp	Pro	
			85						90					95	

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

Val	Cys	Asp	Ile	Phe	Ser	Asp	Gly	Val	Leu	Leu	Asp	Lys	Ala	Leu	Val
1				5				10						15	
Ile	Tyr	Phe	Lys	Ala	Pro	Tyr	Ser	Phe	Thr	Gly	Glu	Asp	Val	Cys	Glu
			20					25					30		

Ile Gln Cys His Gly Ser Pro Leu Leu Ala Gln Asn Ile Leu Gln Ala
35 40 45

Cys Leu Asn Leu Gly Ala Arg Leu Ala Lys Ala Gly Glu Phe Ser Lys
50 55 60

Lys Ala Phe Leu Asn His Lys Met Asp Leu Ser Glu Ile Glu Ala Ser
65 70 75 80

Val Gln Leu Ile Leu Cys Glu Asp Glu Ser Val Leu Asn Ala Leu Ala
85 90 95

Arg Gln Leu Gln Gly Gly
100

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

Met Phe Lys Lys Met Cys Leu Ser Leu Leu Met Ile Ser Gly Val Cys
1 5 10 15

Val Gly Ala Lys Asp Leu Asp Phe Lys Leu Asp Tyr Arg Ala Thr Gly
20 25 30

Gly Lys Phe Met Gly Lys Met Thr Asp Ser Ser Leu Leu Ser Ile Thr
35 40 45

Ser Met Asn Asp Glu Pro Val Val Ile Lys Asn Leu Ile Val Asn Arg
50 55 60

Gly Asn Ser Val Glu Ala Thr Lys Lys Val Glu Pro Lys Phe Gly Asp
65 70 75 80

Lys Phe Lys Lys Glu Lys Leu Phe Asp His Glu Leu Lys Tyr Ser Gln
85 90 95

Gln Ile Phe Tyr Arg Leu Asp Cys Lys Pro Asn Gln Leu Leu Glu Val
100 105 110

Lys Ile Ile Thr Asp Lys Gly Glu Tyr Tyr His Lys Phe Ser Lys
115 120 125

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...502
- (D) OTHER INFORMATION: /note= "SULFATE TRANSPORT ATP-BINDING PROTEIN CYSA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

Met	Thr	Leu	Lys	Pro	Tyr	Pro	Thr	Lys	Glu	Thr	Gly	Leu	Ala	Ser	Gln
1				5					10					15	
Leu	Ser	Gly	His	Trp	Phe	Phe	Gln	Leu	Ser	Leu	Phe	Asn	Lys	Thr	Asn
			20					25					30		
Phe	Asn	Pro	Asn	Lys	Ile	Trp	Ile	Pro	Leu	Glu	Phe	Asn	Lys	Arg	Ser
			35				40					45			
Lys	Ile	Lys	Phe	Asp	Lys	Asp	Leu	Glu	Ile	Tyr	Phe	Asp	Ser	His	Glu
	50					55					60				
Ser	Phe	Asn	Ile	Ser	Lys	Lys	Tyr	Leu	Gln	Glu	Ile	Asp	Gln	Glu	Ser
65					70					75					80
Leu	Lys	Lys	Ile	Lys	Gln	Ser	Lys	Asp	Phe	Phe	Ser	Ile	Gln	Lys	Ile
				85					90					95	
Glu	Ser	Lys	His	Asp	Asn	Asn	Asp	Ile	Leu	Gln	Leu	Glu	Phe	Phe	Glu
			100					105					110		
Asn	Asp	Thr	Ser	Phe	Leu	Phe	Ala	Lys	Gly	Ser	Phe	Ala	Glu	Ile	Leu
			115				120					125			
Glu	Tyr	Asn	Met	Gln	Leu	Lys	Ile	Asp	Ser	Leu	Ile	Thr	Lys	Glu	Phe
	130					135					140				
Asn	Lys	Leu	Leu	Ala	Ile	Val	Gln	Asp	Ser	Pro	Gln	Asp	Ser	Tyr	Gln
145					150					155					160
Leu	Lys	Ile	Arg	Val	Arg	His	Asn	Asn	Lys	Leu	Pro	Arg	Glu	Lys	Tyr
				165					170					175	
Thr	Glu	His	Glu	Ile	Lys	Leu	Glu	Val	Tyr	Asp	Cys	Arg	Lys	Ser	His
			180					185					190		
Asp	His	Asn	Glu	Pro	Ile	Ile	Leu	Ser	Gln	Gln	Ser	Thr	Gly	Phe	Gln

195					200					205					
Trp	Ala	Phe	Asn	Phe	Met	Phe	Gly	Phe	Leu	Tyr	Asn	Val	Gly	Ser	His
	210					215					220				
Phe	Ser	Phe	Asn	His	Asn	Ile	Ile	Tyr	Val	Met	Asp	Glu	Pro	Ala	Thr
225					230					235					240
His	Leu	Ser	Val	Pro	Ala	Arg	Lys	Glu	Phe	Arg	Lys	Phe	Leu	Lys	Glu
				245					250					255	
Tyr	Ala	His	Lys	Asn	His	Val	Thr	Phe	Val	Leu	Ala	Thr	His	Asp	Pro
			260					265					270		
Phe	Leu	Val	Asp	Thr	Asp	His	Leu	Asp	Glu	Ile	Arg	Ile	Val	Glu	Lys
		275					280					285			
Glu	Thr	Glu	Gly	Ser	Val	Ile	Lys	Asn	His	Phe	Asn	Tyr	Pro	Leu	Asn
	290					295					300				
Asn	Ala	Ser	Lys	Asp	Ser	Asp	Ala	Leu	Asp	Lys	Ile	Lys	Arg	Ser	Leu
305					310					315					320
Gly	Val	Gly	Gln	His	Val	Phe	His	Asn	Pro	Gln	Lys	His	Arg	Ile	Ile
				325					330					335	
Phe	Val	Glu	Gly	Ile	Thr	Asp	Tyr	Cys	Tyr	Leu	Ser	Ala	Phe	Lys	Leu
			340					345					350		
Tyr	Leu	Arg	Tyr	Lys	Glu	Tyr	Lys	Asp	Asn	Pro	Ile	Pro	Phe	Thr	Phe
		355					360					365			
Leu	Pro	Ile	Ser	Gly	Leu	Lys	Asn	Asp	Ser	Asn	Asp	Met	Lys	Glu	Thr
	370					375					380				
Ile	Glu	Lys	Leu	Cys	Glu	Leu	Asp	Asn	His	Pro	Ile	Val	Leu	Thr	Asp
385					390					395					400
Asp	Asp	Arg	Lys	Cys	Val	Phe	Asn	Gln	Gln	Ala	Thr	Ser	Glu	Arg	Phe
				405					410					415	
Lys	Arg	Ala	Asn	Glu	Glu	Met	His	Asp	Pro	Ile	Thr	Ile	Leu	Gln	Leu
			420					425					430		
Ser	Asp	Cys	Asp	Arg	His	Phe	Lys	Gln	Ile	Glu	Asp	Cys	Phe	Ser	Ala
		435					440					445			
Asn	Asp	Arg	Asn	Lys	Tyr	Ala	Lys	Asn	Lys	Gln	Met	Glu	Leu	Ser	Met
	450				455						460				
Ala	Phe	Lys	Thr	Arg	Leu	Leu	Tyr	Gly	Gly	Glu	Asp	Ala	Ile	Glu	Lys
465					470					475					480
Gln	Thr	Lys	Arg	Asn	Phe	Leu	Lys	Leu	Phe	Lys	Trp	Ile	Ala	Trp	Ala
				485					490					495	
Thr	Asn	Leu	Ile	Lys	Asn										
			500												

(2) INFORMATION FOR SEQ ID NO:600:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

```
Val Tyr Phe Phe Leu Ala Leu Ser Gly Glu Lys Val Leu Leu Pro Val
1           5              10              15

Ile Gly Gly Leu Glu Lys Asn Ala Leu Glu Ala Gly Leu Leu Lys Gly
          20              25              30

Asp Arg Ile Leu Leu Ser Thr Ile Lys Lys
        35              40
```

(2) INFORMATION FOR SEQ ID NO:601:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 341 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

```
Met Glu Asn Phe Lys Leu Ile Asn Phe Phe Thr Gly Gln Asn Asp Ala
1           5              10              15

Gly Lys Thr Asn Leu Leu Glu Ala Leu Tyr Thr Asn Thr Gly Leu Cys
          20              25              30

Asp Pro Thr Ala Asn Gln Val Ser Leu Pro Pro Glu His Ala Val Asn
        35              40              45

Ile Ser Glu Phe Arg Lys Ile Lys Leu Asp Ala Asp Asn Leu Lys Thr
        50              55              60

Phe Phe Tyr Gln Gly Asn Thr Ala Asn Pro Ile Ser Ile Arg Thr Glu
65           70              75              80
```


Phe	Glu	His	Ala	Thr	Ile	Pro	Leu	Thr	Ile	Gln	Tyr	Pro	Thr	Gln	Thr	85	90	95
Ser	Tyr	Ser	Lys	Asp	Ile	Asn	Leu	Asn	Ser	Asp	Asp	Ala	His	Met	Thr	100	105	110
Asn	Leu	Ile	Asn	Thr	Thr	Ile	Thr	Lys	Pro	Gln	Leu	Gln	Phe	Ser	Tyr	115	120	125
Asn	Pro	Ser	Leu	Ser	Pro	Met	Thr	Met	Thr	Tyr	Glu	Phe	Glu	Arg	Gln	130	135	140
Asn	Leu	Gly	Leu	Ile	His	Ser	Asn	Leu	Asp	Lys	Ile	Ala	Gln	Thr	Tyr	145	150	155
Lys	Glu	Asn	Ala	Met	Phe	Ile	Pro	Ile	Glu	Leu	Ser	Ile	Val	Asn	Ser	165	170	175
Leu	Lys	Ala	Leu	Glu	Asn	Leu	Gln	Leu	Ala	Ser	Lys	Glu	Lys	Glu	Leu	180	185	190
Ile	Glu	Ile	Leu	Gln	Cys	Phe	Asn	Pro	Asn	Ile	Leu	Asn	Ala	Asn	Thr	195	200	205
Ile	Arg	Lys	Ser	Val	Tyr	Ile	Gln	Ile	Lys	Asp	Glu	Asn	Thr	Pro	Leu	210	215	220
Glu	Glu	Ser	Pro	Lys	Arg	Leu	Leu	Asn	Leu	Phe	Gly	Trp	Gly	Phe	Ile	225	230	235
Lys	Phe	Phe	Ile	Met	Val	Ser	Ile	Leu	Ile	Asp	Asn	Arg	Val	Lys	Tyr	245	250	255
Leu	Phe	Ile	Asp	Glu	Ile	Glu	Ser	Gly	Leu	His	His	Thr	Lys	Met	Gln	260	265	270
Glu	Phe	Leu	Lys	Ala	Leu	Phe	Lys	Leu	Ala	Gln	Lys	Leu	Gln	Ile	Gln	275	280	285
Ile	Phe	Ala	Thr	Thr	His	Asn	Lys	Glu	Phe	Leu	Leu	Asn	Ala	Ile	Asn	290	295	300
Thr	Ile	Ser	Asp	Asn	Glu	Thr	Gly	Val	Phe	Lys	Asp	Ile	Ala	Leu	Phe	305	310	315
Glu	Leu	Glu	Lys	Glu	Ser	Ala	Ser	Asp	Phe	Ile	Arg	His	Ser	Tyr	Ser	325	330	335
Met	Leu	Glu	Lys	Ala												340		

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

Met	Asp	Phe	Lys	Lys	Cys	Pro	Asn	Phe	Glu	Lys	Lys	Cys	Ala	Phe	Leu	
1			5						10					15		
Cys	Phe	Ser	Asn	Leu	Val	Leu	Leu	Ile	Glu	Ile	His	Ser	Lys	Gly	Leu	
			20					25					30			
His	Met	Gln	Lys	Lys	Lys	Pro	Lys	Asn	Pro	Gln	Pro	Asn	Leu	Phe	Ser	
		35					40					45				
Ile	Leu	Asp	Lys	Gly	Asp	Val	Ala	Thr	Asn	Asn	Pro	Val	Glu	Glu	Ser	
	50					55					60					
Asp	Lys	Ala	Asn	Lys	Ile	Gln	Glu	Pro	Leu	Pro	Tyr	Val	Val	Lys	Thr	
65				70				75							80	
Gln	Ile	Asn	Lys	Ala	Ser	Met	Ile	Ser	Arg	Asp	Pro	Ile	Glu	Trp	Ala	
			85					90						95		
Lys	Tyr	Leu	Ser	Phe	Glu	Lys	Arg	Val	Tyr	Lys	Asp	Asn	Ser	Lys	Glu	
		100						105					110			
Asp	Val	Asn	Phe	Phe	Ala	Asn	Gly	Glu	Ile	Lys	Glu	Ser	Ser	Arg	Val	
		115					120					125				
Tyr	Glu	Ala	Asn	Lys	Glu	Gly	Phe	Glu	Arg	Arg	Ile	Thr	Lys	Arg	Tyr	
	130					135					140					
Asp	Leu	Ile	Asp	Arg	Asn	Ile	Asp	Arg	Asn	Arg	Glu	Phe	Phe	Ile	Lys	
145				150					155						160	
Glu	Ile	Glu	Ile	Leu	Thr	His	Thr	Asn	Ser	Leu	Lys	Glu	Leu	Lys	Glu	
			165					170					175			
Gln	Gly	Leu	Glu	Ile	Gln	Leu	Thr	His	His	Asn	Glu	Thr	His	Lys	Lys	
		180					185						190			
Ala	Leu	Glu	Asn	Gly	Asn	Glu	Ile	Val	Lys	Glu	Tyr	Asp	His	Leu	Lys	
		195					200					205				
Asp	Ile	Tyr	Gln	Glu	Val	Glu	Arg	Thr	Lys	Asp	Gly	Gly	Leu	Val	Arg	
	210					215					220					
Glu	Ile	Ile	Pro	Ser	Ile	Ser	Ser	Ala	Glu	Tyr	Phe	Lys	Leu	Tyr	Asn	
225				230					235						240	
Lys	Leu	Pro	Phe	Glu	Ser	Ile	Asn	Asn	Glu	Asn	Thr	Lys	Leu	Asn	Thr	
			245						250					255		

Asn Asp Asn Glu Glu Val Lys Lys Leu Glu Phe Glu Leu Ala Lys Glu
 260 265 270
 Val His Ile Leu Ile Leu Glu Gln Gln Leu Leu Ser Ala Thr Asn Tyr
 275 280 285
 Tyr Ser Trp Ile Asp Lys Asp Asp Asn Ala Asn Phe Ala Trp Lys Met
 290 295 300
 His Arg Leu Ile Asn Glu Asn Lys Leu Lys Glu Asn His Leu Ser Ala
 305 310 315 320
 Asn Asn Ala Asn Lys Ile Lys Gln Phe Phe Phe Asn Asn Gly Ser Ile
 325 330 335
 Leu Gly Trp Thr Lys Glu Glu Gln Ser Ala Ile Gln Glu Asn Arg Asp
 340 345 350
 Tyr Ser Leu Arg Ser Ala Leu Leu Ser Leu Glu Glu Ile Ala Gln Ala
 355 360 365
 Lys Ile Glu Leu Gln Lys Tyr Tyr Glu Ser Val Tyr Val Asn Gly Asp
 370 375 380
 Gly Asn Lys Arg Glu Ile Lys Pro Phe Lys Glu Ile Leu Arg Asp Thr
 385 390 395 400
 Asn Asn Phe Glu Lys Ala Tyr Lys Glu Arg Tyr Asp Lys Leu Val Ser
 405 410 415
 Leu Ser Ala Ala Ile Ile Gln Ala Lys Glu Gly Gly Asn Glu Arg Gln
 420 425 430
 Asn Ser Ser Ala Asn Asn Asn Asn Pro Ile Lys Asn Thr Ile Glu Thr
 435 440 445
 Asn Thr Ser Asn Asn Ile Ile Gln Asn Asn Asp Asn Ile Ile Ile Gln
 450 455 460
 Ile
 465

(2) INFORMATION FOR SEQ ID NO:603:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

Met Ala Leu Glu Val Val Leu Trp Asp Phe Asp Gly Val Ile Phe Asp
1 5 10 15

Ser Met His Leu Lys Tyr Glu Gly Phe Lys Ala Leu Phe Gln Lys His
 20 25 30

Gly Asn Asp Ser Lys Glu Gly Leu Lys Gln Phe Glu Val Tyr His Tyr
 35 40 45

Gln Ser Gly Gly Ile Ser Arg Asn Glu Lys Ile Gln Tyr Phe Tyr Asn
 50 55 60

Glu Ile Leu Lys Thr Pro Ile Ala Gln Glu Glu Ile Asp Ala Leu Ala
65 70 75 80

Leu Glu Phe Gly Ala Ile Ile Glu Gln Lys Leu Phe Asp Arg Gly His
 85 90 95

Leu Asn Ser Glu Val Met Ala Phe Ile Asp Lys His Tyr Gln Asn Tyr
 100 105 110

Ile Phe His Ile Ala Ser Ala Ala Leu His Ser Glu Leu Gln Val Leu
 115 120 125

Cys Glu Phe Leu Gly Ile Thr Lys Tyr Phe Lys Ser Val Glu Gly Ser
 130 135 140

Pro Pro Asp Lys Pro Lys Ile Ile Ala Asn Ile Ile Gln Lys Tyr Ala
145 150 155 160

Tyr Asp Pro Ser Arg Met Leu Met Ile Ala Ile Ala Ser Met Ile Met
 165 170 175

Lys Ala Leu Arg Leu Ile Lys Trp Arg Phe Trp Ala Ile Thr Ala Arg
 180 185 190

Phe

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

Met Leu Lys Lys Lys Ile Asp Leu His Lys Asp Ser Ile Arg Lys Leu

1	5	10	15
Phe Phe Tyr Tyr Phe Ile Pro Leu Val Phe Ser Met Ile Ser Leu Ser	20	25	30
Thr Tyr Ser Met Val Asp Asp Met Phe Val Gly Lys Lys Leu Gly Lys	35	40	45
Glu Ala Ile Ala Ala Val Asn Ile Ala Trp Pro Ile Phe Pro Gly Leu	50	55	60
Ile Ala Tyr Glu Leu Leu Phe Gly Phe Gly Ala Ala Ser Ile Val Gly	65	70	75
Tyr Phe Leu Gly Gln Asn Lys Thr His Arg Ala Arg Leu Val Phe Ser	85	90	95
Ser Val Phe Tyr Phe Val Ala Leu Ser Ala Phe Ile Leu Ser Met Ala	100	105	110
Leu Leu Pro Phe Ser Glu Asn Ile Ala Gln Phe Phe Gly Ser Asn Asp	115	120	125
Ala Leu Leu Asn Met Ser Asn Ala Ile Leu Lys Ser Phe	130	135	140

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

Val Lys Cys Leu Leu Ile Lys Lys Ser Leu Leu Phe Ala Leu Lys Pro	1	5	10	15
Leu Pro Asp Leu Lys Thr Thr Thr Pro Ile Leu Ala Pro Met Ser Val	20	25	30	
Val Ala Gly Arg Leu Xaa Xaa His Leu Val Gln His Tyr Leu Leu Ala	35	40	45	
Leu Glu His Val Lys Gly Phe Met Gly Lys Gly Val Ile Leu Gly Gly	50	55	60	
Leu Ser Gly Ala Gln Arg Ala Lys Ile Val Val Ile Gly Gly Gly Val	65	70	75	80

Val	Gly	Met	Glu	Ser	Ala	Lys	Val	Leu	Xaa	Gln	Met	Gly	Xaa	Lys	Val	85	90	95
Thr	Ile	Leu	Glu	Leu	Asp	Tyr	Ala	Lys	Leu	Gln	Asn	His	Pro	Tyr	Tyr	100	105	110
His	Leu	Tyr	Asp	Leu	Glu	Val	Leu	Ser	Val	Asn	Glu	Ala	Asn	Ile	Ile	115	120	125
Gln	Ala	Leu	Asn	Gly	Xaa	Val	Gly	Leu	Val	Gly	Ala	Val	Leu	Val	Thr	130	135	140
Xaa	Ser	Gln	Thr	Pro	Lys	Val	Xaa	Leu	Arg	Arg	His	Leu	Lys	Tyr		145	150	155

(2) INFORMATION FOR SEQ ID NO:606:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

Met	Leu	Ala	Lys	Ile	Val	Phe	Ser	Ser	Leu	Val	Ala	Phe	Gly	Val	Leu	1	5	10	15
Ser	Ala	Asn	Val	Glu	Gln	Phe	Gly	Ser	Phe	Phe	Asn	Glu	Ile	Lys	Lys	20	25	30	
Glu	Gln	Glu	Glu	Val	Ala	Ala	Lys	Glu	Asp	Ala	Leu	Lys	Ala	Arg	Lys	35	40	45	
Lys	Leu	Leu	Asn	Asn	Thr	His	Asp	Phe	Leu	Glu	Asp	Leu	Val	Phe	Arg	50	55	60	
Lys	Gln	Lys	Ile	Lys	Glu	Leu	Val	Asp	Tyr	Arg	Ala	Lys	Val	Leu	Leu	65	70	75	80
Asp	Leu	Glu	Asn	Lys	Tyr	Lys	Lys	Glu	Lys	Glu	Ala	Leu	Glu	Lys	Glu	85	90	95	
Thr	Arg	Gly	Lys	Ile	Leu	Thr	Ala	Lys	Ser	Lys	Ala	Tyr	Gly	Asp	Leu	100	105	110	
Glu	Gln	Ala	Leu	Lys	Asp	Asn	Pro	Leu	Tyr	Lys	Lys	Leu	Leu	Pro	Asn	115	120	125	
Pro	Tyr	Ala	Tyr	Val	Leu	Asn	Gln	Glu	Thr	Phe	Thr	Gln	Glu	Asp	Lys	130	135	140	

Glu	Arg	Leu	Ser	Tyr	Tyr	Tyr	Pro	Gln	Val	Lys	Thr	Ser	Ser	Ile	Phe	145	150	155	160
Lys	Lys	Thr	Thr	Ala	Thr	Thr	Lys	Asp	Lys	Ala	Gln	Ala	Leu	Leu	Gln	165	170	175	
Met	Gly	Val	Phe	Ser	Leu	Asp	Glu	Glu	Gln	Asn	Lys	Lys	Ala	Ser	Arg	180	185	190	
Leu	Ala	Leu	Ser	Tyr	Lys	Gln	Ala	Ile	Glu	Glu	Tyr	Ser	Asn	Asn	Ile	195	200	205	
Ser	Asn	Leu	Leu	Ser	Arg	Lys	Glu	Leu	Asp	Asn	Ile	Asp	Tyr	Tyr	Leu	210	215	220	
Gln	Leu	Glu	Arg	Asn	Lys	Phe	Asp	Ser	Lys	Ala	Lys	Asp	Ile	Ala	Gln	225	230	235	240
Lys	Ala	Thr	Asn	Thr	Leu	Ile	Phe	Asn	Ser	Glu	Arg	Leu	Ala	Phe	Ser	245	250	255	
Met	Ala	Ile	Asp	Lys	Ile	Asn	Glu	Lys	Tyr	Leu	Arg	Gly	Tyr	Glu	Ala	260	265	270	
Phe	Ser	Asn	Leu	Leu	Lys	Asn	Val	Lys	Asp	Asp	Val	Glu	Leu	Asn	Thr	275	280	285	
Leu	Thr	Lys	Asn	Phe	Thr	Asn	Gln	Lys	Leu	Ser	Phe	Ala	Gln	Lys	Gln	290	295	300	
Lys	Leu	Cys	Leu	Leu	Val	Leu	Asp	Ser	Phe	Asn	Phe	Asp	Thr	Gln	Ser	305	310	315	320
Lys	Lys	Ser	Ile	Leu	Lys	Lys	Thr	Asn	Glu	Tyr	Asn	Ile	Phe	Val	Asp	325	330	335	
Ser	Asp	Pro	Met	Met	Ser	Asp	Lys	Thr	Thr	Met	Gln	Lys	Glu	His	Tyr	340	345	350	
Lys	Ile	Phe	Asn	Phe	Phe	Lys	Thr	Val	Val	Ser	Ala	Tyr	Arg	Asn	Asn	355	360	365	
Val	Ala	Lys	Asn	Asn	Pro	Phe	Glu									370	375		

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

Met	Asp	Phe	Val	Gly	Phe	Glu	Asp	Leu	Lys	Cys	Lys	Asp	Lys	Glu	Asn	
1				5					10					15		
Ser	Gln	Lys	Val	Phe	Val	Ile	Arg	Asn	Asp	Lys	Leu	Gly	Asp	Phe	Ile	
			20					25					30			
Leu	Glu	Ile	Pro	Ala	Leu	Ile	Ala	Leu	Lys	His	Ala	Phe	Leu	Glu	Lys	
			35				40					45				
Gly	Val	Glu	Val	Tyr	Leu	Gly	Val	Val	Val	Pro	Ser	Tyr	Thr	Thr	Pro	
	50					55					60					
Ile	Ala	Leu	Glu	Phe	Pro	Phe	Ile	Asp	Glu	Val	Ile	Ile	Glu	Asp	Asn	
65					70				75						80	
His	Leu	Ala	Thr	Thr	His	Lys	Asn	Arg	Ser	Ile	Asp	Ala	Leu	Ile	Phe	
				85					90					95		
Leu	Phe	Ser	Asn	Phe	Lys	Asn	Ala	Lys	Leu	Ala	Phe	Ser	Leu	Arg	Lys	
			100					105					110			
Ser	Ile	Pro	Tyr	Ile	Leu	Ala	Pro	Lys	Thr	Lys	Ile	Tyr	Ser	Trp	Leu	
		115					120					125				
Tyr	Gln	Lys	Arg	Val	Arg	Gln	Asn	Arg	Ser	Leu	Cys	Leu	Lys	Thr	Glu	
	130					135					140					
Tyr	Glu	Tyr	Asn	Leu	Asp	Leu	Ile	His	Ala	Phe	Cys	Lys	Asp	Tyr	Asp	
145					150				155						160	
Leu	Pro	Asn	Ala	Gln	Leu	Lys	Lys	Ile	Ala	Trp	Lys	Leu	Lys	Asp	Lys	
				165					170					175		
Ser	Lys	Glu	Arg	Ser	Ile	Ile	Ala	Ser	Lys	Leu	Asn	Ala	Asn	Val	Asp	
			180					185					190			
Leu	Leu	Trp	Ile	Gly	Val	His	Met	His	Ser	Gly	Gly	Ser	Ser	Pro	Val	
	195						200					205				
Leu	Pro	Ala	Ser	His	Phe	Ile	Glu	Leu	Ile	Ala	Ile	Leu	His	Glu	Lys	
	210					215					220					
Leu	Ser	Cys	Glu	Ile	Ile	Leu	Ile	Cys	Gly	Pro	Gly	Glu	Arg	Lys	Ala	
225					230				235						240	
Thr	Glu	Glu	Leu	Leu	Lys	Glu	Val	Pro	Phe	Ala	His	Leu	Tyr	Asp	Thr	
			245						250					255		
Ser	His	Ser	Leu	Val	Asp	Leu	Ala	Lys	Leu	Cys	Ala	Asn	Leu	Ser	Val	
			260					265					270			
Cys	Ile	Gly	Asn	Ala	Ser	Gly	Pro	Leu	His	Val	Asn	Ala	Leu	Phe	Asp	
	275						280					285				

Asn Gln Ser Ile Gly Phe Tyr Pro Asn Glu Leu Thr Ala Ser Ile Ala
 290 295 300
 Arg Trp Arg Pro Phe Asn Glu Gln Phe Leu Gly Ile Thr Pro Pro Asn
 305 310 315 320
 Gly Ser Asn Asp Met Gly Leu Ile Asp Ile Gln Lys Glu Ser Glu Lys
 325 330 335
 Ile Met Gly Phe Ile Thr Lys Asn Leu Ser His His Met Gln Glu Arg
 340 345 350

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

Val Gly Val Leu Ser Leu Lys Ile Glu Ala Ile Ser Asn Phe Tyr Gly
 1 5 10 15
 Leu Cys Val Leu Gly Val Leu Leu Ala Cys Phe Tyr Leu Leu Asp Ala
 20 25 30
 Tyr Tyr Leu Met Gln Glu Arg Leu Phe Arg Glu Gln Tyr Gln Trp Leu
 35 40 45
 Ile Lys Asn Arg Leu Lys Thr Asp Glu Arg Leu Phe Glu Val Phe Pro
 50 55 60
 Ile His Gln Thr Cys Gln Ser Thr Gln Phe Leu Ser Pro Cys Val Arg
 65 70 75 80
 Leu Val Phe Ser Pro Ile Gly Arg
 85

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

```
Met Ser Leu Gly Ala Val Val Ser Ser Leu Leu Cys His Lys Leu Glu
1          5          10          15
Gly Ala Ile Leu Asp Leu Arg Ala Tyr Arg Xaa Xaa Ala Tyr Tyr His
          20          25          30
Glu Asn Lys Asp Thr Leu Leu Ile Lys Gly Lys Lys Arg Leu Leu Tyr
          35          40          45
Asn Tyr Ile Lys Ala His Ile Xaa Leu Asn Leu Leu Trp Thr Ile Arg
          50          55          60
Asn Arg Thr Xaa Ser Leu Gly Lys Phe Thr Gln Asn Pro Thr Glu Gln
65          70          75          80
Pro Pro Thr Asn Asn His
          85
```

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

```
Met Lys Lys Thr Thr Leu Phe Val Leu Gly Leu Leu Phe Asn Ser Ser
1          5          10          15
Leu Ser Ala Val Asp Gly Ile Ser Gln Thr Glu Pro Ser Ser Leu Asn
          20          25          30
Leu Ala Glu Asp Ser Leu Pro Leu Asn His Ser Asn Ala Gln Lys Leu
          35          40          45
Ser Leu Lys Asn Ala Trp Asn Arg Val Leu Ser Asn His Glu Gly Leu
          50          55          60
His Ala Gln Asn Thr Pro Leu Ser Glu Arg Val Lys
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

Val Lys Lys Val Glu Ser Met Asn Val Val Pro Phe Ile Asp Ile Met
1 5 10 15
Leu Val Leu Leu Val Ile Val Leu Thr Thr Ala Ser Phe Val Gln Thr
 20 25 30
Ser Lys Leu Pro Ile Ser Ile Pro Gln Val Asp Lys Asp Ser Thr Asp
 35 40 45
Ser Lys Asp Val Leu Asp Lys Lys Gln Val Thr Ile Ala Ile Ser Asn
 50 55 60
Lys Gly Ser Phe Tyr Phe Asp Asp Lys Glu Ile Ser Phe Glu Asn Leu
65 70 75 80
Lys His Lys Val Ser Thr Leu Ala Lys Asp Thr Pro Ile Val Phe Ala
 85 90 95
Arg Arg

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

Met Gly Ser Tyr Thr Phe Pro Leu Ile Leu Lys Pro Ile Phe Ile Asn
1 5 10 15
Lys Val Pro Val Thr Ile Asp Phe Tyr Ala Asn Ala Asn Tyr Phe Leu
 20 25 30

Asp Leu Val Asp Ala Val Phe Val Glu Gln
50 55

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...66
- (D) OTHER INFORMATION: /note= "N-ACETYLMURAMATE--ALANINE LIGASE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

Val Cys Gly Ala His Gly Lys Ser Ser Ile Thr Xaa Met Leu Ser Ala
1 5 10 15
Ile Cys Pro Ala Phe Gly Xaa Ile Ile Gly Arg His Ser Lys Glu Phe
20 25 30
Asp Ser Asn Val Xaa Glu Ser Ala Asp Met Ser Leu Val Phe Glu Xaa
35 40 45
Asp Glu Ser Asp Ser Ser Phe Phe Ile Phe Gln Pro Phe Leu Arg Asp
50 55 60
Cys Ala
65

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...77
- (D) OTHER INFORMATION: /note= "ONE OF THE DIFFERENT ANTIGENIC SEROTYPES OF PROTEIN M"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

Val	Asn	Glu	Leu	Lys	Asn	Ser	Lys	Gln	Val	Leu	Gly	Asn	Gly	Lys	Ala
1				5				10						15	
Asp	Leu	Ser	Asn	Glu	Asn	Thr	Lys	Val	Arg	Gln	Thr	Lys	Thr	Asn	Leu
			20					25					30		
Thr	Glu	Lys	Asn	Gln	Arg	Leu	Thr	Thr	Glu	Lys	Thr	Glu	Leu	Asn	Asn
			35				40					45			
Lys	Ile	Thr	Gly	Leu	Ala	Thr	Glu	Lys	Glu	Arg	Leu	Ala	Ala	Asp	Lys
	50					55					60				
Glu	Asn	Leu	Thr	Lys	Glu	Ser	Arg	Gln	Arg	Lys	Pro	Asn			
65					70					75					

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

Met	Asp	Leu	Gln	Gln	Ile	Asp	Glu	Leu	Glu	Asn	Lys	Phe	Glu	Glu	Gln
1				5				10						15	

Glu Glu Gln Ala Gln Asp Thr Pro Leu Lys Gln Glu Pro Ser Thr Lys
 20 25 30
 Glu Val Lys Ile Pro Lys Lys Arg Gly Arg Lys Lys Ser Leu Leu Asp
 35 40 45
 Glu Asp Lys Lys Lys Ser Phe Asn Ile Ala Phe Ser Pro Cys Val Ile
 50 55 60
 Lys Glu Leu Asn Glu Phe Leu Leu Glu Phe Gly Ser Phe Lys Glu Thr
 65 70 75 80
 Arg Ser Thr Phe Ile Glu Glu Ala Leu Ile Arg His Leu Lys His Arg
 85 90 95
 Lys Asn Thr Gln Glu Gln Lys Leu Leu Lys Gln Leu Glu Arg Leu Gln
 100 105 110
 Asn Lys Glu Lys Gly Ile Met Lys Thr Met Asn Leu Asn Glu Phe Phe
 115 120 125
 Thr His Lys Ile Ile Tyr Lys Asp Thr Pro Leu Lys Phe Lys Asp Thr
 130 135 140
 Leu Glu Gln Glu Ile Ser Gln Ala Ser Leu Val Glu Lys Leu Ile Leu
 145 150 155 160
 Ala Asn Ile Leu Ala Asn Met Val Phe Ala Lys Ile Ser Asn Glu Asn
 165 170 175

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

Met Gly Cys Tyr Gly Ile Gly Ile Ser Arg Leu Leu Ser Val Ile Leu
 1 5 10 15
 Glu Gln Lys Ser Asp Asp Leu Asp Cys Val Trp Thr Lys Asn Thr Ala
 20 25 30
 Pro Phe Asp Val Val Ile Val Val Ser Asn Leu Lys Asp Glu Ala Gln
 35 40 45
 Lys Lys Leu Ala Phe Glu Val Tyr Glu Arg Leu Leu Gln Lys Gly Val
 50 55 60

Asp Ala Leu Leu Asp Asp Arg Asp Ala Arg Phe Gly Ala Lys Met Arg
 65 70 75 80
 Asp Phe Glu Leu Ile Gly Glu Arg Leu Ala Leu Ile Val Gly Lys Gln
 85 90 95
 Thr Leu Glu Ser Lys Glu Phe Glu Cys Ile Lys Arg Ala Asn Leu Glu
 100 105 110
 Lys Gln Thr Ile Lys Asp Ile Gly Ile Arg Arg Lys Asn Phe Arg Asn
 115 120 125
 Val Ser Glu Arg Ile Arg Gly Gly Asn Gly Lys Asn Ser Asp Trp Leu
 130 135 140

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...90
- (D) OTHER INFORMATION: /note= "vacuolating cytotoxin of Hpylori"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

Met Glu Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser
 1 5 10 15
 Leu Val Leu Ala Gly Ala Leu Ile Ser Ala Ile Pro Gln Glu Ser His
 20 25 30
 Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile
 35 40 45
 Ala Thr Gly Thr Ala Val Gly Thr Val Ser Gly Leu Leu Ser Trp Gly
 50 55 60
 Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys
 65 70 75 80
 Val Trp Arg Ile Gln Ala Gly Lys Gly Leu
 85 90

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 268 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:SEQ ID NO:621:

Met	Ser	Glu	Lys	Glu	Arg	Leu	Asn	Glu	Val	Ile	Leu	Glu	Glu	Glu	Asn	1	5	10	15
Asn	Gly	Ser	Gly	Thr	Lys	Lys	Val	Phe	Leu	Ile	Val	Ala	Ile	Ala	Ile	20	25	30	
Ile	Ile	Leu	Ala	Val	Leu	Leu	Met	Val	Phe	Trp	Lys	Ser	Thr	Arg	Val	35	40	45	
Ala	Pro	Lys	Glu	Thr	Phe	Leu	Gln	Thr	Asp	Ser	Gly	Met	Gln	Lys	Ile	50	55	60	
Gly	Asn	Thr	Lys	Asp	Glu	Lys	Lys	Asp	Asp	Glu	Phe	Glu	Ser	Leu	Asn	65	70	75	80
Met	Asp	Ser	Pro	Lys	Gln	Glu	Asp	Lys	Leu	Asp	Lys	Val	Val	Asp	Asn	85	90	95	
Ile	Lys	Lys	Gln	Glu	Ser	Glu	Asn	Ser	Met	Pro	Ile	Gln	Thr	Asp	Gln	100	105	110	
Ala	Gln	Met	Glu	Met	Lys	Thr	Thr	Glu	Glu	Lys	Gln	Glu	Ser	Gln	Lys	115	120	125	
Glu	Leu	Lys	Ala	Val	Glu	Pro	Ile	Pro	Met	Ser	Thr	Gln	Lys	Glu	Ser	130	135	140	
Gln	Ala	Val	Ala	Lys	Lys	Glu	Thr	Pro	His	Lys	Lys	Pro	Lys	Val	Ala	145	150	155	160
Pro	Lys	Asp	Lys	Glu	Ala	His	Lys	Asp	Lys	Ala	Lys	His	Ala	Ala	Lys	165	170	175	
Glu	Pro	Lys	Val	Lys	Lys	Glu	Ala	Arg	Lys	Glu	Val	Ser	Lys	Lys	Ala	180	185	190	
Asn	Ser	Lys	Thr	Asn	Leu	Thr	Lys	Gly	His	Tyr	Leu	Gln	Val	Gly	Val	195	200	205	
Phe	Ala	His	Thr	Pro	Asn	Lys	Ala	Phe	Leu	Gln	Glu	Phe	Asn	Gln	Phe	210	215	220	
Pro	His	Lys	Ile	Glu	Asp	Arg	Gly	Ala	Thr	Lys	Arg	Tyr	Leu	Ile	Gly				

225		230		235		240									
Pro	Tyr	Lys	Ser	Lys	Gln	Glu	Ala	Leu	Met	His	Ala	Asp	Glu	Val	Ser
				245					250					255	
Lys	Lys	Met	Thr	Lys	Pro	Val	Val	Ile	Glu	Val	Arg				
			260					265							

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...171
- (D) OTHER INFORMATION: /note= "ferric enterobactin transport protein fepC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

Val	Glu	Tyr	Tyr	Ala	Phe	Asn	Phe	Ser	Val	Leu	Asp	Phe	Val	Leu	Met
1				5				10						15	
Gly	Lys	Ala	Thr	His	Leu	Asn	Leu	Phe	Ala	Met	Pro	Lys	Ala	Lys	His
			20					25					30		
Ile	Lys	Glu	Ala	Thr	Ser	Val	Leu	Glu	Arg	Leu	Asp	Leu	Glu	Ser	Leu
		35					40				45				
Lys	Asp	Gln	Gly	Ile	Asn	Asp	Leu	Ser	Gly	Gly	Gln	Arg	Gln	Met	Val
	50					55					60				
Leu	Leu	Ala	Arg	Ser	Leu	Leu	Gln	Arg	Thr	Pro	Leu	Leu	Leu	Leu	Asp
65					70				75					80	
Glu	Pro	Thr	Ser	Ala	Leu	Asp	Leu	Lys	Asn	Gln	Ala	Leu	Phe	Phe	Asp
			85						90					95	
Ala	Ile	Lys	Asp	Glu	Met	Lys	Lys	Arg	Glu	Leu	Ser	Val	Leu	Val	Asn
			100					105					110		
Ile	His	Asp	Pro	Asn	Leu	Val	Ala	Arg	His	Ser	Thr	His	Val	Val	Met
		115					120					125			
Leu	Lys	Asp	Lys	Lys	Leu	Phe	Leu	Gln	Ala	Ser	Thr	Pro	Ile	Ala	Met
	130					135					140				

Thr Ser His Asn Leu Ser Ala Leu Tyr Asp Thr Pro Leu Xaa Ala Ile
 145 150 155 160

Trp His Asp Asp Lys Leu Val Val Tyr Ala Leu
 165 170

(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

Met	Met	Ala	His	Ser	Leu	Ile	Leu	Val	Ser	Lys	Thr	Ser	Leu	Ser	Asn
1				5					10					15	
Leu	Leu	Ile	Phe	Val	Val	Gln	Pro	Asp	Gly	Lys	Leu	Ser	Met	Thr	Asp
			20					25					30		
Ala	Ala	Ile	Asp	Pro	Asn	Met	Thr	Asn	Ser	Gly	Leu	Arg	Trp	Tyr	Arg
		35					40					45			
Val	Asn	Glu	Ile	Ala	Glu	Lys	Phe	Lys	Leu	Ile	Lys	Asp	Lys	Ala	Leu
	50					55					60				
Val	Thr	Val	Ile	Asn	Lys	Gly	Tyr	Gly	Lys	Asn	Pro	Leu	Thr	Lys	Asn
65				70					75					80	
Tyr	Asn	Ile	Lys	Asn	Tyr	Gly	Glu	Leu	Glu	Arg	Val	Ile	Lys	Lys	Leu
			85					90						95	
Pro	Leu	Val	Arg	Asp	Lys										
			100												

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

Leu Lys Val Thr Asn Pro His Leu Leu Val Val Ile Gln Asp Leu Asn
1 5 10 15
Ala Arg Ile Ala Leu Met Lys Leu Leu Phe Gln Asn Val Lys Ser Ala
20 25 30
Asn Lys Glu Leu Val Phe Cys Asn Lys Glu Lys Arg Leu Ile Arg Ser
35 40 45
Phe Asp Ala Gln Lys Glu Tyr Gly Ile Thr Pro Val Glu Asn Ile Leu
50 55 60
Ser Val Leu Asp Thr Ala Met Asn Pro Asn Ser Ala Leu Val Ile Asp
65 70 75 80
Asn Leu Asn Glu Ala Lys Glu Leu His Asp Lys Val Gly Ala Glu Lys
85 90 95
Leu Lys Ser Phe Leu Glu Lys Ala Xaa Arg Gln Arg Ala Val Leu Arg
100 105 110
His Phe Cys Ala
115

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

Val Leu Asn Glu Glu Gln Asn Ser Leu Glu Glu Lys Gly Gly Glu Asn
1 5 10 15
Lys Asn Glu Lys Glu Thr Pro Leu Lys Gly Ile His Ser Lys Ile Pro
20 25 30
Ser Leu Lys Gln Ala Leu Glu Gln Thr Ile Ser Lys Ile Lys Ser Ser
35 40 45
Lys Glu Phe Phe Lys Gln Leu Leu His Asn Lys Lys Lys Leu Tyr Ile
50 55 60
Ala Leu Gly Ile Leu Leu Ser Leu Ile Ala Leu Ile Val Ala Leu Ser
65 70 75 80

Leu Leu Leu Gly His Lys Lys Glu Asn Lys Gln Thr Ser Leu Gln Thr
 85 90 95
 Asn Thr Ala Thr Thr Asn Asn Glu Thr Pro Asn Asp Thr Asn Asn Ala
 100 105 110
 Glu Ala Glu Gly Gln Ile Glu Asn Leu Asp Leu Pro Asp Leu Ile Gly
 115 120 125
 Lys Asp Ser Leu Lys Arg Asn Asp Glu Ser Gln Val Asp Ala Met Met
 130 135 140
 Gln Lys Ala Ser Leu Leu Tyr Glu Gln Gly Gln Lys Asp Glu Ala Leu
 145 150 155 160
 His Leu Phe Asp Lys Ile Ala Ser Phe Ser Gln Gly Ile Ala Ser His
 165 170 175
 Asn Leu Gly Val Ile Lys Phe Lys Glu Lys Asp Phe Asn Gly Ala Leu
 180 185 190
 Asp Leu Phe Asp Ser Ser Ile Ala Ser Lys Glu Asn Ala Ser Val Ser
 195 200 205
 Ala Ile Asp Ala Leu Val Thr Ala Tyr His Leu Gln Asp Ala Asp Leu
 210 215 220
 Tyr Tyr His Tyr Leu Lys Ile Val Lys Arg His Phe Val
 225 230 235

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

Met Lys Glu Ser Phe Tyr Ile Glu Gly Met Thr Cys Thr Ala Cys Ser
 1 5 10 15
 Ser Gly Ile Glu Arg Ser Leu Gly Arg Lys Ser Phe Val Lys Lys Ile
 20 25 30
 Glu Val Ser Leu Leu Asn Lys Ser Ala Asn Ile Glu Phe Asn Glu Asn
 35 40 45
 Glu Thr Asn Leu Asp Glu Ile Phe Lys Leu Ile Glu Lys Leu Gly Tyr

50	55	60
Ser Pro Lys Lys Thr Leu Ala Glu Glu Lys Lys Glu Phe Phe Ser Pro		
65	70	75 80
Asn Val Lys Leu Ala Leu Ala Val Ile Phe Thr Leu Phe Val Val Tyr		
	85	90 95
Leu Ser Met Gly Ala Met Leu Ser Pro Ser Leu Leu Pro Glu Ser Leu		
	100	105 110
Leu Thr Ile Asn His His Ser Asn Phe Leu Asn Ala Cys Leu Gln Leu		
	115	120 125
Ile Gly Ala Leu Ile Val Met His Leu Gly Arg Asp Phe Tyr Ile Gln		
	130	135 140
Gly Phe Lys Ala Leu Trp His Arg Gln Pro Asn Met Ser Ser Leu Ile		
	145	150 155 160
Ala Ile Gly Thr Ser Ala Ala Leu Ile Ser Ala Cys Gly Asn Cys Ile		
	165	170 175
Trp Phe Ile Pro Ile Ile Ile Pro Ile Ser Gly Leu Met Gly Ile Ile		
	180	185 190
Ile Leu Lys Ala Cys Ala		
	195	

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...225
- (D) OTHER INFORMATION: /note= "HEAT SHOCK PROTEIN HTPX PRECURSOR"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

Met Asn Thr Ser Leu Leu Thr Gln Ala Gln Val Leu Ser Ser Lys Glu
1 5 10 15
Asn Gln Ile His Arg Leu Leu Leu Glu Leu Leu Glu Glu Ala Lys Leu
20 25 30
His Phe Glu Pro Lys Leu Tyr Ile Ile Asn Ala Pro Tyr Met Asn Ala

35		40		45											
Phe	Ala	Ser	Gly	Trp	Asp	Glu	Ser	Asn	Ser	Leu	Ile	Ala	Leu	Thr	Ser
50						55					60				
Ala	Leu	Ile	Glu	Arg	Leu	Asp	Arg	Asp	Glu	Leu	Lys	Ala	Val	Ile	Ala
65					70					75					80
His	Glu	Leu	Ser	His	Ile	Arg	His	Asn	Asp	Ile	Arg	Leu	Thr	Met	Cys
				85					90					95	
Val	Gly	Ile	Leu	Ser	Asn	Ile	Met	Leu	Leu	Val	Ala	Asn	Phe	Ser	Val
			100					105					110		
Tyr	Phe	Phe	Met	Gly	Asn	Arg	Lys	Asn	Ser	Gly	Ala	Asn	Leu	Ala	Arg
			115					120					125		
Met	Ile	Leu	Trp	Val	Leu	Gln	Ile	Ile	Leu	Pro	Phe	Leu	Thr	Leu	Leu
			130			135					140				
Leu	Gln	Met	Tyr	Leu	Ser	Arg	Thr	Arg	Glu	Tyr	Met	Ala	Asp	Ser	Gly
145					150					155					160
Ala	Ala	Phe	Leu	Met	His	Asp	Asn	Lys	Pro	Met	Ile	Arg	Ala	Leu	Gln
				165					170					175	
Lys	Ile	Ser	Asn	Asp	Tyr	Thr	Asn	Asn	Asp	Tyr	Lys	Glu	Ile	Asp	Lys
			180					185					190		
Asn	Ser	Thr	Arg	Ser	Ala	Ala	Tyr	Leu	Phe	Asn	Ala	Glu	Met	Phe	Ser
		195					200					205			
Thr	His	Pro	Ser	Ile	Lys	Asn	Arg	Ile	Gln	Ser	Leu	Arg	Lys	Arg	Val
	210					215					220				
Ile															
225															

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

Val	Gly	Ile	Val	Pro	Asp	Asn	Leu	Trp	Lys	Leu	Lys	Arg	Phe	Asn	Gln
1				5					10					15	

Asp Trp Arg Val Gly Asp Thr Leu Ile Thr Ala Ile Gly Gln Gly Ser
 20 25 30
 Phe Leu Ala Thr Pro Leu Gln Val Leu Ala Tyr Thr Gly Leu Ile Ala
 35 40 45
 Thr Gly Lys Leu Ala Thr Pro His Phe Ala Ile His Asn Gln Gln Pro
 50 55 60
 Leu Lys Asp Pro Leu Asn Arg Phe Ser Lys Lys Glu Ala Pro Ser Leu
 65 70 75 80
 Ala Arg Gly His Val
 85

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

Met Phe Asn Ile Lys Arg Thr Phe Leu Ile Thr Ile Ile Ser Phe Phe
 1 5 10 15
 Leu Ile Val Pro Asn Trp Leu Lys Ala Ile Asp Leu Pro Ile Val Ser
 20 25 30
 Asn Leu Lys Ile Tyr Gln Thr Val Tyr Cys Met Leu Ile Pro Ser Tyr
 35 40 45
 Val Leu Thr Asn Lys Ser Phe Ala Asp Ile Leu Thr Gly Tyr Thr Ser
 50 55 60
 Ile Gly Ala Ser Gly Ser Gly Lys Ser Ser Gly Gln Gly Val Ile Glu
 65 70 75 80
 Ala Leu Ser Thr Pro Leu Ala Thr Ser Leu Ala Ala Ser Asn Leu Val
 85 90 95
 Lys Tyr Leu Asn Thr Leu Gly Pro Leu Trp Gly Ser Ala Trp Ala Ser
 100 105 110
 Val Ala Thr Ala Ile Gln Gly Phe Ala Leu Thr Pro Ser Ser Gly Cys
 115 120 125
 Asn Phe Gly Trp Asn Ala Leu Ile Asn Lys Asn Ile Asp Val Ser Met
 130 135 140

Asp	Ser	Val	Leu	Asp	Asn	Leu	Ser	Asn	Lys	Ile	Gln	Asn	Phe	Thr	Lys	
145					150					155					160	
Gly	Gly	Val	Glu	Asp	Asn	Val	Lys	Gly	Asn	Ile	Leu	Leu	Gln	Ile	Ile	
				165					170					175		
Gly	Ser	Ile	Thr	Ala	Gln	Ala	Ser	Thr	Asn	Ile	Thr	Ala	Asp	Gly	Leu	
			180					185					190			
Ile	Trp	Leu	Ile	Gly	Lys	Glu	Phe	Thr	Ala	Asn	Lys	Leu	Gln	Asn	Asn	
		195					200					205				
Thr	Ile	Ala	Met	Leu	Ala	Phe	Ala	Ala	Leu	Glu	Ser	Val	Val	Lys	Gly	
	210					215						220				
Ala	Asp	Ala	Ala	Val	Leu	Pro	Ala	Tyr	Gly	Val	Val	Asn	Leu	Pro	Asp	
225					230					235					240	
Ile	Ile	Ile	Gly	Gln	Gly	Ser	Tyr	Leu	Asp	Phe	Val	Ser	Tyr	Leu	Ile	
				245					250					255		
Tyr	Ile	Val	Phe	Gly	Ile	Phe	Val	Phe	Ile	Ser	Phe	Met	Lys	Leu	Arg	
			260					265					270			
Asp	Ile	Ser	Asn	Gly	Ile	Gln	Ile	Asn	Ile	Gly	Phe	Glu	Tyr	Met	Arg	
		275					280					285				
Phe	Val	Gly	Gly	Thr	Leu	Phe	Lys	Met	Ala	Met	Val	Ser	Phe	Ile	Ala	
	290					295					300					
Tyr	Ala	Gly	Phe	Gly	Tyr	Leu	Tyr	Lys	Ile	Ser	Tyr	Ser	Ile	Tyr	Phe	
305					310					315					320	
Gly	Leu	Ala	Gly	Ala	Phe	Gly	Leu	Asn	Gln	Val	Leu	Phe	Trp	Ala	Leu	
				325					330					335		
Asp	Leu	Val	Leu	Asn	Tyr	Thr	Val	Asn	Ser	Ile	Leu	Pro	Ala	Val	Arg	
			340					345					350			
Ala	Val	Phe	Ser	Asn	Val	Gly	Asn	Asn	Ala	Pro	Ser	Leu	Leu	Gln	Gly	
		355					360					365				
Leu	Gln	Val	Ala	Gly	Ile	Ser	Leu	Phe	Ala	Ile	Phe	Met	Gln	Val	Thr	
	370					375					380					
Ile	Ile	Met	Arg	Ile	Ser	Thr	Val	Val	Val	Lys	Pro	Leu	Ile	Ala	Gly	
385					390					395					400	
Ala	Phe	Ser	Gly	Ile	Val	Phe	Pro	Ile	Ala	Val	Cys	Leu	Ile	Val	Leu	
				405					410					415		
Asp	Trp	Phe	Lys	Asp	Ser	Met	Lys	Asn	Ile	Leu	Ile	Trp	Phe	Ile	Asn	
			420					425					430			
Asn	Leu	Phe	Ile	Leu	Val	Leu	Ala	Ile	Pro	Ile	Leu	Leu	Phe	Gly	Val	
		435					440					445				

Leu Ala Leu Leu Ala Phe Asn Leu Thr Ile Thr Pro Ser Val Ala Ile
 450 455 460
 Gln Asn Ile Asn Gln Gly Gly Leu Gly Ile Asp Ser Thr Ile Ala Ser
 465 470 475 480
 Leu Ile Thr Leu Phe Ile Leu Lys Gly Phe Ile Glu Thr Ile Ile Glu
 485 490 495

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

Met Ala Phe Trp Gln Ala Ile Arg Trp Trp Ile Leu Lys Leu Pro Phe
 1 5 10 15
 Met Met Gly Ala Thr Met Met Trp Ile Leu Ser Glu Met Ala Phe Lys
 20 25 30
 Ile Ala Gly Xaa Met Ala Phe Lys Glu Ala Ser Arg Ala Ala Asn Pro
 35 40 45
 Val Leu Leu Glu Pro Met Met Lys Val Glu Val Glu Val Pro Glu Glu
 50 55 60
 Tyr Met Gly Asp Val Ile Gly Asp Leu Asn Arg Arg Arg Gly Gln Ile
 65 70 75 80
 Asn Ser Met Asp Asp Arg Leu Gly Leu Lys Ile Val Asn Ala Phe Val
 85 90 95
 Pro Leu Val Glu Met Phe Gly Tyr Ser Thr Asp Leu Arg Ser Ala Thr
 100 105 110
 Gln Gly Arg Gly Thr Tyr Ser Met Glu Phe Asp His Tyr Gly Glu Val
 115 120 125
 Pro Ser Asn Ile Ala Lys Glu Ile Val Glu Lys Arg Lys Gly
 130 135 140

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

Met	Gln	Asn	Leu	Pro	Gly	Met	Ala	Arg	Ala	Ala	Met	Leu	Thr	Thr	Ser
1				5				10						15	
Ser	Ala	Pro	Ala	Pro	Glu	Gly	Glu	Gly	Ala	Phe	Arg	Ala	Met	Lys	Met
			20					25					30		
Ala	Ser	Glu	Met	Ala	Lys	Val	Glu	Val	Gly	Tyr	Val	Asn	Ala	His	Gly
			35				40					45			
Thr	Ser	Thr	His	Tyr	Asn	Asp	Trp	Tyr	Glu	Ser	Ile	Ala	Leu	Lys	Asn
	50					55					60				
Val	Leu	Ala	Leu	Lys	Lys	Lys	Ser	Leu	Leu	Leu	Ala	Pro	Leu	Lys	Gly
65					70					75					80
Arg	Leu	Gly	Leu	Leu	Gly	Cys	Cys	Gly	Val	Arg	Ser	Arg	Tyr	Ser	Ile
				85					90					95	
Met	Ala	Met	Xaa	Gln	Gly	Ile	Leu	Pro	Pro	Thr	Ile	Asn	Gln	Glu	Thr
			100					105					110		
Pro	Asp	Pro	Glu	Cys	Xaa	Leu	Asp	Tyr	Ile	Pro	Asn	Thr	Ala	Arg	Glu
		115					120					125			
Lys	Gln	Val	Asn	Ala	Val	Met	Ser	Asn	Ser	Phe	Gly	Phe	Gly	Gly	Thr
	130					135					140				
Asn	Gly	Val	Val	Ile	Phe	Lys	Lys	Ala							
145						150									

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 343 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

Met	Gln	Asn	Leu	Leu	Ile	Gln	Ala	Glu	Asn	Ala	Ile	Ala	Leu	Leu	Phe	1	5	10	15
Leu	Leu	Asn	Asp	Lys	Asn	Leu	Lys	Gly	Lys	Ile	Asp	Leu	Ile	Tyr	Ile	20	25	30	
Asp	Pro	Pro	Phe	Ala	Thr	Asn	Asn	His	Phe	Thr	Ile	Thr	Asn	Gly	Arg	35	40	45	
Ala	Thr	Thr	Ile	Ser	Asn	Ser	Lys	Asn	Gly	Asp	Ile	Ala	Tyr	Ser	Asp	50	55	60	
Lys	Val	Val	Gly	Met	Asp	Phe	Met	Glu	Phe	Leu	Lys	Gln	Arg	Leu	Val	65	70	75	80
Leu	Leu	Lys	Glu	Leu	Leu	Ser	Glu	Gln	Gly	Ser	Ile	Tyr	Val	His	Thr	85	90	95	
Asp	Tyr	Lys	Ile	Gly	His	Tyr	Val	Lys	Val	Met	Leu	Asp	Glu	Ile	Phe	100	105	110	
Gly	Ile	Gln	Asn	Phe	Arg	Asn	Glu	Ile	Thr	Arg	Ile	Lys	Cys	Asn	Pro	115	120	125	
Lys	Asn	Phe	Lys	Arg	Ile	Gly	Tyr	Gly	Asn	Ile	Lys	Asp	Met	Ile	Leu	130	135	140	
Phe	Tyr	Ser	Lys	Gly	Lys	Asn	Pro	Ile	Phe	Asn	Glu	Pro	Lys	Ile	Pro	145	150	155	160
Tyr	Thr	Pro	Gln	Asp	Leu	Glu	Lys	Arg	Phe	Pro	Lys	Ile	Asp	Lys	Asp	165	170	175	
Lys	Arg	Arg	Tyr	Thr	Thr	Val	Pro	Ile	His	Ala	Pro	Gly	Glu	Val	Glu	180	185	190	
Ser	Gly	Glu	Cys	Ser	Lys	Ala	Phe	Lys	Gly	Met	Leu	Pro	Pro	Lys	Gly	195	200	205	
Arg	His	Trp	Arg	Thr	Asp	Ile	Ala	Thr	Leu	Glu	Arg	Trp	Asp	Lys	Glu	210	215	220	
Gly	Leu	Ile	Glu	Tyr	Ser	Asn	Asn	Asn	Asn	Pro	Arg	Lys	Lys	Ile	Tyr	225	230	235	240
Ala	Leu	Glu	Gln	Val	Gly	Lys	Arg	Val	Gln	Asp	Ile	Trp	Glu	Phe	Lys	245	250	255	
Asp	Pro	Gln	Tyr	Pro	Ser	Tyr	Pro	Thr	Glu	Lys	Asn	Ala	Gln	Leu	Leu	260	265	270	
Asp	Leu	Ile	Ile	Lys	Thr	Ser	Ser	Asn	Lys	Asp	Ser	Ile	Val	Leu	Asp	275	280	285	
Cys	Phe	Cys	Gly	Ser	Gly	Thr	Thr	Leu	Lys	Ser	Ala	Phe	Leu	Leu	Gln	290	295	300	

Arg Lys Phe Ile Gly Ile Asp Asn Ser Asp Leu Ala Ile Gln Ala Cys
 305 310 315 320

Lys Asn Lys Leu Glu Thr Ile Thr Lys Asp Leu Phe Val Ser Gln Asn
 325 330 335

Phe Tyr Asp Phe Leu Val Phe
 340

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

Met Ile Leu Lys Asn Leu Ile Leu Leu Phe Leu Ala Lys Arg Lys Leu
 1 5 10 15

Ile Phe Ile Glu Ala Asn Phe Tyr Thr Ile Ser Gly Ser Lys Leu Asn
 20 25 30

Glu Val Ala Arg Ser Tyr Gln Asp Leu Ala Leu Lys Phe Glu Ala Phe
 35 40 45

Pro Asn Tyr Glu Phe Ile Trp Ile Thr Asp Gly Ile Gly Trp Leu Asp
 50 55 60

Ala Lys Ser Lys Leu Gln Glu Ala Tyr Lys Ser Val Glu Ile Tyr Asn
 65 70 75 80

Leu Ser Tyr Val Asn Asp Phe Ile Ser Lys Val Gln Lys
 85 90

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

Met	Thr	Ser	Val	Val	Ile	Lys	Pro	His	Ala	Tyr	Gly	Glu	Gln	Val	Gln	
1				5					10					15		
Glu	Ile	Glu	Glu	Glu	Ser	Asp	Ser	Asp	Tyr	Glu	Lys	Asn	Asn	Asp	Gln	
			20					25					30			
Glu	Ala	Ile	Asn	Phe	Gly	Ile	Ala	Leu	His	Lys	Gly	Leu	Glu	Tyr	Gln	
			35				40					45				
Tyr	Ala	Tyr	Asn	Ile	Pro	Lys	Gln	Ser	Val	Leu	Glu	Tyr	Leu	Asn	Tyr	
	50					55				60						
His	Tyr	Gly	Phe	Tyr	Gly	Leu	Asp	Tyr	Gln	Ala	Leu	Glu	Glu	Ser	Leu	
65					70				75						80	
Glu	Leu	Phe	Glu	Asn	Asp	Ala	Gly	Ile	Gln	Ala	Leu	Phe	Lys	Asn	His	
				85					90					95		
Ala	Leu	Lys	Gly	Glu	Ala	Ala	Phe	Leu	Phe	Gln	Gly	Val	Val	Ser	Arg	
			100					105					110			
Ile	Asp	Val	Leu	Leu	Trp	Asp	Arg	Gly	Gln	Asn	Leu	Tyr	Val	Leu	Asp	
	115						120					125				
Tyr	Lys	Ser	Ser	Gln	Asn	Tyr	Gln	Gln	Ser	His	Lys	Ala	Gln	Val	Ser	
	130					135					140					
His	Tyr	Ala	Glu	Phe	Leu	Arg	Thr	Gln	Xaa	Pro	His	Phe	Lys	Ile	Gln	
145					150				155						160	
Ala	Gly	Ile	Ile	Tyr	Ala	His	Lys	Arg	Leu	Leu	Glu	Lys	Xaa	Trp	Xaa	
				165					170					175		

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...88
- (D) OTHER INFORMATION: /note= "flagellar biosynthetic protein fliQ"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

Met Glu Ser Gln Leu Met Lys Leu Ala Ile Glu Thr Tyr Lys Ile Thr
1 5 10 15

Leu Met Ile Ser Leu Pro Val Leu Leu Ala Gly Leu Val Val Gly Leu
20 25 30

Leu Val Ser Ile Phe Gln Ala Thr Thr Gln Ile Asn Glu Met Thr Leu
35 40 45

Ser Phe Val Pro Lys Ile Leu Ala Val Ile Gly Val Leu Ile Leu Thr
50 55 60

Met Pro Trp Met Thr Asn Met Leu Leu Asp Tyr Thr Lys Thr Leu Ile
65 70 75 80

Lys Leu Ile Pro Lys Ile Ile Gly
85

(2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

Met Lys Phe Phe Thr Arg Ile Thr Asp Ser Tyr Lys Lys Val Val Val
1 5 10 15

Thr Leu Gly Leu Val Val Thr Thr Asn Pro Leu Met Ala Val Thr Ser
20 25 30

Pro Ala Thr Gly Val Thr Glu Thr Lys Ser Leu Val Ile Gln Ile Ile
35 40 45

Ser Val Leu Ala Ile Val Gly Gly Cys Ala Leu Gly Val Lys Gly Ile
50 55 60

Ala Asp Ile Trp Lys Ile Ser Asp Asp Ile Lys Arg Gly Gln Ala Thr
65 70 75 80

Val Phe Ala Tyr Ala Gln Pro Ile Ala Met Leu Ala Val Ala Gly Gly
85 90 95

Ile Ile Tyr Leu Ser Thr Lys Phe Gly Phe Asn Ile Gly Glu Ser Gly
100 105 110

Gly Ala Ser

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

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Met Ser Glu Asp Leu Pro Phe Ala Ser Asp Ser Gln Phe Thr Tyr Asn
1           5           10           15
Gly Val Ser Ile Thr Arg Pro Thr Asn Glu Val Asn Asp Val Ile Ser
20           25           30
Gly Val Asn Ile Thr Leu Glu Gln Thr Thr Glu Pro Asn Lys Pro Ala
35           40           45
Ile Ile Ser Val Ser Arg Asp Asn Gln Ala Ile Ile Asp Ser Leu Lys
50           55           60
Glu Phe Val Lys Ala Tyr Asn Glu Leu Ile Pro Lys Leu Asp Glu Asp
65           70           75           80
Thr Arg Tyr Asp Ala Asp Thr Lys Ile Ala Gly Ile Phe Asn Gly Val
85           90           95
Gly Asp Ile Arg Ala Ile Arg Ser Ser Leu Asn Asn Val Phe Ser Tyr
100          105          110
Ser Val His Thr Asp Asn Gly Val Glu Ser Leu Met Lys Tyr Gly Leu
115          120          125
Ser Leu Asp Asp Lys Gly Val Met Ser Leu Asp Glu Ala Lys Leu Ser
130          135          140
Ser Ala Leu Asn Ser Asn Pro Lys Ala Thr Gln Asp Phe Phe Tyr Gly
145          150          155          160
Ser Asp Ser Lys Asp Met Gly Gly Arg Glu Ile His Gln Glu Gly Ile
165          170          175
Phe Ser Lys Phe Asn Gln Val Ile Ala Asn Leu Ile Asp Gly Gly Asn
180          185          190
Ala Lys Leu Lys Ile Tyr Glu Asp Ser Leu Asp Arg Asp Ala Lys Ser
195          200          205

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Leu Thr Lys Asp Lys Glu Asn Ala Gln Glu Leu Leu Lys Thr Arg Tyr
 210 215 220
 Asn Ile Met Ala Glu Arg Phe Ala Ala Tyr Asp Ser Gln Ile Ser Lys
 225 230 235 240
 Ala Asn Gln Lys Phe Asn Ser Val Gln Met Met Ile Asp Gln Ala Ala
 245 250 255
 Ala Lys Lys Asn
 260

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

Met Lys Asn Pro Gln Ala Asn Val Leu Lys Leu Phe Leu Asn Gln Val
 1 5 10 15
 Ala Asp Gln Lys Tyr Ile Asp Met Asn Asp Glu Lys Asn Tyr Asp Pro
 20 25 30
 Arg Glu Pro Glu Pro Pro Tyr Gly Thr Lys Gly Ala Leu Asp Glu Ile
 35 40 45
 Ile Arg Thr Asp Ala Arg Ser Trp Ala Asn Thr Pro Asp Asp Glu Phe
 50 55 60
 Gly Ser Ile Met Ser Ser Phe Lys Arg Phe Met Tyr Val Tyr Lys Asp
 65 70 75 80
 Pro Lys Val Arg Glu Ala Thr Ser Lys Met Ser Phe Asp Tyr Glu Glu
 85 90 95
 Leu Arg Thr Gly Asn Ile Ser Ile Tyr Ile Val Ile Ala Gln Ile Asp
 100 105 110
 Ile Gly Thr Leu Ser Ser Leu Val Arg Ala Phe Leu Glu Ser Ile Ala
 115 120 125
 Lys Asn Leu Met Val Lys Glu Ser Ser Lys Pro Glu Glu Arg Ile Phe
 130 135 140
 Ile Ile Ala Asp Glu Phe Val Arg Phe Gly Lys Leu Pro Phe Leu Leu
 145 150 155 160

Glu	Met	Pro	Ala	Leu	Cys	Arg	Ser	Tyr	Asn	Val	Val	Pro	Leu	Phe	Ile
				165					170					175	
Thr	Gln	Asp	Tyr	Ala	Met	Ile	Arg	Asn	Thr	Ile	Ala	Met	Met	Ile	
				180				185					190		

(2) INFORMATION FOR SEQ ID NO:639:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

Met	Ile	Ser	Glu	Ile	Ile	Lys	Phe	Gln	Leu	Lys	Gly	Ile	Lys	Met	Ile
1				5					10					15	
Arg	Leu	Lys	Gly	Leu	Asn	Lys	Thr	Leu	Lys	Thr	Ser	Leu	Leu	Ala	Gly
			20					25					30		
Val	Leu	Leu	Gly	Ala	Thr	Ala	Pro	Leu	Met	Ala	Lys	Pro	Leu	Leu	Ser
		35					40					45			
Asp	Glu	Asp	Leu	Leu	Lys	Arg	Val	Lys	Leu	His	Asn	Ile	Lys	Glu	Asp
	50					55					60				
Thr	Leu	Thr	Ser	Cys	Asn	Ala	Lys	Val	Asp	Gly	Ser	Gln	Tyr	Leu	Asn
65					70					75					80
Ser	Gly	Trp	Asn	Leu	Ser	Lys	Glu	Phe	Pro	Gln	Glu	Tyr	Arg	Glu	Lys
				85					90					95	
Ile	Phe	Glu	Cys	Val	Glu	Glu	Glu	Lys	His	Lys	Gln	Ala	Leu	Asn	Leu
			100					105					110		
Ile	Asn	Lys	Glu	Asp	Thr	Glu	Asp	Lys	Glu	Glu	Leu	Ala	Lys	Lys	Ile
		115					120					125			
Lys	Glu	Ile	Lys	Glu	Lys	Ala	Lys	Val	Leu	Arg	Gln	Lys	Phe	Met	Ala
	130					135					140				
Phe	Glu	Met	Lys	Glu	His	Ser	Lys	Glu	Phe	Pro	Asn	Lys	Lys	Gln	Leu
145					150					155					160
Gln	Thr	Met	Leu	Glu	Asn	Ala	Phe	Asp	Asn	Gly	Ala	Glu	Ser	Phe	Ile
				165					170					175	
Asp	Asp	Trp	His	Glu	Arg	Phe	Gly	Gly	Ile	Ser	Arg	Glu	Asn	Thr	Tyr

180	185	190
Lys Ala Leu Gly Ile Lys Glu Tyr Ser Asp Glu Gly Lys Ile Leu Ala		
195	200	205
Phe Gly Glu Arg Ser Tyr Ile Arg Gln Tyr Lys Lys Asp Phe Glu Glu		
210	215	220
Ser Thr Tyr Asp Thr Arg Gln Thr Leu Ser Ala Met Ala Asn Met Ser		
225	230	235
Gly Glu Asn Asp Tyr Lys Ile Thr Trp Leu Lys Pro Lys Tyr Gln Leu		
245	250	255
His Ser Ser Asn Asn Ile Lys Pro Leu Met Ser Asn Thr Glu Leu Leu		
260	265	270
Asn Met Ile Glu Leu Thr Asn Ile Lys Lys Glu Tyr Val Met Gly Cys		
275	280	285
Asn Met Glu Ile Asp Gly Ser Lys Tyr Pro Ile His Lys Asp Trp Gly		
290	295	300
Phe Phe Gly Lys Ala Lys Val Pro Glu Thr Trp Arg Asn Lys Ile Trp		
305	310	315
Glu Cys Ile Lys Asn Lys Val Lys Ser Tyr Asp Asn Thr Thr Ala Glu		
325	330	335
Ile Gly Ile Val Trp Lys Lys Asn Thr Tyr Ser Ile Ser His His		
340	345	350

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...351
- (D) OTHER INFORMATION: /note= "flagellar motor switch protein flIM"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

Met	Ala	Asp	Ile	Leu	Ser	Gln	Glu	Glu	Ile	Asp	Ala	Leu	Leu	Glu	Val
1				5					10					15	

Val	Asp	Glu	Asn	Val	Asp	Ile	Gln	Asn	Val	Gln	Lys	Lys	Asp	Ile	Ile	20	25	30	
Pro	Gln	Arg	Ser	Val	Thr	Leu	Tyr	Asp	Phe	Lys	Arg	Pro	Asn	Arg	Val	35	40	45	
Ser	Lys	Glu	Gln	Leu	Arg	Ser	Phe	Arg	Ser	Ile	His	Asp	Lys	Met	Ala	50	55	60	
Arg	Asn	Leu	Ser	Ser	Gln	Val	Ser	Ser	Ile	Met	Arg	Ser	Ile	Val	Glu	65	70	75	80
Ile	Gln	Leu	His	Ser	Val	Asp	Gln	Met	Thr	Tyr	Gly	Glu	Phe	Leu	Met	85	90	95	
Ser	Leu	Pro	Ser	Pro	Thr	Ser	Phe	Asn	Val	Phe	Ser	Met	Lys	Pro	Met	100	105	110	
Gly	Gly	Thr	Gly	Val	Leu	Glu	Ile	Asn	Pro	Ser	Ile	Ala	Phe	Pro	Met	115	120	125	
Ile	Asp	Arg	Leu	Leu	Gly	Gly	Lys	Gly	Ser	Ala	Tyr	Asp	Gln	Asn	Arg	130	135	140	
Glu	Phe	Ser	Asp	Ile	Glu	Leu	Asn	Leu	Leu	Asp	Thr	Ile	Leu	Arg	Gln	145	150	155	160
Val	Met	Gln	Ile	Leu	Lys	Glu	Val	Trp	Ser	Pro	Val	Val	Glu	Met	Tyr	165	170	175	
Pro	Thr	Ile	Asp	Ala	Lys	Glu	Ser	Ser	Ala	Asn	Val	Val	Gln	Ile	Val	180	185	190	
Ala	Gln	Asn	Glu	Ile	Ser	Ile	Met	Val	Val	Leu	Glu	Ile	Ile	Ile	Gly	195	200	205	
His	Ser	Arg	Gly	Met	Met	Asn	Ile	Cys	Tyr	Pro	Val	Ile	Ser	Ile	Glu	210	215	220	
Ser	Ile	Leu	Ser	Lys	Met	Gly	Ser	Arg	Asp	Phe	Met	Leu	Ser	Glu	Thr	225	230	235	240
Asn	Ser	Lys	Lys	Ser	Arg	Asn	Lys	Glu	Leu	Gln	Ala	Leu	Leu	Ser	Gly	245	250	255	
Val	Ser	Val	Asp	Met	Met	Val	Phe	Leu	Gly	Ala	Val	Glu	Leu	Ser	Leu	260	265	270	
Lys	Glu	Met	Leu	Asp	Leu	Asp	Val	Gly	Asp	Thr	Ile	Arg	Leu	Asn	Lys	275	280	285	
Val	Ala	Asn	Asp	Glu	Val	Ser	Val	Tyr	Val	His	Lys	Lys	Lys	Arg	Tyr	290	295	300	
Leu	Ala	Ser	Val	Gly	Phe	Gln	Gly	Tyr	Arg	Lys	Thr	Ile	Gln	Ile	Lys	305	310	315	320
Glu	Val	Val	Tyr	Ser	Glu	Lys	Glu	Arg	Thr	Lys	Glu	Ile	Leu	Glu	Met				

325

330

335

Leu Glu Glu Gln Arg Arg Arg Gln Ser Trp Ala Met Leu Trp Ser
 340 345 350

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

Met Arg Ile Val Phe Met Gly Thr Pro Ser Phe Ala Glu Val Ile Leu
 1 5 10 15

Arg Ala Leu Val Glu Asn Glu Asp Lys Lys Ile Glu Val Val Gly Leu
 20 25 30

Phe Thr Gln Arg Asp Lys Pro Phe Gly Arg Lys Lys Glu Leu Lys Ala
 35 40 45

Pro Glu Thr Lys Thr Tyr Ile Leu Glu Asn His Leu Asn Ile Pro Ile
 50 55 60

Phe Gln Pro Gln Ser Leu Lys Glu Pro Glu Val Gln Ile Leu Lys Gly
 65 70 75 80

Leu Lys Pro Asp Phe Ile Val Val Val Ala Tyr Gly Lys Ile Leu Pro
 85 90 95

Lys Glu Val Leu Thr Ile Ala Pro Cys Ile Asn Leu His Ala Ser Leu
 100 105 110

Leu Pro Lys Tyr Arg Gly Ala Ser Pro Ile His Glu Met Ile Leu Asn
 115 120 125

Asp Asp Arg Ile Tyr Gly Ile Ser Thr Met Leu Met Xaa Phe Gly Ile
 130 135 140

Gly
 145

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1...190
 (D) OTHER INFORMATION: /note= "PHOSPHO-N-ACETYLMURAMOYL-PENTAPEPTIDE-TRANSFERASE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

Met	Pro	Thr	Met	Leu	Ala	Val	Gly	Phe	Trp	Val	Leu	Val	Phe	Leu	Ser	1	5	10	15
Thr	Ser	Asn	Ala	Val	Asn	Leu	Thr	Asp	Gly	Leu	Asp	Gly	Leu	Ala	Ser	20	25	30	
Val	Pro	Ser	Ile	Phe	Thr	Leu	Leu	Ser	Leu	Ser	Ile	Phe	Val	Tyr	Val	35	40	45	
Ala	Gly	Asn	Ala	Glu	Phe	Ser	Lys	Tyr	Leu	Leu	Tyr	Pro	Lys	Val	Ile	50	55	60	
Asp	Val	Gly	Glu	Leu	Phe	Val	Ile	Ser	Leu	Ala	Leu	Val	Gly	Ser	Leu	65	70	75	80
Phe	Gly	Phe	Leu	Trp	Tyr	Asn	Cys	Asn	Pro	Ala	Ser	Val	Phe	Met	Gly	85	90	95	
Asp	Ser	Gly	Ser	Leu	Ala	Ile	Gly	Gly	Phe	Ile	Ala	Tyr	Asn	Ala	Ile	100	105	110	
Val	Ser	His	Asn	Glu	Ile	Leu	Leu	Val	Leu	Met	Gly	Ser	Ile	Phe	Val	115	120	125	
Ile	Glu	Thr	Leu	Ser	Val	Ile	Leu	Gln	Val	Gly	Ser	Tyr	Lys	Thr	Arg	130	135	140	
Lys	Lys	Arg	Leu	Phe	Leu	Met	Ala	Pro	Ile	His	His	His	Phe	Glu	Gln	145	150	155	160
Lys	Gly	Trp	Ala	Glu	Asn	Lys	Val	Ile	Val	Arg	Phe	Trp	Ile	Ile	Ser	165	170	175	
Met	Leu	Ser	Asn	Leu	Val	Ala	Leu	Leu	Ser	Leu	Lys	Val	Cys	180	185	190			

(2) INFORMATION FOR SEQ ID NO:643:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 489 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

Val	Arg	Phe	Glu	Asn	Phe	Ile	Asn	Arg	Leu	Ala	Phe	Tyr	Met	Ala	Thr
1				5					10					15	
Gly	Ser	Gly	Lys	Thr	Ile	Val	Ile	Ile	Lys	Leu	Val	Glu	Leu	Leu	Ser
			20					25					30		
Val	Ala	Met	Gly	Met	Gly	Leu	Ile	Pro	Lys	Lys	Asn	Ile	Met	Phe	Phe
		35					40					45			
Ser	Ala	Asn	Glu	His	Leu	Ile	Lys	Gln	Phe	Glu	Lys	Glu	Ile	Glu	Lys
	50					55					60				
Tyr	Asn	Arg	Asn	Lys	Asp	Tyr	Ser	Lys	Gln	Ile	Asp	Phe	Lys	Asn	Leu
65					70					75					80
Lys	Ser	Val	Lys	Asn	Lys	Asp	Phe	Tyr	Arg	Ala	Pro	Lys	Asp	Ser	Leu
				85					90					95	
Met	Lys	Glu	Ile	Ala	Leu	Phe	Tyr	Tyr	Arg	Ala	Asp	Leu	Met	Ser	Asp
			100						105				110		
Glu	Glu	Ser	Lys	Glu	Asn	Leu	Leu	Asn	Tyr	Lys	Asp	Cys	Trp	Asp	Asn
		115					120					125			
Gly	Glu	Asn	Tyr	Val	Ile	Leu	Asp	Glu	Ala	His	Lys	Gly	Asn	Lys	Thr
	130						135					140			
Glu	Ser	Lys	Arg	Gln	Ala	Ile	Phe	Ser	Leu	Leu	Ser	Leu	Lys	Gly	Phe
145					150					155					160
Leu	Phe	Asn	Phe	Ser	Ala	Thr	Phe	Thr	Glu	Glu	Ser	Asp	Leu	Ile	Thr
				165					170					175	
Ala	Val	Tyr	Asn	Leu	Ser	Val	Gly	Glu	Trp	Val	Lys	Leu	Gly	Tyr	Gly
			180					185					190		
Lys	Glu	Ser	Val	Leu	Leu	Lys	Lys	Asn	Asn	Leu	Asn	Ala	Phe	Lys	Glu
		195					200					205			
Leu	Lys	Asp	Leu	Asn	Asp	Arg	Glu	Lys	Glu	Ile	Ala	Leu	Leu	Lys	Ala
	210					215					220				
Leu	Leu	Leu	Leu	Gly	Met	Gln	Lys	Arg	Tyr	Lys	Val	Glu	Gly	Tyr	Phe
225					230					235					240
His	Asp	Pro	Leu	Met	Leu	Val	Phe	Thr	His	Ser	Val	Asn	Met	Glu	Asn

245										250					255				
Ser	Asp	Ala	Xaa	Ile	Phe	Phe	Lys	Thr	Leu	Ala	Arg	Val	Ile	Glu	Asn				
			260						265					270					
Asp	Asp	Glu	Ser	Asp	Phe	Ser	Lys	Ala	Lys	Asp	Asp	Leu	Leu	Glu	Glu				
		275					280					285							
Leu	Lys	Asn	Pro	Glu	Phe	Leu	Phe	Ser	Asp	Gly	Lys	Asp	Lys	Glu	Lys				
	290					295					300								
Asp	Tyr	Lys	Ile	Glu	Val	Phe	Lys	Glu	Ser	Leu	Lys	Gly	Met	Asp	Phe				
305					310					315					320				
Lys	Gly	Leu	Lys	Glu	Ala	Val	Phe	Tyr	Ala	Ser	Asn	Gly	His	Ile	Glu				
				325					330					335					
Val	Ile	Ile	Asn	Pro	Lys	Asn	Asn	Gln	Glu	Ile	Ala	Phe	Lys	Leu	Asn				
			340					345					350						
Thr	Ser	Asp	Lys	Val	Phe	Cys	Leu	Ile	Arg	Ile	Gly	Asp	Ile	Thr	Glu				
		355					360					365							
Trp	Ile	Arg	Glu	Lys	Leu	Lys	Ser	Val	Lys	Val	Val	Ser	Lys	Asn	Leu				
	370					375					380								
Ser	Phe	Lys	Glu	Glu	Ser	Tyr	Phe	Ser	Gln	Ile	Asp	Lys	Ser	Ser	Ile				
385					390					395					400				
Asn	Ile	Leu	Val	Gly	Ser	Arg	Ala	Phe	Asp	Thr	Gly	Trp	Asp	Ser	Thr				
			405						410					415					
Arg	Pro	Ser	Val	Ile	Leu	Phe	Leu	Asn	Ile	Gly	Leu	Asp	Asp	Asp	Ala				
			420					425					430						
Lys	Lys	Leu	Val	Lys	Gln	Ser	Phe	Gly	Arg	Gly	Val	Arg	Ile	Glu	Ser				
		435					440					445							
Val	Lys	Asn	Gln	Arg	Gln	Arg	Leu	Ala	Tyr	Leu	Glu	Ile	Asp	Glu	Ala				
	450					455					460								
Ile	Lys	Glu	Gln	Ala	Glu	Thr	Lys	Arg	Cys	Asn	Ala	Gly	Asn	Ala	Phe				
465					470				475					480					
Cys	Asp	Thr	Tyr	Gln	Pro	Cys	Lys	Pro											
				485															

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

```
Met Arg Phe Tyr Phe Lys Phe Leu Trp Leu Leu Gly Ile Phe Leu Ile
1          5          10          15

Phe Tyr Phe Leu Asp Ile Lys Gly Ser Ser Ser Tyr Ile Ser Asp Arg
20          25          30

Val Lys Ser Ala Leu Met Ser Ala Lys Asn Ser Leu Leu Asp Asn Val
35          40          45

Gln Ala Tyr Phe Phe Gln Ala Gln Asn Ile Lys Glu Phe Gln Lys Glu
50          55          60

Arg Leu Ile Leu Glu Ala Leu Lys Leu Glu Asn Ala Asp Leu Lys Glu
65          70          75          80

Arg Leu Asn Ser Ile Tyr Pro Leu Glu Asn Pro Lys Met Thr Tyr Thr
85          90          95

Pro Thr Phe Met Thr Ser Phe Ile Asn Leu Glu Asp Thr His Ser Val
100         105         110

Ser Leu Asn Pro Ile Val Asn Leu Glu Glu Asn Lys Ile Tyr Gly Leu
115         120         125

Val Ser His Asn Gln Ala Ile Gly Ile Ala Val Leu Glu Lys Gly Arg
130         135         140

Leu Asn Gly Phe Leu Asn Ala His Lys Arg Cys Ala Tyr Ser Val Met
145         150         155         160

Ile Gly Gln Asn Gln Val Leu Gly Phe Ile Gly Thr Asn Phe Lys Gln
165         170         175

Glu Leu Val Val Asp Phe Ile Val Pro Ser Ala Glu Ile Asn Ile Gly
180         185         190

Asp Gln Val Leu Thr Ser Gly Leu Asp Gly Ile Phe Gly Ala Gly Val
195         200         205

Phe Val Gly Glu Val Ser Ser Val Glu Asp His Tyr Thr Tyr Lys Ser
210         215         220

Ala Val Leu Lys Asn Ala Phe Leu Ser Glu Ala Lys Leu Leu Arg His
225         230         235         240

Val Phe Leu Ser Gly Val Lys Asn
245
```

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

Leu	Ala	Leu	Arg	Leu	Pro	Phe	Leu	Ile	Ala	His	Val	Ile	Asn	Met	Phe
1				5				10						15	
Leu	Phe	Tyr	Leu	Ile	Gly	Arg	Lys	Ile	Leu	Lys	Lys	Pro	Lys	Asp	Ala
			20				25						30		
Leu	Tyr	Val	Val	Leu	Thr	Tyr	Ala	Leu	Leu	Pro	Gly	Val	Asn	Leu	Phe
			35				40						45		
Ala	Ile	Leu	Leu	Ala	Lys	Ser	Val	Leu	Val	Leu	Ser	Leu	Gly	Leu	Leu
	50					55					60				
Ile	Ser	Tyr	Leu	Tyr	Ile	Lys	Thr	Gln	Lys	Ile	Pro	Tyr	Leu	Thr	Leu
65					70					75					80
Ser	Ala	Cys	Ala	Phe	Leu	Asp	Gly	Ala	Phe	Ile	Pro	Leu	Leu	Leu	Gly
				85					90						95
Val	Phe	Ala	Tyr	Ala	Leu	Arg	Lys	Thr	Ala	Ile	Leu	Arg	Ala	Arg	Ser
			100					105					110		
Leu	Leu	Trp	Trp	Phe	Xaa	Leu									
			115												

(2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

Val	Asn	Leu	Met	Asp	Tyr	Phe	Ser	Lys	Ser	Leu	Phe	Leu	Asn	Ser	Leu
1				5				10						15	
Asn	Thr	Gln	Arg	Leu	Ile	Val	Ser	Asn	Lys	Leu	Ala	Ile	Asp	Val	Gln

20							25							30						
Tyr	Gly	Met	Leu	Gln	Ser	Val	Arg	Lys	Asn	Tyr	Pro	Asp	Val	Val	Asp					
		35					40					45								
Gly	Gly	Val	Arg	Glu	Gly	Pro	Phe	Trp	Val	Leu	Ala	Gly	Ala	Leu	Met					
	50					55					60									
Pro	Ser	Ile	Leu	Ile	Glu	Ile	Gly	Tyr	Asn	Ser	His	Ala	Ile	Glu	Ser					
65					70					75					80					
Lys	Arg	Ile	Gln	Ser	Lys	Pro	Tyr	Gln	Lys	Ile	Leu	Ala	Lys	Gly	Ile					
				85					90					95						
Ala	Asp	Gly	Ile	Asp	Ser	Phe	Phe	Ser	Lys	Asn	Asp									
			100					105												

Asp Val Phe Ser Ala Lys Ile Arg Phe Ser Gly Ile Ser Phe Ala Tyr
 130 135 140
 Asn Ile Ala Tyr Ala Ile Thr Ala Gly Phe Thr Pro Gln Leu Ser Ser
 145 150 155 160
 Trp Leu Asn Ala Lys Ala Ile Ala Val Pro Glu Ser Leu Gln Ser Tyr
 165 170 175
 Gly Leu Ser Phe Tyr Ile Leu Ile Val Ser Leu Ile Ala Phe Ile Thr
 180 185 190
 Ser Leu Leu Met Ala Pro Ile Tyr His Lys Ser Asn Thr Gln His Glu
 195 200 205
 Val Ser Pro Thr Ala
 210

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

Leu Ala Ser Arg Tyr Ser Val Ala Val Gly Asn Leu Phe Ser Glu His
 1 5 10 15
 Leu Tyr Asp Leu Arg Asn Glu Thr Met Thr Asn Leu Ile Gly Phe Leu
 20 25 30
 Leu Val Leu Ala Ser Ile Trp Val Phe Phe Leu Ala Leu Gly Val Leu
 35 40 45
 Leu Gly Lys Met Leu Val Phe Ser Gly Leu Gly Ile Ile Asp Lys Ala
 50 55 60
 Leu Gly Phe Ile Phe Ser Cys Leu Lys Thr Phe Leu Val Leu Ser Phe
 65 70 75 80
 Ile Leu Tyr Ala Leu Ser Lys Met Asp Leu Met Lys Asp Ala Asn Ala
 85 90 95
 Tyr Leu Gln Glu Lys Xaa Xaa Ile Phe Pro Thr Xaa Lys Xaa Xaa Xaa
 100 105 110
 Ser Lys Ile Met Arg Leu Asp Gly Val Lys His Val Glu Lys Asn Leu
 115 120 125

Lys Asp Asn Leu Glu Glu Met Ser Asp Glu Val Lys Asn Lys Gly Ser
 130 135 140
 Ile Asp Asn Ala Lys Glu Ser Phe Asn Lys Gly Tyr Gly
 145 150 155

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...312
- (D) OTHER INFORMATION: /note= "flagellar basal body
L-ring protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

Met Lys Ser Asp Lys Pro Phe Leu Glu Arg Tyr Phe Tyr Asp Pro Thr
 1 5 10 15
 Leu Leu Gln Lys Gly Leu Ile Phe Ala Leu Tyr Pro Phe Ser Leu Ile
 20 25 30
 Tyr Gln Cys Ile Ala Thr Ile Lys Arg Lys Thr Ala Lys Lys His Asp
 35 40 45
 Phe Lys Ile Pro Ile Ile Ser Ile Gly Asn Leu Ile Ala Gly Gly Ser
 50 55 60
 Gly Lys Thr Pro Phe Ile Leu Glu Ile Ala Pro Arg Tyr Gln Glu Val
 65 70 75 80
 Ala Val Val Ser Arg Gly Tyr Gln Arg Asp Ser Lys Gly Leu Val Val
 85 90 95
 Val Ser Val Lys Gly Asn Ile Leu Val Pro Gln Lys Thr Ala Gly Asp
 100 105 110
 Glu Ala Tyr Leu Leu Ala Leu Asn Leu Lys Gln Ala Ser Val Ile Val
 115 120 125
 Ser Glu Lys Arg Glu Leu Gly Val Leu Lys Ala Leu Glu Leu Gly Ser
 130 135 140
 Lys Ile Val Phe Leu Asp Asp Gly Phe Arg Phe Asn Phe Asn Gln Phe

145		150		155		160									
Asn	Ala	Leu	Leu	Lys	Pro	Lys	Val	Pro	Pro	Tyr	Tyr	Pro	Phe	Cys	Leu
				165					170					175	
Pro	Ser	Gly	Leu	Tyr	Arg	Glu	Asn	Ile	Lys	Ser	Tyr	Lys	Glu	Ala	His
			180					185					190		
Leu	Val	Ile	Thr	Glu	Asp	Lys	Asp	Tyr	Gln	Arg	Ile	Thr	Ser	Ile	Thr
		195					200					205			
Asn	Pro	Thr	Lys	Arg	Met	Leu	Leu	Val	Thr	Ala	Ile	Ala	Asn	Pro	Ser
	210					215					220				
Arg	Leu	Asp	Ala	Phe	Leu	Pro	Lys	Glu	Val	Val	Lys	Lys	Leu	Tyr	Phe
225					230					235					240
Arg	Asp	His	Ala	Pro	Phe	Asp	Leu	Lys	Leu	Leu	Glu	Lys	Glu	Phe	Tyr
			245						250					255	
Gln	Asn	Asn	Ala	Thr	Ser	Leu	Leu	Val	Thr	Ser	Lys	Asp	Leu	Val	Lys
			260					265					270		
Leu	Gln	Asp	Cys	Lys	Leu	Pro	Leu	Ser	Val	Leu	Asp	Leu	Lys	Leu	Glu
		275					280					285			
Ile	Cys	Pro	Lys	Val	Leu	Glu	Glu	Ile	Asp	Arg	Tyr	Ile	Leu	Ser	Tyr
	290					295				300					
Pro	Cys	Asn	Ile	Lys	Glu	His	Leu								
305					310										

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

Met	Ser	Leu	Gly	Ala	Val	Ile	Arg	Leu	Ile	Phe	Cys	Tyr	Lys	Leu	Glu
1				5					10					15	
Gly	Val	Ile	Leu	Asp	Leu	Lys	Arg	Ile	Asn	Phe	Lys	Ser	Tyr	Tyr	Pro
			20					25					30		
Asn	Asn	Lys	Asn	Ala	Leu	Phe	Ile	Asn	Asn	Lys	Lys	Asn	Pro	Leu	Ser
		35					40					45			

Ser Thr Ser Lys Phe Ile Leu Leu
50 55

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...199
- (D) OTHER INFORMATION: /note= "cell division and sporulation protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

Met	Leu	Glu	Thr	Thr	Ile	Asp	Phe	Ser	Arg	Tyr	Ser	Ser	Val	Lys	Ile	1	5	10	15
Gly	Ala	Pro	Leu	Lys	Val	Ser	Val	Leu	Glu	Asn	Asp	Asn	Glu	Ile	Ser	20	25	30	
Gln	Glu	His	Gln	Ile	Ile	Gly	Leu	Ala	Asn	Asn	Leu	Leu	Ile	Ala	Pro	35	40	45	
Asp	Val	Lys	Asn	Leu	Ala	Leu	Leu	Gly	Lys	Asn	Tyr	Asp	Tyr	Ile	Cys	50	55	60	
Asp	Lys	Gly	Glu	Trp	Val	Glu	Val	Gly	Gly	Ala	Ala	Asn	Ala	Ser	Lys	65	70	75	80
Ile	Phe	Asn	Tyr	Phe	Arg	Ala	Asn	Asp	Leu	Glu	Gly	Leu	Glu	Phe	Leu	85	90	95	
Gly	Gln	Leu	Pro	Gly	Thr	Leu	Gly	Ala	Leu	Val	Lys	Met	Asn	Ala	Gly	100	105	110	
Met	Lys	Glu	Phe	Glu	Ile	Lys	Asn	Val	Leu	Glu	Ser	Ala	Cys	Val	Asn	115	120	125	
Gly	Glu	Trp	Leu	Glu	Lys	Glu	Ala	Leu	Gly	Leu	Asp	Tyr	Arg	Ser	Ser	130	135	140	
Gly	Phe	Asn	Gly	Val	Val	Leu	Arg	Ala	Arg	Phe	Lys	Lys	Thr	His	Gly	145	150	155	160
Phe	Arg	Glu	Gly	Val	Leu	Lys	Ala	Cys	Lys	Ser	Met	Arg	Lys	Ser	His	165	170	175	

Pro Lys Leu Pro Asn Phe Gly Ser Cys Phe Lys Asn Pro Pro Asn Asp
180 185 190
Tyr Ala Gly Arg Leu Leu Glu
195

(2) INFORMATION FOR SEQ ID NO:652:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

Leu	Ser	Lys	Gln	Ser	Ala	Asp	Ile	Val	Ile	Thr	Asn	Asp	Ser	Leu	Ser
1				5					10					15	
Ser	Leu	Val	Lys	Val	Leu	Ala	Ile	Ala	Lys	Lys	Thr	Lys	Ser	Ile	Thr
			20					25					30		
Trp	Gln	Asn	Ile	Leu	Phe	Ala	Leu	Gly	Ile	Lys	Ala	Val	Phe	Ile	Val
		35					40					45			
Leu	Gly	Leu	Met	Gly	Val	Ala	Ser	Leu	Trp	Glu	Ala	Val	Phe	Gly	Asp
	50					55					60				
Val	Gly	Val	Thr	Leu	Leu	Ala	Leu	Ala	Asn	Ser	Xaa	Arg	Thr	Met	Arg
65					70					75				80	

Ala

(2) INFORMATION FOR SEQ ID NO:653:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION: 1...89

(D) OTHER INFORMATION: /note= "chemotaxis protein cheY"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

```
Met Leu Lys Asn Gly Asp Lys Ile Pro Asp Ala Ile Leu Val Asp Ile
1           5           10           15
Glu Met Pro Lys Met Asp Gly Tyr Thr Phe Ala Ser Glu Val Arg Lys
          20           25           30
Tyr Asn Lys Phe Lys Asn Leu Pro Leu Ile Ala Val Thr Ser Arg Val
          35           40           45
Thr Lys Thr Asp Arg Met Arg Gly Val Glu Ser Gly Met Thr Glu Tyr
          50           55           60
Ile Thr Lys Pro Tyr Ser Gly Glu Tyr Leu Thr Thr Val Val Lys Arg
65           70           75           80
Ser Ile Lys Leu Glu Gly Asp Gln Ser
          85
```

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

```
Val Phe Glu Pro Val Ile Ala Tyr Lys Leu Phe His Ser Phe Val Ile
1           5           10           15
Leu Gly Cys Ala Ile Glu Thr Leu Thr Thr Lys Cys Val Glu Gly Ile
          20           25           30
Thr Ala Asn Glu Lys Ile Cys His Asp Tyr Val Phe Asn Ser Ile Gly
          35           40           45
Ile Val Thr Ala Leu Asn Pro His Ile Gly Tyr Glu Lys Ser Ala Met
          50           55           60
Ile Ala Lys Glu Ala Leu Lys Ser Asp Arg Ser Ile Tyr Asp Ile Ala
65           70           75           80
Leu Glu Lys Lys Ile Leu Thr Lys Glu Gln Leu Asp Asp Ile Phe Lys
          85           90           95
```

Pro Glu Asn Met Leu Arg Thr His Ala Phe Lys Lys His Lys Asp
100 105 110

(2) INFORMATION FOR SEQ ID NO:655:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

Met Leu Arg Leu Leu Ala Gln Lys Ser Ala Ile Lys Leu Ile Leu Ile
1 5 10 15
Pro Pro Ser Ala Asn Ala Leu Gly Ile Ala Ser Ile Cys Glu Leu Ser
20 25 30
Glu Glu Val Phe Glu His Glu Lys Ile Val Gly Ile Arg Ala Gln Gly
35 40 45
Asp Phe Thr Ile Asn Ser Asp Asp Arg Gly Phe Trp Glu Arg Arg Cys
50 55 60
Gln
65

(2) INFORMATION FOR SEQ ID NO:656:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 268 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

Met Lys Lys Leu Leu Leu Leu Glu His Lys Ile Val Lys Ile Gly
1 5 10 15
Leu Ile Ile Val Ile Val Leu Val Gly Phe Phe Leu Phe Tyr Glu Gln
20 25 30

Glu	Ile	Lys	Glu	Lys	Ala	Val	Asn	Val	Ser	Gln	Gly	Lys	Phe	Pro	Thr	35	40	45	
Ser	Ser	Tyr	Leu	Phe	Gln	Ala	Tyr	Glu	Gly	Ile	Lys	Asn	Lys	Ile	Asp	50	55	60	
Thr	Ile	Asn	Gln	Val	Lys	Pro	Asn	Asp	Glu	Thr	Lys	Ser	Val	Asn	Glu	65	70	75	80
Asn	Ile	Glu	Lys	Thr	Gln	Lys	Asp	Leu	Asp	Asp	Phe	Asn	Ala	Leu	Val	85	90	95	
Gln	Lys	Leu	Pro	Asn	Leu	Pro	Lys	Asp	Phe	Asn	Lys	Thr	Leu	Ile	Lys	100	105	110	
Pro	Gln	Ser	Pro	Phe	Phe	Asn	Tyr	Asn	Thr	Ala	Asn	Glu	Asp	Glu	Lys	115	120	125	
Asn	Arg	Leu	Val	Ile	Leu	Ala	Ser	Arg	Ile	Ser	Ser	Gln	Lys	Glu	Thr	130	135	140	
Gln	Pro	Pro	Ile	Ser	Ile	Lys	Asn	Ser	Val	Ser	His	Ile	Lys	Ser	Lys	145	150	155	160
Glu	Lys	Arg	Glu	Leu	Glu	Lys	Glu	Trp	Ala	Lys	Pro	Ser	Val	Ser	Phe	165	170	175	
Gly	Ser	Phe	Ser	Leu	Leu	Ser	Ser	Ser	Ser	Ser	Phe	Ser	Ser	Phe	Glu	180	185	190	
Val	Ser	Phe	Leu	Ser	Arg	Gly	Ile	Gly	Leu	Asp	Cys	Glu	Lys	Leu	Lys	195	200	205	
Ser	Phe	Leu	Lys	Ala	Phe	Ser	Ser	Ser	Leu	Phe	Ser	Leu	Leu	Ser	Ser	210	215	220	
Leu	Phe	Cys	His	Pro	Leu	Ser	Leu	Phe	Cys	Ser	Leu	Ile	Gly	Leu	Ile	225	230	235	240
Phe	Cys	Phe	Ser	Lys	Phe	Ser	Arg	Glu	Leu	Val	Asn	Ala	Ser	Asn	Asn	245	250	255	
Ser	Leu	Glu	Phe	Ser	Ser	Leu	Ser	Arg	Leu	Gly	Ser					260	265		

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...100

(D) OTHER INFORMATION: /note= "UDP-N-ACETYLMURAMYL-TRYPEPTIDE
SYNTHETASE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

```
Met Gly Ala Ile Ala Ser Cys Tyr Ala His Gln Ile Ile Leu Thr Ser
1           5           10           15
Asp Asn Pro Arg Ser Glu Asn Glu Glu Asp Ile Ile Lys Asp Ile Leu
20           25           30
Lys Gly Ile Asn Asn Ser Ser Lys Val Ile Val Glu Lys Asp Arg Lys
35           40           45
Lys Ala Ile Leu Asn Ala Leu Glu Asn Leu Lys Asp Asp Glu Val Leu
50           55           60
Leu Ile Leu Gly Lys Gly Asp Glu Asn Ile Gln Ile Phe Lys Asp Lys
65           70           75           80
Thr Ile Phe Phe Ser Asp Gln Glu Val Val Lys Asp Tyr Tyr Leu Asn
85           90           95
Leu Lys Gln Gly
100
```

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...80

(D) OTHER INFORMATION: /note= "FLAGELLAR MOTOR SWITCH PROTEIN F"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

```
Val Met Asp Lys Leu Thr Lys Ser Leu Gln Thr Gln Lys Asn Phe Ala
1           5           10           15
Tyr Leu Gly Lys Ile Lys Pro Gln Gln Leu Ala Asp Phe Ile Ile Asn
20           25           30
```

Glu	His	Pro	Gln	Thr	Ile	Ala	Leu	Ile	Leu	Ala	His	Met	Glu	Xaa	Pro
		35					40					45			
Asn	Ala	Ala	Glu	Thr	Leu	Ser	Tyr	Phe	Pro	Asp	Glu	Met	Lys	Ala	Glu
	50					55					60				
Ile	Ser	Ile	Arg	Met	Ala	Asn	Phe	Arg	Arg	Asn	Ile	Ala	Pro	Ser	Gly
65					70					75					80

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

Met	Arg	Tyr	Phe	Arg	Ser	Ala	Phe	Leu	Leu	Phe	Phe	Met	Thr	Leu	Phe
1				5				10						15	
Phe	Val	Ser	Cys	Ser	Lys	His	Pro	Phe	Ser	Lys	Gln	Thr	Pro	Lys	Thr
			20					25					30		
Lys	Glu	Arg	Ile	Arg	Gln	Glu	Glu	Ala	Asn	Lys	Lys	Arg	Glu	Glu	Thr
		35				40						45			
Leu	Asn	Ala	Leu	Arg	Gln	Phe	Arg	Leu	Ile	Tyr	Ile	Asn	Thr	Pro	Val
	50					55					60				
Phe	Arg	Phe	Tyr	Asp	Tyr	Gly	Thr	Ile	Lys	Thr	Asp	Lys	Asp	His	Asn
65					70					75					80
Thr	Glu	Val	Thr	Leu	Tyr	Lys	Leu	Ser	Gln	Lys	Val	Gly	Asp	Ile	Tyr
				85					90					95	
Met	Thr	Lys	Arg	Ser	Ile	Cys	Phe	Ser	Gln	Lys	Cys	Ser	Ala	Lys	Trp
			100					105					110		
Ile	Ala	Ala	Arg	Asp	Leu	Phe	Gly	Lys	Val	Ser	Tyr	Gly	Asp	Leu	Phe
		115					120					125			
Asp	Asp	Ile	Val	Leu	Gly	Arg	Asp	Ile	Phe	Lys	Gly	Leu	Gly	Lys	Arg
	130					135					140				
His	Leu	Thr	Pro	Glu	Tyr	Val	Ile	Gln	Arg	Phe	Gln	Lys	Ser	Gly	Glu
145					150					155					160
Ile	Ile	Leu	Tyr	Glu	Arg	Lys	Asn	Gly	Leu	Ile	Ser	Phe	Gln	Asn	Leu

	165		170		175										
Thr	Gln	Lys	Ile	Ala	Ile	Arg	Ile	Glu	Pro	Tyr	Glu	Pro	Ser	Leu	Gln
			180					185					190		
Asp	Leu	Glu	Asp	Asn	Glu	Asn	Ala	Asp	Ser	Glu	Leu	Gln			
		195					200					205			

(2) INFORMATION FOR SEQ ID NO:660:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...124
 - (D) OTHER INFORMATION: /note= "flagellar hook polypeptide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

Met	Arg	Ile	Glu	Glu	Asn	Gly	Val	Ile	Ser	Leu	Ala	Phe	Ser	Asn	Gly
1				5					10					15	
Val	Val	Glu	Pro	Val	Ala	Arg	Ile	Gly	Ile	Xaa	Ala	Phe	Thr	Asn	Asp
			20					25					30		
Gln	Gly	Leu	Arg	Lys	Ile	Gly	Gly	Asn	Leu	Tyr	Glu	Met	Gln	Glu	Gly
		35					40					45			
Thr	Ile	Asn	Gly	Glu	Asn	Arg	Pro	Leu	Xaa	Gly	Asn	Pro	Ile	Leu	Gly
		50				55					60				
Trp	Asp	Glu	Glu	Gly	Lys	Leu	Lys	Phe	Gly	Lys	Ile	Arg	His	Lys	Tyr
65					70					75				80	
Leu	Glu	Thr	Ser	Asn	Val	Asn	Ala	Gly	Asn	Ala	Leu	Thr	Asn	Leu	Ile
				85					90					95	
Leu	Met	Gln	Arg	Gly	Tyr	Ser	Met	Asn	Ala	Arg	Ala	Phe	Gly	Ala	Gly
			100					105					110		
Asp	Asp	Met	Ile	Lys	Glu	Ala	Ile	Ser	Leu	Lys	Lys				
			115				120								

(2) INFORMATION FOR SEQ ID NO:661:

- (i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 1...93

(D) OTHER INFORMATION: /note= " vacuolating cytotoxin -
Helicobacter pylor"

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:661:

Val Glu Ala Arg Tyr Tyr Tyr Gly Asp Thr Ser Tyr Phe Tyr Leu His
1 5 10 15

Val	Gly	Val	Leu	Gln	Glu	Phe	Ala	His	Phe	Gly	Ser	Asn	Asp	Val	Ala
			20					25					30		

Ser Leu Asn Thr Phe Lys Ile Asn Ala Ala Arg Ser Pro Leu Ser Thr
35 40 45

Tyr Ala Arg Ala Met Met Gly Gly Glu Leu Gln Leu Ala Lys Glu Val
50 55 60

Phe Leu Asn Leu Gly Val Val Tyr Leu His Asn Leu Ile Ser Asn Ala
65 70 75 80

Ser His Phe Ala Ser Asn Leu Gly Met Arg Tyr Ser Phe
85 90

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

Met Lys Asn Leu Arg His Phe Arg Lys Leu Ile Ala Phe Leu Gly Phe
1 5 10 15

Ser Pro Leu Leu Leu Gln Ala Asp Met Thr Thr Phe Phe Asn Ser Ile

	20		25		30										
Glu	Gln	Gln	Leu	Thr	Ser	Pro	Thr	Ala	Lys	Gly	Ile	Leu	Met	Val	Ile
	35						40					45			
Phe	Leu	Gly	Leu	Ala	Ile	Phe	Ile	Trp	Lys	Asn	Leu	Asp	Arg	Trp	Lys
	50					55					60				
Glu	Ile	Leu	Met	Thr	Val	Leu	Ala	Leu	Lys	Xaa	Val	Pro	Met	Gln	Xaa
65					70					75				80	

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

Val	Glu	Glu	Leu	Ala	Lys	Leu	Ile	Asn	Asn	Asn	Asn	Asn	Asn	Lys	Lys
1				5				10						15	
Leu	Arg	Gly	Phe	Phe	Leu	Lys	Val	Leu	Leu	Ser	Leu	Val	Val	Phe	Ser
			20					25					30		
Ser	Tyr	Gly	Ser	Ala	Asn	Asp	Asp	Lys	Glu	Ala	Lys	Lys	Glu	Ala	Leu
		35					40					45			
Glu	Lys	Glu	Lys	Asn	Thr	Pro	Asn	Gly	Leu	Val	Tyr	Thr	Asn	Leu	Asp
	50					55					60				
Phe	Asp	Ser	Phe	Lys	Ala	Thr	Ile	Lys	Asn	Leu	Lys	Asp	Lys	Lys	Val
65					70					75					80
Thr	Phe	Lys	Glu	Val	Asn	Pro	Asp	Ile	Ile	Lys	Asp	Glu	Val	Phe	Asp
				85					90					95	
Phe	Val	Ile	Val	Asn	Arg	Val	Leu	Lys	Lys	Ile	Lys	Asp	Leu	Lys	His
			100					105					110		
Tyr	Asp	Pro	Val	Ile	Glu	Lys	Ile	Phe	Asp	Glu	Lys	Gly	Lys	Glu	Met
		115					120					125			
Gly	Leu	Asn	Val	Glu	Leu	Gln	Ile	Asn	Pro	Glu	Val	Lys	Asp	Phe	Phe
	130					135					140				
Thr	Phe	Lys	Ser	Ile	Ser	Thr	Thr	Asn	Lys	Gln	Arg	Cys	Phe	Leu	Ser
145					150					155					160

Leu His Gly Glu Thr Arg Glu Ile Leu Cys Asp Asp Lys Leu Tyr Asn
 165 170 175
 Val Leu Leu Ala Val Phe Asn Ser Tyr Asp Pro Asn Asp Leu Leu Lys
 180 185 190
 His Ile Ser Thr Ile Glu Ser Leu Lys Lys Ile Phe Tyr Thr Ile Thr
 195 200 205
 Cys Glu Ala Val Tyr Leu
 210

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

Val Gly Gly Ile Val Ala Asn Met Asn Asp Leu Ser Thr Tyr Met Val
 1 5 10 15
 Glu Asn Leu Leu Met Gly Leu Tyr Leu Phe Ser Ser Ala Leu Asp Leu
 20 25 30
 Gly Val Lys Lys Ala Ile Asn Leu Ala Ser Ser Cys Ala Tyr Pro Lys
 35 40 45
 Tyr Ala Pro Asn Pro Leu Lys Glu Ser Asp Leu Leu Asn Gly Ser Leu
 50 55 60
 Glu Pro Thr Asn Glu Gly Tyr Ala Leu Pro Asn Ser Leu Xaa
 65 70 75

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

Met Lys Lys Arg Lys His Val Ser Lys Lys Val Phe Asn Val Ile Ile
1 5 10 15
Leu Phe Val Ala Val Phe Thr Leu Leu Val Val Ile His Lys Thr Leu
20 25 30
Ser Asn Gly Ile His Ile Gln Asn Leu Lys Ile Gly Lys Leu Gly Ile
35 40 45
Ser Glu Leu Tyr Leu Lys Leu Asn Asn Lys Leu Ser Leu Glu Val Glu
50 55 60
Arg Val Asp Leu Ser Ser Phe Phe His Gln Lys Pro Thr Lys Lys Arg
65 70 75 80
Leu Glu Val Ser Asp Leu Ile Lys Asn Ile Arg Tyr Gly Ile Trp Ala
85 90 95
Val Ser Tyr Phe Glu Lys Leu Lys Val Lys Glu Ile Ile Leu Asp Asp
100 105 110
Lys Asn Lys Ala Asn Ile Phe Phe Asp Gly Asn Lys Tyr Glu Xaa Arg
115 120 125
Ile Ser Arg Asn Gln Arg Gly Ile Phe Pro Arg Arg Arg Leu Lys Ile
130 135 140
Ser Ser Leu Lys Ser Ser Ile Cys Phe Leu Lys Met Leu Lys Ser Lys
145 150 155 160
Trp Met Ala Thr Pro Thr Ile Xaa Pro Lys Pro Gly Lys Trp Arg Ser
165 170 175
Ile

(2) INFORMATION FOR SEQ ID NO:666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

Val Ser Cys Trp Gly Ala Ser Lys Lys Arg Phe Leu Gly Phe Cys Val
1 5 10 15

Trp	Gly	Arg	Cys	Val	Tyr	Ala	Gly	Gly	Leu	Met	Ala	Glu	Gln	Asp	Pro			
			20					25					30					
Lys	Glu	Leu	Ile	Phe	Ser	Gly	Ile	Thr	Ile	Tyr	Thr	Asp	Lys	Asn	Phe			
		35					40					45						
Thr	Arg	Ala	Lys	Lys	Tyr	Phe	Glu	Lys	Ala	Cys	Lys	Ser	Asn	Asp	Ala			
	50					55					60							
Asp	Gly	Cys	Ala	Ile	Leu	Arg	Glu	Val	Tyr	Ser	Ser	Gly	Lys	Ala	Ile			
65					70					75					80			
Ala	Arg	Glu	Asn	Ala	Arg	Glu	Ser	Ile	Glu	Lys	Ala	Leu	Glu	His	Thr			
			85						90					95				
Ala	Thr	Ala	Lys	Val	Cys	Lys	Leu	Asn	Asp	Ala	Glu	Lys	Cys	Lys	Asp			
		100						105					110					
Leu	Ala	Glu	Phe	Tyr	Phe	Asn	Val	Asn	Asp	Leu	Lys	Asn	Ala	Leu	Glu			
	115						120					125						
Tyr	Tyr	Ser	Lys	Ser	Cys	Lys	Leu	Asn	Asn	Val	Glu	Gly	Cys	Met	Leu			
	130					135					140							
Ser	Ala	Thr	Phe	Tyr	Asn	Asp	Met	Ile	Lys	Gly	Leu	Lys	Lys	Asp	Lys			
145					150					155					160			
Lys	Asp	Leu	Glu	Tyr	Tyr	Ser	Lys	Ala	Cys	Glu	Leu	Asn	Asn	Gly	Gly			
			165						170					175				
Gly	Cys	Ser	Lys	Leu	Gly	Gly	Asp	Tyr	Phe	Phe	Gly	Glu	Gly	Val	Thr			
		180						185					190					
Lys	Asp	Phe	Lys	Lys	Ala	Phe	Glu	Tyr	Ser	Ala	Lys	Ala	Cys	Glu	Leu			
		195					200					205						
Asn	Asp	Ala	Lys	Gly	Cys	Tyr	Ala	Leu	Ala	Ala	Phe	Tyr	Asn	Glu	Gly			
	210					215					220							
Lys	Gly	Val	Ala	Lys	Asp	Glu	Lys	Gln	Thr	Thr	Glu	Asn	Leu	Glu	Lys			
225					230					235				240				
Ser	Cys	Lys	Leu	Gly	Leu	Lys	Glu	Ala	Cys	Asp	Ile	Leu	Lys	Glu	Gln			
			245						250					255				

Lys Gln

(2) INFORMATION FOR SEQ ID NO:667:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

Lys Gln Ser Ile Glu Asn Trp Asn Ala Gln Asn Leu Leu Arg Asn Lys
 115 120 125
 Tyr Leu Gln Gln Gln Cys Pro Trp Leu Asn Val Asn Ala Leu Thr Asn
 130 135 140
 Asn Lys Ile Val Asn Leu Lys Asp Leu Asn Asn Leu Ile Thr Lys Asn
 145 150 155 160
 Gly Glu Gln Thr Gln Thr Ala Arg Asp Val Gln Asn Leu Ile Gln Ser
 165 170 175
 Ile Ser Gly Ser Gly Tyr Gly Asn Met Gln Ser Leu Ala Gly Glu Leu
 180 185 190
 Ser Gly Arg Ala Trp Gly Glu Met Leu Cys Lys Met Val Asn Asp Ser
 195 200 205
 Asn Tyr Glu Ser Glu Gln Ala Leu Leu Ala Thr Gly Asn Asn Pro Glu
 210 215 220
 Glu Gln Lys Arg Arg Phe Leu Leu Arg Val Lys Lys Lys Val Asn Asp
 225 230 235 240
 Asn Lys Gln Leu Lys Asp Lys Leu Asp Pro Phe Leu Lys Arg Leu Asp
 245 250 255
 Val Leu Gln Thr Glu Phe Gly Val Thr Asp Pro Thr Ala Asn His Asn
 260 265 270
 Lys Gln Gly Ile His Tyr Cys Thr Glu Asn Lys Glu Thr Gly Lys Cys
 275 280 285
 Asp Pro Ile Lys Asn Val Phe Arg Thr Thr Arg Leu Asp Asn Glu Leu
 290 295 300
 Glu Gln Glu Ile Gln Thr Leu Thr Leu Asp Leu Ile Lys Ala Ser Asn
 305 310 315 320
 Lys Asp Ala Gln Ser Gln Ala Tyr Ala Asn Phe Asn Gln Arg Ile Lys
 325 330 335
 Leu Leu Thr Leu Lys Tyr Leu Lys Glu Ile Thr Asn Gln Met Leu Phe
 340 345 350
 Leu Asn Gln Thr Met Ala Met Gln Ser Glu Ile Met Thr Asp Asp Tyr
 355 360 365
 Phe Arg Gln Asn Asn Asp Gly Phe Gly Glu Lys Glu Asn His Ile Asp
 370 375 380
 Glu Gln Leu Thr Gln Lys Arg Ile Asn Glu Arg Glu Arg Ala Arg Ile
 385 390 395 400
 Tyr Phe Gln Asn Pro Asn Val Lys Phe Asp Gln Phe Gly Phe Pro Ile
 405 410 415

Phe Ser Ile Trp Asp
420

(2) INFORMATION FOR SEQ ID NO:669:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...81
 - (D) OTHER INFORMATION: /note= "sodium/glutamate symport carrier protein"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

Met	Ser	Val	Asn	Leu	Leu	Glu	Leu	Leu	Lys	Leu	Ala	Val	Pro	Leu	Ala
1			5						10					15	
Val	Ile	Leu	Ser	Val	Gln	Val	Ala	Val	Met	Ile	Leu	Tyr	Val	Val	Leu
		20					25						30		
Val	Thr	Phe	Arg	Val	Cys	Gly	Lys	Asp	Tyr	Asp	Ala	Ala	Val	Leu	Cys
		35					40					45			
Ala	Gly	His	Cys	Gly	Phe	Gly	Leu	Gly	Ala	Thr	Pro	Thr	Ala	Met	Val
	50					55					60				
Asn	Met	Gln	Thr	Ile	Thr	Asn	His	Tyr	Gly	Pro	Ser	His	Val	Ala	Phe
65					70					75					80

Ile

(2) INFORMATION FOR SEQ ID NO:670:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

Met	Gln	Leu	Ser	Pro	Leu	Gln	Ser	Ala	Leu	Leu	Tyr	Phe	Arg	Tyr	Phe	
1				5					10					15		
Ile	Tyr	Pro	Glu	Lys	Lys	Thr	Arg	Ser	Phe	Asp	Leu	Ser	Asp	Leu	Ile	
			20					25					30			
Phe	Ile	Val	Met	Val	Phe	Leu	Val	Leu	Ala	Leu	Gly	Leu	Leu	Met	Ser	
		35					40					45				
Glu	Glu	Ile	Ser	Ile	Ser	Tyr	Asn	Glu	Ala	Lys	Asp	Phe	Phe	Tyr	Ser	
	50					55					60					
Asp	Ala	Trp	Phe	Val	Lys	Ile	Ala	Gln	Lys	Ser	Val	Ala	Ile	Leu	Arg	
65					70					75					80	
Pro	Lys	Arg	Phe	Gly	Phe	Lys	Ile	Ala	Phe	Phe	Asp	Arg	Ser	Arg	His	
			85						90					95		
Gln	His	Val	Phe	Ile	Leu	Pro	His	Arg	Ala	Lys	Asp	Phe	Lys	Lys	Ala	
		100						105					110			

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

Leu	Ala	Gly	Leu	Xaa	Val	Gly	Cys	Xaa	Arg	Met	Lys	Gln	Thr	Phe	Trp	
1				5					10					15		
Xaa	Leu	Ser	Trp	Gly	Glu	Lys	Ser	Gln	Lys	Val	Cys	Val	His	Arg	Pro	
			20					25					30			
Trp	Tyr	Ala	Ile	Trp	Ser	Cys	Asp	Lys	Trp	Glu	Glu	Lys	Thr	Gln	Gln	
		35					40					45				
Phe	Thr	Gly	Asn	Gln	Leu	Ile	Thr	Lys	Thr	Trp	Ala	Gly	Gly	Asn	Ala	
	50					55					60					
Ala	Asn	Tyr	Tyr	His	Ser	Gln	Asn	Asn	Gln	Asp	Ile	Thr	Ala	Asn	Leu	
65				70					75						80	
Lys	Asn	Asp	Asn	Gly	Thr	Tyr	Phe	Leu	Ser	Gly	Leu	Tyr	Asn	Tyr	Thr	
			85						90					95		

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

Leu	Leu	Ser	Leu	Val	Lys	Gly	Lys	Thr	Met	Leu	Arg	Ser	Leu	Tyr	Ser	
1				5					10					15		
Ala	Thr	Ser	Gly	Met	Leu	Ala	Gln	Gln	Thr	His	Ile	Asp	Thr	Thr	Ser	
			20					25					30			
Asn	Asn	Ile	Ala	Asn	Val	Asn	Thr	Thr	Gly	Phe	Lys	Lys	Ser	Arg	Ala	
		35					40					45				
Asp	Phe	Asn	Asp	Leu	Phe	Tyr	Gln	Ala	Met	Gln	Tyr	Ala	Gly	Thr	Asn	
	50					55					60					
Thr	Ser	Asn	Thr	Thr	Leu	Ser	Pro	Asp	Gly	Met	Glu	Val	Gly	Leu	Gly	
65					70					75					80	
Val	Arg	Pro	Ser	Ala	Ile	Thr	Lys	Met	Phe	Ser	Gln	Gly	Ser	Pro	Lys	
				85					90					95		
Glu	Thr	Glu	Asn	Asn	Leu	Asp	Ile	Ala	Ile	Thr	Gly	Lys	Gly	Phe	Phe	
			100					105					110			
Gln	Val	Gln	Leu	Pro	Asp	Gly	Thr	Thr	Ala	Tyr	Thr	Arg	Ser	Gly	Asn	
		115					120					125				
Phe	Lys	Leu	Asp	Glu	Gln	Gly	Asn	Leu	Val	Thr	Ser	Glu	Gly	Tyr	Leu	
	130					135					140					
Leu	Ile	Pro	Gln	Ile	Thr	Leu	Pro	Glu	Asp	Thr	Thr	Gln	Val	Asn	Ile	
145				150						155					160	
Gly	Val	Asp	Gly	Thr	Val	Ser	Val	Thr	Gln	Gly	Leu	Gln	Thr	Thr	Ser	
				165					170					175		
Asn	Val	Ile	Gly	Gln	Ile	Thr	Leu	Ala	Asn	Phe	Val	Asn	Pro	Ala	Gly	
			180					185					190			
Leu	His	Ser	Met	Gly	Asp	Asn	Leu	Phe	Ser	Ile	Thr	Asn	Ala	Ser	Gly	
		195					200					205				
Asp	Ala	Ile	Val	Gly	Asn	Pro	Asp	Ser	Gln	Gly	Leu	Gly	Lys	Leu	Arg	
	210					215					220					
Gln	Gly	Phe	Leu	Glu	Leu	Ser	Asn	Val	Arg	Leu	Val	Glu	Glu	Met	Thr	
225				230						235					240	
Asp	Leu	Ile	Thr	Ala	Gln	Arg	Ala	Tyr	Glu	Ala	Asn	Ser	Lys	Ser	Ile	
				245					250					255		
Gln	Thr	Ala	Asp	Ala	Met	Leu	Gln	Thr	Val	Asn	Ser	Leu	Lys	Arg		
			260					265					270			

(2) INFORMATION FOR SEQ ID NO:673:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

Val	Tyr	Ala	Leu	Met	Val	Ala	Phe	Phe	Ala	Tyr	Met	Ser	Tyr	Cys	Leu
1				5					10					15	
Gly	Tyr	Gln	Phe	Ser	Lys	Phe	Val	Ser	Lys	Asn	Asn	Ile	Ser	Ser	Leu
			20					25					30		
Ser	Ser	Leu	Leu	Ser	Ser	Cys	Val	Arg	Val	Val	Ser	Val	Leu	Ile	Leu
		35					40					45			
Ser	Leu	Ser	Ser	Leu	Glu	Leu	Arg	Tyr	Phe	Ser	Pro	Leu	Thr	Ile	Ile
	50					55					60				
Thr	Met	His	Phe	Ala	Leu	Thr	Leu	Ile	Ile	Leu	Phe	Phe	Phe		
65					70					75					

(2) INFORMATION FOR SEQ ID NO:674:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

Met	Arg	Ser	Trp	Met	Lys	Lys	Lys	Tyr	Phe	Thr	Leu	Leu	Leu	Gln	Ser
1				5					10					15	
Ser	Val	Val	Leu	Ala	Val	Phe	Ile	Gly	Cys	Ser	Ser	Thr	Arg	Asn	His
			20					25					30		
Thr	Phe	Ser	Ala	Leu	Ser	Asn	Gln	Glu	Asn	Thr	Asp	Asp	Lys	Leu	Pro
		35					40					45			
Val	Val	His	Ser	Ile	Lys	Thr	Ile	Asn	Asp	Val	Ser	Ser	Val	Gly	Phe
	50					55					60				

Glu Trp Ser Lys Val Ala Asp Thr Tyr Asp Ile Asp Gly Phe Val Leu
 65 70 75 80
 Tyr Arg Leu Lys Lys Asp Ser Lys Leu Lys Arg Ile Ala Thr Ile Lys
 85 90 95
 Asn Pro Tyr Ala Thr His Tyr Tyr Asp Glu Gly Leu Glu Thr Glu Ser
 100 105 110
 Ser Tyr Thr Tyr Gln Leu Ala Thr Tyr Lys Gly Asp Lys Ile Ser Lys
 115 120 125
 Leu Ser Glu Pro Ile Leu Val Lys Thr Ser Phe Ile Asn Pro Val Glu
 130 135 140
 Ser Val Phe Ala Ser Leu Glu Tyr Pro Lys Ser Val Lys Val Phe Trp
 145 150 155 160
 Ser Pro His Pro Asn Pro Ser Val Ser Lys Tyr Ile Ile Gln Arg Gln
 165 170 175
 Asn Lys Asp Gly Lys Phe Leu Asn Val Gly Ala Val Lys Asn Arg Leu
 180 185 190
 Phe Val Glu Phe Phe Asp Lys Asp Leu Glu Asp Gly Gln Lys Tyr Arg
 195 200 205
 Tyr Gln Ile Ile Ala Glu Asn Phe Met Gly Asp Lys Ser Arg Pro Ser
 210 215 220
 Val Ile Val Glu Gly Lys Thr Lys Asp Leu Pro Lys Glu Ile Ala Asn
 225 230 235 240
 Val Arg Val Ser Gln Asn Leu Thr Arg Gln Ile Glu Leu Ser Trp Asp
 245 250 255
 Lys Ser Pro Glu Glu Asp Val Ile Ala Tyr Arg Ile Tyr Ala Ser Asn
 260 265 270
 Asn Arg Asn Asp Lys Tyr Lys Phe Ile Ala Gln Thr Thr Asn Thr Ser
 275 280 285
 Tyr Val Asp Lys Ile Glu Lys Asp Asn Leu Thr Arg Tyr Tyr Lys Val
 290 295 300
 Val Ala Val Asp Lys Thr His Leu Glu Gly Ala Leu Pro Lys Glu Pro
 305 310 315 320
 Ala Met Gly Glu Thr Ser Asp Arg Pro Glu Ala Pro Ile Ile Thr Lys
 325 330 335
 Gly Thr Ile Gln Asp Ser Ser Ala Leu Ile Gln Trp Glu Asn Asn Pro
 340 345 350
 Ser Pro Lys Ile Ala Thr Tyr Ala Val Tyr Arg Phe Glu Ala Asn Ser
 355 360 365
 Lys Thr Pro Leu Arg Phe Gly Asn Ile Thr Gln Asn Gln Phe Val Asp

370	375	380
Lys Asp Met Lys Val Gly Val Ala Tyr Arg Tyr Gln Val Val Ser Val		
385	390	395 400

(2) INFORMATION FOR SEQ ID NO:675:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

Met	Gln	Asn	Gly	Tyr	Tyr	Ala	Ala	Thr	Gly	Ala	Met	Ala	Thr	Gln	Phe
1				5					10					15	
Asn	Arg	Leu	Asp	Leu	Thr	Ser	Asn	Asn	Leu	Ala	Asn	Leu	Asn	Thr	Asn
		20						25					30		
Gly	Phe	Lys	Arg	Asp	Asp	Ala	Ile	Thr	Gly	Asp	Phe	Leu	Arg	Leu	Tyr
		35					40					45			
Gln	Glu	Tyr	Arg	Glu	Gln	Leu	Pro	Leu	Glu	Asp	Gln	Thr	Lys	Ala	Ser
	50					55					60				
Ala	Lys	Tyr	Leu	Asn	Arg	Xaa	Leu	Asn	Arg	Val	Pro	Ile	Leu	Ser	Xaa
65					70					75					80
Ile	Tyr	Thr	Xaa	Arg	Xaa	Leu	Gly	Xaa	Val						
				85					90						

(2) INFORMATION FOR SEQ ID NO:676:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

Met Leu Pro Thr Lys Thr Arg Ile Arg Asp Pro Asn Lys Gln Glu Leu

1	5	10	15
Thr Gln Pro Lys Ile Lys Gly Leu Ser Met Gly Lys Ile Leu Ala Ser	20	25	30
Leu Leu Gly Gly Gly Thr Asn Leu Phe Thr Gly Leu Ser Ser Asp Leu	35	40	45
Phe Ser Met Ile Leu Asn Phe Leu Phe Phe Leu Met Leu Met Met Gly	50	55	60
Leu Asn Glu Ala Leu Gly Lys Lys Phe Asn Leu Pro Met Asp Asn Ile	65	70	75
Lys Asn Phe Met Ala Glu Val Leu Lys Asn Gly Phe Asp Ser Ile Lys	85	90	95
Asn Met Gly Ser Ala Leu Val Gly Asn Gly Phe Gly Ser Ser Lys Ser	100	105	110
Asp Lys Thr Thr Asn Lys Met Ser Val Pro Gln Val Arg Leu	115	120	125

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

Val Gly Ala Met Pro Thr Ile Gln Ile Arg Xaa Phe Gly Ala Gly Gly	1	5	10	15
Ser Gly His Ser Asp Ala Thr Leu Met Leu Val Asn Gly Ile Pro Val	20	25	30	
Tyr Met Ala Pro Tyr Ala His Ile Glu Leu Asp Ile Phe Pro Val Thr	35	40	45	
Phe Gln Ala Ile Asp Arg Ile Asp Val Ile Lys Gly Gly Gly Ser Val	50	55	60	
Gln Tyr Gly Pro Asn Thr Tyr Gly Gly Ile Val Asn Ile Ile Thr Lys	65	70	75	80
Pro Ile Pro Asn Gln Trp Glu Asn Gln Ala Ala Glu Arg Xaa Thr Tyr	85	90	95	

Trp Ala Lys Ala Arg Asn Ala Gly Phe Ala Ala Pro Xaa Asp Lys Thr
 100 105 110
 Gly Asp Pro Ser Phe Ile Lys Ser Leu Gly Asn Asn Leu Leu Tyr Asn
 115 120 125
 Thr Tyr Val Arg Ser Gly Gly Met Ile Asn Lys His Val Gly Ile Gln
 130 135 140
 Arg Lys Leu Thr Gly Leu Glu Ala Lys Ala Leu Gly Thr Ile Ala Pro
 145 150 155 160
 Leu Val Phe Gln Thr Ile Gly Trp Met Gly Ser Met Thr Ser Met Lys
 165 170 175
 Ala Met Gly Leu Lys Pro Ile Thr Asn Thr Thr Ile Leu Ala Ile Xaa
 180 185 190
 Gln Pro Gly
 195

(2) INFORMATION FOR SEQ ID NO:678:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...72
 - (D) OTHER INFORMATION: /note= "OXYGEN-INSENSITIVE NAD(P)H
NITROREDUCTASE"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

Met Ala Asn Met Met Met Ala Ala Ala Met Leu Gly Ile Asp Ser Cys
 1 5 10 15
 Pro Ile Glu Gly Tyr Asp Gln Glu Lys Val Glu Ala Tyr Leu Glu Glu
 20 25 30
 Lys Gly Tyr Leu Asn Thr Ala Glu Phe Gly Val Ser Val Met Ala Ser
 35 40 45
 Phe Gly Tyr Arg Asn Gln Glu Ile Thr Pro Lys Thr Arg Trp Lys Thr
 50 55 60
 Glu Val Ile Tyr Glu Val Ile Glu
 65 70

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

Met	Ala	Gly	Leu	Val	Leu	Met	Val	Leu	Leu	Ala	Ser	Tyr	Glu	Ser	Phe
1				5					10					15	
Val	Ser	Lys	Leu	Asp	Lys	Val	Asp	Ala	Ser	Glu	Ile	Thr	Trp	Leu	Lys
			20					25					30		
His	Thr	Asp	Phe	Asn	Ala	Leu	Lys	Leu	Lys	Val	Ser	Leu	Ser	Ile	Val
		35					40					45			
Ala	Ile	Ser	Ala	Ile	Phe	Leu	Leu	Lys	Arg	Tyr	Met	Ser	Leu	Glu	Asp
	50					55					60				
Val	Leu	Ser	Ser	Ile	Pro	Lys	Asp	Thr	Pro	Leu	Ser	His	Asn	Pro	Ile
65				70						75				80	
Phe	Trp	Gln	Val	Val	Ile	His	Leu	Val	Phe	Val	Cys	Ser	Ala	Leu	Leu
			85					90						95	
Thr	Ala	Val	Thr	Asn	Asn	Ile	Ala	Phe	Ser	Gln	Lys	Glu	Arg	His	
		100					105						110		

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

Met	Ile	Thr	Ile	Val	Ile	Ala	Lys	Ala	Gly	Asn	Ile	Val	Lys	Xaa	Asp
1				5					10					15	

Ile Phe Thr His Ile Ser Asp Ile Lys Met Gly Leu Ile Lys Gly Gly
 20 25 30
 Gln Trp Gly Val Ile Gly Leu Gly Asn Ile Gly Lys Arg Val Ala Lys
 35 40 45
 Leu Ala Gln Ala Phe Gly Ala Lys Val Val Tyr Phe Ser Pro Lys Asp
 50 55 60
 Lys Lys Glu Glu Tyr Glu Arg Leu Ser Leu Glu Glu Leu Leu Lys Thr
 65 70 75 80
 Ser Gly Ile Ile Ser Ile His Ala Pro Leu Asn Glu Ser Thr Arg Asp
 85 90 95
 Leu Ile Ala Leu Lys Glu Leu Gln Ser Leu Lys Asp Gly Ala Ile Leu
 100 105 110
 Ile Asn Val Gly Arg Gly Gly Ile Val Asn Glu Lys Xaa Leu Ala Xaa
 115 120 125
 Xaa Leu Glu Thr Thr Asp Leu Tyr Tyr Ala Ser Asp Val Phe
 130 135 140

(2) INFORMATION FOR SEQ ID NO:681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...63
- (D) OTHER INFORMATION: /note= "vacuolating cytotoxin of Hpylori"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

Val Asn Phe Asn Ala Lys Asn Ile Ser Ile Asp Asn Leu Val Glu Ile
 1 5 10 15
 Asn Asn Arg Val Gly Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val
 20 25 30
 Leu Thr Leu Gln Ala Ser Glu Gly Ile Thr Xaa Ser Lys Asn Ala Glu
 35 40 45
 Ile Ser Leu Tyr Asp Gly Ala Thr Xaa Ile Trp Leu Gln Thr Gly
 50 55 60

(2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

Met	Arg	Thr	Leu	Ile	Leu	Ser	Leu	Leu	Lys	His	Ala	Ile	Leu	Met	Gly
1				5					10					15	
Met	Leu	Leu	Lys	Glu	Cys	Gln	Glu	Lys	Leu	Lys	Arg	Ser	Leu	Asn	Leu
			20					25					30		
Ser	Ala	Asn	His	Cys	Val	Leu	Ser	Ala	Gly	Tyr	Gly	Ala	Ser	Ser	Ala
		35					40					45			
Ile	Lys	Lys	Phe	Gln	Glu	Ile	Leu	Gly	Val	Cys	Ile	Pro	Ser	Lys	Thr
	50						55				60				
Lys	Lys	Asn	Leu	Glu	Pro	Tyr	Leu	Lys	Asp	Met	Ala	Leu	Lys	Arg	Val
65					70				75					80	
Ile	Val	Gly	Pro	Tyr	Glu	His	His	Ser	Asn	Glu	Val	Ser	Trp	Arg	Glu
				85					90					95	
Gly	Leu	Cys	Glu	Val	Val	Arg	Ile	Pro	Leu	Asn	Glu	His	Gly	Leu	Leu
			100					105					110		
Asp	Leu	Glu	Ile	Leu	Glu	Gln	Thr	Leu	Lys	Lys	Thr	Pro	Asn	Ser	Leu
		115					120					125			
Val	Ser	Val	Ser	Ala	Ala	Ser	Asn	Val	Thr	Gly	Ile	Leu	Thr	Pro	Leu
	130					135					140				
Lys	Glu	Val	Ser	Ser	Leu	Cys	Lys	Glu	Tyr	Arg	Ala	Ile	Leu	Ala	Leu
145					150				155						160
Asp	Leu	Ala	Asn	Phe	Ser	Ala	His	Ala	Asn	Pro	Lys	Asp	Cys	Glu	Tyr
			165					170					175		
Gln	Thr	Gly	Phe	Tyr	Ala	Pro	His	Lys	Leu	Leu	Gly	Gly	Val	Gly	Gly
			180					185					190		
Cys	Gly	Leu	Leu	Gly	Ile	Ser	Lys	Asp	Leu	Ile	Asp	Thr	Gln	Ile	Pro
	195						200				205				
Thr	Ser	Phe	Ser	Ala	Gly	Gly	Val	Ile	Lys	Tyr	Ala	Asn	Arg	Thr	Arg

210		215		220
His Glu Phe Ile Asp	Glu Leu Pro Leu Arg	Glu Glu Phe Gly Thr Pro		
225	230	235		240
Gly Leu Leu Gln Phe Tyr Arg Ser Ala Leu Ala Tyr Gln Leu Arg Asp				
	245	250		255
Glu Cys Gly Leu Asp Phe Ile His Lys Lys Glu Asn Asn Leu Leu Arg				
	260	265		270
Val Leu Val Tyr Gly Leu Lys Asp Leu Pro Ala Ile Asn Ile Tyr Gly				
	275	280		285
Asn Leu Thr Ala Ser Arg Val Gly Val Val Thr Phe Asn Ile Gly Gly				
	290	295		300
Ile Ser Pro Tyr Asp Leu				
305	310			

(2) INFORMATION FOR SEQ ID NO:683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu Met Gln Lys			
1	5	10	15
Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser Ile Leu Ala			
	20	25	30
Ile Lys Arg Gln Val Glu Asp Lys Asn Ala Pro Ile Leu Val Leu Gly			
	35	40	45
Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala Leu Lys Gln			
	50	55	60
Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu Phe Val Pro			
65	70	75	80
Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu Thr Cys Met			
	85	90	95
His Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val Ile Ile Leu			
	100	105	110

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

Met Xaa Met Ser His Ile Ile Lys Ser Ile Glu Ala Leu Asp Asp Tyr
1 5 10 15
Thr Ile Arg Phe Thr Leu Asn Gly Pro Glu Ala Pro Phe Leu Ala Asn
20 25 30
Leu Gly Met Asp Phe Leu Ser Ile Leu Ser Lys Asp Tyr Ala Asp Tyr
35 40 45
Leu Ala Gln Asn Asn Lys Lys Asp Glu Leu Ala Lys Xaa Pro Val Gly
50 55 60
Thr Gly Pro Phe Lys Phe Phe Leu Trp Asn Lys Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

Leu Met Arg Lys Ile Phe Ser Tyr Ile Ser Lys Val Leu Leu Phe Ile
1 5 10 15
Gly Val Val Tyr Ala Glu Pro Asp Ser Lys Val Glu Ala Leu Glu Gly
20 25 30
Arg Lys Gln Glu Ser Ser Leu Asp Lys Lys Ile Arg Gln Glu Leu Lys
35 40 45
Ser Lys Glu Leu Lys Asn Lys Glu Leu Lys Asn Lys Asp Leu Lys Asn
50 55 60
Lys Glu Glu Lys Lys Glu Thr Lys Ala Lys Arg Lys Pro Arg Ala Glu
65 70 75 80
Val His His Gly Asp Ala Lys Asn Pro Thr Pro Lys Ile Thr Pro Pro
85 90 95
Lys Ile Lys Gly Ser Ser Lys Gly Val Gln Asn Gln Gly Val Gln Asn
100 105 110

Asn Ala Pro Lys Pro Glu Glu Lys Asp Thr Thr Pro Gln Ala Thr Glu
 115 120 125
 Lys Asn Lys Glu Thr Ser Pro Ser Ser Gln Phe Asn Ser Ile Phe Gly
 130 135 140
 Asn Pro Asn Asn Ala Thr Asn Asn Thr Leu Glu Asp Lys Val Val Gly
 145 150 155 160
 Gly Ile Ser Leu Leu Val Asn Gly Ser Pro Ile Thr Leu Tyr Gln Ile
 165 170 175
 Gln Glu Glu Gln Glu Lys Ser Lys Val Ser Xaa Ala Xaa Ala Arg Asp
 180 185 190
 Arg Leu Xaa Xaa
 195

(2) INFORMATION FOR SEQ ID NO:687:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

Val Leu Trp Val Leu Tyr Phe Leu Thr Ser Leu Phe Ile Cys Ser Leu
 1 5 10 15
 Ile Val Leu Trp Ser Lys Lys Ser Met Leu Phe Val Asp Asn Ala Asn
 20 25 30
 Lys Ile Gln Gly Phe His His Ala Arg Thr Pro Arg Ala Gly Gly Leu
 35 40 45
 Gly Ile Phe Leu Ser Phe Ala Leu Ala Cys Tyr Leu Glu Pro Phe Glu
 50 55 60
 Met Pro Phe Lys Gly Pro Phe Val Phe Leu Gly Leu Ser Leu Val Phe
 65 70 75 80
 Leu Ser Gly Phe Leu Glu Asp Ile Asn Leu Ser Leu Ser Pro Lys Ile
 85 90 95
 Arg Leu Ile Leu Gln Ala Val Gly Val Val Cys Ile Ile Ser Ser Thr
 100 105 110
 Pro Leu Val Val Ser Asp Phe Ser Pro Leu Phe Ser Leu Pro Tyr Phe
 115 120 125

Ile Ala Phe Leu Phe Ala Ile Phe Tyr Ala Gly Gly Tyr Gln
 130 135 140

(2) INFORMATION FOR SEQ ID NO:688:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

Met Ala Cys Lys Phe Cys Pro Lys Ile Arg Lys Thr Asp Trp Ile Phe
 1 5 10 15

Ile Leu Ile Ala Ala Leu Gly Phe Tyr Ser Val Asn Lys Leu Gly Tyr
 20 25 30

Ala Pro Lys Phe Asn Thr Pro Thr Pro Lys Ser Ser Arg Pro Leu Ser
 35 40 45

Arg Pro Ile Glu Lys Pro Asn Asn Met Thr Glu Glu Glu Arg Lys Lys
 50 55 60

Arg Phe Ile Glu Leu Gln Lys Ala Cys Leu Leu His Lys Asp Lys Lys
 65 70 75 80

Ala Cys Glu Glu Val Phe
 85

(2) INFORMATION FOR SEQ ID NO:689:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...121
- (D) OTHER INFORMATION: /note= "PREPROTEIN TRANSLOCASE

SECA SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

```

Val Asp Ser Ile Leu Ile Asp Glu Ala Arg Thr Pro Leu Ile Ile Ser
1           5           10           15
Gly Pro Val Asp Arg Arg Met Glu Asn Tyr Asn Lys Ala Asp Glu Val
          20           25           30
Ala Lys Ser Met Gln Val Glu Val Asp Phe Thr Ile Asp Glu Lys Asn
          35           40           45
Arg Ala Ile Leu Ile Thr Glu Glu Gly Ile Lys Lys Ala Glu Asn Leu
          50           55           60
Phe Gly Val Asp Asn Leu Tyr Lys Ile Glu Asn Ala Ala Leu Ser His
65           70           75           80
His Leu Asp Gln Ala Leu Lys Ala Asn Tyr Leu Phe Phe Ile Asp Lys
          85           90           95
Asp Tyr Ile Val Ala Asn Asn Glu Val Val Ile Val Asp Lys Phe Thr
          100          105          110
Asp Arg Leu Asn Glu Gly Glu Ala Leu
          115          120

```

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

```

Met Thr Ile Thr Thr Leu Ser Phe Leu Phe Thr Thr Pro Glu Val Phe
1           5           10           15
Val Asn Gln Asp Phe Pro Trp Leu Ser Gly Ala Gly Arg Leu Val Val
          20           25           30
Lys Asp Leu Ala Leu Phe Ala Gly Gly Leu Phe Val Ala Gly Phe Asp
          35           40           45
Arg Asn Ala Ile Trp Arg Val Lys Gly Phe Ala
          50           55

```


(2) INFORMATION FOR SEQ ID NO:691:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...142
 - (D) OTHER INFORMATION: /note= "similar to E.coli hypothetical nucleoside transport protein"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

Val	Phe	Ser	Gly	Asn	Lys	Arg	Ala	Ile	Asn	Tyr	Arg	Thr	Ile	Val	Ser
1				5				10						15	
Ala	Phe	Val	Ile	Gln	Val	Ala	Leu	Gly	Ala	Leu	Ala	Leu	Tyr	Val	Pro
			20					25					30		
Leu	Gly	Arg	Glu	Ile	Leu	Gln	Gly	Leu	Ala	Ser	Gly	Ile	Gln	Ser	Val
		35					40					45			
Ile	Gly	Tyr	Gly	Tyr	Glu	Gly	Val	Arg	Phe	Leu	Phe	Gly	Asn	Leu	Ala
	50					55				60					
Pro	Asn	Ala	Lys	Gly	Asp	Gln	Gly	Ile	Gly	Gly	Phe	Ile	Phe	Ala	Ile
65					70				75					80	
Asn	Val	Leu	Ala	Ile	Ile	Ile	Phe	Phe	Ala	Ser	Leu	Ile	Ser	Leu	Leu
				85					90					95	
Tyr	Tyr	Leu	Lys	Ile	Met	Pro	Leu	Val	Ile	Asn	Leu	Ile	Gly	Gly	Ala
			100					105					110		
Leu	Gln	Lys	Cys	Leu	Gly	Thr	Ser	Lys	Ala	Glu	Ser	Met	Ser	Ala	Ala
		115					120					125			
Ala	Asn	Xaa	Xaa	Val	Ala	His	Thr	Glu	Asp	Xaa	Leu	Ser	His		
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:692:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...80

(D) OTHER INFORMATION: /note= "sequence predicts membrane bound protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

```
Met Leu Val Gly Ile Ser Asn Ala Ile Asn Ile Ile Asp Gly Phe Asn
1           5           10           15
Gly Leu Ala Ser Gly Ile Cys Ala Ile Ala Leu Leu Val Ile His Tyr
20           25           30
Ile Asp Xaa Ser Ser Leu Ser Cys Leu Leu Ala Tyr Met Val Leu Gly
35           40           45
Val Tyr Gly Val Lys Xaa Pro Phe Arg Lys Asp Phe Leu Gly Arg Ser
50           55           60
Gly Gly Arg Ile Phe Trp Val Trp Xaa Xaa Xaa Phe Leu Ser Cys Ile
65           70           75           80
```

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

```
Met Lys Arg Ser Ser Val Phe Ser Phe Leu Val Ala Phe Leu Leu Val
1           5           10           15
Val Gly Cys Ser His Lys Met Asp Asn Lys Thr Val Ala Gly Asp Val
20           25           30
Ser Thr Lys Ala Val Gln Thr Ala Pro Val Thr Thr Glu Pro Ala Pro
35           40           45
Glu Lys Glu Glu Pro Lys Gln Glu Pro Ala Pro Val Val Glu Glu Lys
50           55           60
```

Pro Ala Ile Glu Ser Gly Thr Ile Ile Ala Ser Ile Tyr Phe Asp Phe
 65 70 75 80
 Asp Lys Tyr Glu Ile Lys Glu Ser Asp Gln Glu Thr Leu Asp Glu Ile
 85 90 95
 Val Gln Lys Ala Lys Glu Asn His Met Gln Val Leu Leu Glu Gly Asn
 100 105 110
 Thr Asp Glu Phe Gly Ser Ser Glu Tyr Asn Gln Ala Leu Gly Val Lys
 115 120 125
 Arg Thr Leu Ser Val Lys Asn Ala Leu Val Ile Lys Gly Val Glu Lys
 130 135 140
 Asp Met Ile Lys Thr Ile Ser Phe Gly Glu Ser Lys Pro Lys Cys Val
 145 150 155 160
 Gln Lys Thr Arg Glu Cys Tyr Arg Glu Asn Arg Arg Val Asp Val Lys
 165 170 175
 Leu Val Lys

(2) INFORMATION FOR SEQ ID NO:694:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...75
 - (D) OTHER INFORMATION: /note= "invasion protein A"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

Met Leu His Lys Lys Tyr Arg Pro Asn Val Ala Ala Ile Ile Met Ser
 1 5 10 15
 Pro Asp Tyr Pro Asn Thr Cys Glu Val Phe Ile Ala Glu Arg Ile Asp
 20 25 30
 Ile Glu Gly Ala Trp Gln Phe Pro Gln Gly Gly Ile Asp Glu Gly Glu
 35 40 45
 Thr Pro Leu Glu Ala Leu Tyr Arg Glu Leu Leu Glu Glu Ile Gly Thr
 50 55 60
 Asn Glu Ile Glu Ile Leu Ala Gln Tyr Pro Arg

(2) INFORMATION FOR SEQ ID NO:695:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

```

Val Met Leu Met Ala Ile Phe Thr Pro Tyr Ile Leu Ile Leu Lys Met
1           5           10           15
Met Lys Lys Ser Met Ser Leu Phe Ala Asn Met Gly Leu Glu Gln Ile
          20           25           30
Phe Cys Asn Arg Asp Ile Lys Asp Leu Asn Asp Phe Val Phe Gly Ile
          35           40           45
Glu Val Gly Leu Asp Ser Asn Ala Arg Lys Asn Arg Ser Arg Lys Ala
          50           55           60
Met Glu Asn His Leu Ile Gly Leu Phe Val Gln Ala Gln Leu Asn Phe
65           70           75           80
Lys Glu Gln Val Asp Ile Arg Glu Phe Glu Asp Leu Arg Gln Ala Phe
          85           90           95
Gly Asn Asp

```

(2) INFORMATION FOR SEQ ID NO:696:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 209 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: SEQ ID NO:696:

```

Met Ile Arg Leu Ala Ala Phe Phe Leu Ala Leu Ala Cys Ala Ile Thr
1           5           10           15

```

Pro Lys Ser Arg Leu Leu Leu Lys Asn Val Leu Leu Asn Pro Thr Arg
 20 25 30
 Ile Glu Ala Phe Glu Val Leu Lys Lys Met Gly Ala His Ile Glu Tyr
 35 40 45
 Val Ile Gln Ser Lys Asp Leu Glu Val Ile Gly Asp Ile Tyr Ile Glu
 50 55 60
 His Ala Pro Leu Lys Ala Ile Ser Ile Asp Gln Asn Ile Ala Ser Leu
 65 70 75 80
 Ile Asp Glu Ile Pro Ala Leu Ser Ile Ala Met Leu Phe Ala Lys Gly
 85 90 95
 Lys Ser Met Val Arg Asn Ala Lys Asp Leu Arg Ala Lys Glu Ser Asp
 100 105 110
 Arg Ile Lys Ala Val Val Ser Asn Phe Lys Ala Leu Gly Ile Glu Cys
 115 120 125
 Glu Glu Phe Glu Asp Gly Phe Tyr Ile Glu Gly Leu Gly Asp Ala Ser
 130 135 140
 Gln Leu Lys Gln His Phe Ser Lys Ile Lys Pro Pro Ile Ile Lys Ser
 145 150 155 160
 Phe Asn Asp His Arg Ile Ala Met Ser Phe Ala Val Leu Thr Leu Ala
 165 170 175
 Leu Pro Leu Glu Ile Asp Asn Leu Glu Cys Ala Asn Ile Ser Phe Pro
 180 185 190
 Thr Phe Gln Leu Trp Leu Asn Leu Phe Lys Lys Arg Ser Leu Asn Gly
 195 200 205
 Asn

(2) INFORMATION FOR SEQ ID NO:697:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...75
 - (D) OTHER INFORMATION: /note= "PROBABLE COPPER-TRANSPORTING ATPASE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

Val Gly Ser Leu Lys Phe Leu Asn Ala Met Gly Val Asp Leu Lys Val
1 5 10 15
Lys Glu Ser Ala Asn Ile Met Val Gly Phe Ala Lys Asn Lys Thr Leu
20 25 30
Cys Ala Leu Phe Ile Leu Glu Glu Arg Leu Lys Ala Asn Ala Lys Glu
35 40 45
Val Ile Gln Ala Leu Gln Asn Gln Gly Leu Glu Leu Glu Ile Leu Ser
50 55 60
Gly Asp Asn Glu Ser Ser Val Lys Glu Cys Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

Met Glu Ala Leu Asn Ala Leu Asn Ala Gln Ser Asp Glu Gln Ile Leu
1 5 10 15
Cys Glu Gly Tyr Phe Val Leu Leu Gln Ile Leu Glu Pro Met Ile Pro
20 25 30
His Thr Ala Trp Glu Leu Ser Glu Arg Leu Phe Lys Arg Glu Asn Phe
35 40 45
Lys Pro Ile Glu Val Asp Glu Ser Ala Leu Ile Glu Asp Phe Met Thr
50 55 60
Leu Gly Leu Thr Ile Asn Gly Lys Arg Arg Ala Glu Leu Lys Val Asn
65 70 75 80
Ile Asn Ala Ser Lys Glu Glu Ile Ile Ile Leu Ala Lys Lys Glu Leu
85 90 95
Glu Lys Tyr Leu Glu Asn Ala Ser Val Lys Lys Glu Ile Tyr Val Pro
100 105 110
Asn Lys Leu Val Asn Phe Val Thr Ala
115 120

(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

Met	Lys	Glu	Ser	Ile	Lys	Tyr	Leu	Leu	Glu	Ser	Val	Gly	Leu	Val	Leu	
1				5				10					15			
Leu	Met	Ser	Val	Asn	Pro	Gly	Phe	Gly	Gly	Gln	Lys	Phe	Leu	Asp	Leu	
			20					25					30			
Val	Leu	Glu	Lys	Cys	Leu	Lys	Val	Lys	Glu	Leu	Ile	Lys	Arg	Tyr	Asn	
		35					40					45				
Pro	Ser	Cys	Leu	Leu	Glu	Val	Asp	Gly	Gly	Val	Asn	Asp	Lys	Asn	Ile	
	50					55					60					
Phe	Glu	Leu	Gln	Gln	Ala	Gly	Val	Asp	Val	Val	Val	Ser	Gly	Ser	Tyr	
65				70					75						80	
Ile	Phe	Glu	Ser	Lys	Asp	Xaa	Lys	Leu	Ala	Ile	Glu	Gly	Leu	Gln	Asn	
				85				90						95		
Val	Arg	Gln	Pro	Leu	Ala											
				100												

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

Val	His	Asp	Gly	Val	Leu	Gly	Trp	Val	Gly	Phe	Thr	Leu	Ile	Ala	Ser	
1				5				10					15			

Met Tyr His Met Thr Pro Arg Leu Phe Lys Arg Glu Ile Tyr Ser Gly
 20 25 30
 Arg Leu Val Asp Phe Gln Phe Trp Ile Met Thr Leu Gly Ile Val Leu
 35 40 45
 Tyr Phe Ser Ser Met Trp Ile Ala Gly Ile Thr Gln Gly Met Met Trp
 50 55 60
 Arg Asp Val Asp Gln Tyr Gly Asn Leu Thr Tyr Gln Phe Ile Asp Thr
 65 70 75 80
 Val Lys Ala Leu Ile Pro Tyr Tyr Asn Ile Arg Gly Val Gly Gly Leu
 85 90 95
 Met Tyr Phe Ile Gly Phe Ile Ile Phe Ala Tyr Asn Ile Phe Met Thr
 100 105 110
 Ile Thr Ala Gly Lys Lys Leu Glu Arg Glu Pro Asn Tyr Ala Thr Pro
 115 120 125
 Met Ala Lys
 130

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

Met Ile Thr Leu Phe Ser Phe Gly Ala Phe Ala Tyr Tyr Phe Val Ser
 1 5 10 15
 Ser Gln Ile Ser His Glu Asn Tyr Gln Asn Glu Met Arg His Tyr Gln
 20 25 30
 Phe Val Thr Thr Ile Asn Glu Ile Leu Asn Asn Tyr Ser Asp Tyr Arg
 35 40 45
 Ala Ile Glu Asp Tyr Leu Tyr Lys Ile Gly Phe Arg Glu Thr Thr Ile
 50 55 60
 Glu Asn Leu Glu Lys Val Leu Ala Lys Arg Arg His Gln Leu His His
 65 70 75 80
 Arg Asn Ile Trp Tyr Ala Glu Val Phe Lys Phe Ser Asp Met Val Phe

				85				90				95			
Ile	Leu	Leu	Lys 100	Lys	Asp	Glu	His	Phe 105	Val	Leu	Tyr	Lys	Asp 110	Leu	His
Ser	Val	Ser 115	Tyr	Arg	Asn	Tyr	Phe 120	Leu	Ala	Ile	Thr	Val	Gly 125	Leu	Leu
Leu	Ile 130	Leu	Phe	Leu	Phe	Leu 135	Phe	Val	Leu	Gln	Ser 140	Leu	Leu	Pro	Leu
Arg 145	Glu	Leu	Arg	Ser	Gln 150	Val	Lys	Arg	Phe 155	Ala	Gln	Gly	Asp	Lys	Ser 160
Val	Ser	Cys	Lys	Ser 165	Lys	Gln	Lys	Asp 170	Glu	Ile	Gly	Asp	Leu	Ala 175	Asn
Glu	Phe	Asp	Asn 180	Cys	Ile	Gln	Lys	Ile 185	Asn	Ala	Met	Asn	Glu 190	Ser	Arg
Val	Leu	Phe 195	Leu	Arg	Ser	Ile	Met 200	His	Glu	Leu	Arg	Thr 205	Pro	Ile	Thr
Lys	Gly 210	Lys	Ile	Leu	Ser	Ser 215	Met	Leu	Lys	Glu	Glu 220	Leu	Ser	Cys	Lys
Arg 225	Phe	Ser	Ser	Ile	Phe 230	Asp	His	Leu	Asn 235	Met	Leu	Ile	Glu	Gln	Phe 240
Ala	Arg	Ile	Glu	Gln 245	Leu	Ala	Ser	Lys	Asn 250	Tyr	Gly	Ser	Asn	Lys 255	Glu
Lys	Phe	Leu	Met 260	Ser	Asp	Leu	Ile	Asp 265	Lys	Ile	Glu	Lys	Met 270	Leu	Leu
Ile	Asp 275	Glu	Asp	Lys	Lys	Ser	Pro 280	Ile	His	Val	Ser	Ser 285	Ser	Asn	Tyr
Ile 290	Ile	Glu	Ala	Asp	Phe	Glu 295	Leu	Phe	Ala	Ile	Ala 300	Leu	Lys	Asn	Met
Ile 305	Asp	Asn	Ala	Ile	Lys 310	Tyr	Ser	Asp	Asp 315	Lys	Gln	Val	Phe	Leu	Asp 320
Phe	Ile	Gly	Asn 325	Asn	Leu	Val	Val	Ser	Asn 330	Lys	Ser	Lys	Pro	Leu 335	Lys
Glu	Asp	Phe	Glu 340	Lys	Tyr	Leu	Gln	Pro 345	Tyr	Phe	Lys	Ser	Ser 350	Asn	Pro
Ser	Gln	Ala 355	His	Gly	Phe	Gly	Leu 360	Gly	Met	Tyr	Ile	Ile 365	Lys	Asn	Ala
Leu 370	Glu	Ala	Met	Gly	Leu	Asn 375	Leu	Ser	Tyr	His	Tyr 380	Ser	Asn	Gly	Arg
Ile 385	Cys	Phe	Thr	Ile	His 390	Asp	Cys	Val	Phe	Asn 395	Ser	Phe	Tyr	Asp	Leu 400

Glu Ala Asp Asn Glu Glu Leu Pro Pro Pro Glu Asn Leu Arg Glu Val
405 410 415
Lys Gly Met Lys Gly Thr Glu Lys Ala Asn Cys Gly Val Lys Glu Lys
420 425 430
Gln Lys Glu Arg Thr Cys Ser Asn Asp
435 440

(2) INFORMATION FOR SEQ ID NO:702:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...127
 - (D) OTHER INFORMATION: /note= "HYPOTHETICAL 43.6 KD PROTEIN"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

Val Leu Leu Leu Ser Arg Met Gly Ile Ala Phe Ala His Ser Ile Phe
1 5 10 15
Trp Ser Ile Thr Ala Ser Leu Val Ile Arg Val Ala Pro Arg Asn Lys
20 25 30
Lys Gln Gln Ala Leu Gly Leu Leu Ala Leu Gly Ser Ser Leu Ala Met
35 40 45
Ile Leu Gly Leu Pro Leu Gly Arg Ile Ile Gly Gln Ile Leu Asp Trp
50 55 60
Arg Ser Thr Phe Gly Val Ile Gly Gly Val Ala Thr Leu Ile Met Leu
65 70 75 80
Leu Met Trp Lys Leu Leu Pro His Leu Pro Ser Arg Asn Ala Gly Thr
85 90 95
Leu Ala Ser Val Pro Ile Leu Met Lys Arg Pro Leu Leu Val Gly Ile
100 105 110
Tyr Leu His Val Asn His Gly Tyr Phe Trp Ala Phe His His Leu
115 120 125

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

Met	Gly	Thr	Leu	Ile	Glu	Lys	Trp	Phe	Gly	Phe	Ser	Gln	Ile	Arg	Glu	
1				5					10					15		
Glu	Leu	Glu	Ala	Arg	Ile	Ser	Glu	Leu	Glu	Asp	Glu	Asn	Thr	Glu	Leu	
			20					25					30			
Leu	Arg	Glu	Arg	Glu	Tyr	Leu	Ala	Ala	Glu	Thr	Ser	Glu	Leu	Lys	Asp	
		35					40					45				
Ala	Asn	Asp	Gln	Leu	Arg	Gln	Lys	Asn	Asp	Lys	Leu	Phe	Ile	Thr	Lys	
	50					55					60					
Asp	Lys	Leu	Thr	Lys	Glu	Asn	Thr	Glu	Leu	Phe	Ala	Glu	Asn	Glu	Ser	
65				70						75				80		
Leu	Ser	Val	Lys	Ile	Ser	Gly	Leu	Glu	His	Ser	Asn	Asp	Gln	Leu	Trp	
			85						90					95		
Gln	Asn	Asn	Asn	Lys	Leu	Thr	Lys	Glu	Lys	Ala	Glu	Leu	Lys	Thr	Glu	
			100					105					110			
Lys	Asp	Ile	Leu	Ala	Lys	Glu	Asn	Thr	Arg	Leu	Leu	Ala	Ala	Arg	Asp	
		115					120					125				
Arg	Leu	Thr	Glu	Glu	Lys	Arg	Glu	Leu	Thr	Thr	Glu	Lys	Glu	Arg	Leu	
	130					135					140					
Lys	Arg	Glu	Asn	Thr	Glu	Leu	Thr	His	Lys	Ile	Thr	Glu	Leu	Thr	Lys	
145				150					155					160		
Glu	Asn	Lys	Ala	Leu	Thr	Thr	Glu	Asn	Asp	Lys	Leu	Asn	His	Gln	Val	
			165						170					175		
Thr	Ala	Leu	Thr	Asn	Glu	Arg	Asp	Ser	Leu	Glu	Gln	Glu	Arg	Ala	Arg	
		180						185					190			
Leu	Gln	Asp	Ala	His	Gly	Phe	Leu	Glu	Lys	Arg	Cys	Thr	Asn	Leu	Glu	
		195					200					205				
Lys	Glu	Asn	Gln	Arg	Leu	Thr	Asp	Lys	Leu	Lys	Gln	Leu	Glu	Ser	Ala	
	210					215					220					
Gln	Lys	Ser	Leu	Glu	Asn	Thr	Asn	Asn	Gln	Leu	Arg	Gln	Ala	Leu	Glu	

225		230		235		240
Asn Ser Asn Val Gln Leu Ala Gln Ala Lys Glu Xaa Ile Ala Ile Glu						
	245			250		255
Xaa Ser Glu Leu Xaa Arg Arg Asn Arg Thr Leu Glu Glu Leu Arg Gly						
	260		265			270
Tyr Gly Ser Gln Lys Xaa Ile Trp Thr Tyr Thr Xaa Gly Val						
	275		280			285

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

Val Leu Arg Lys Leu Leu Gly Lys Asn Cys Ile Glu Thr His Lys Gly															
1			5				10						15		
Val Gly Tyr Arg Leu Thr His Tyr Glu Lys Lys Ser Leu Lys Leu Phe															
	20					25						30			
Leu Gly Thr Tyr Leu Gly Ser Ser Phe Val Leu Met Leu Val Ile Ser															
	35					40						45			
Val Leu Ala Phe Asn Tyr Glu Lys Asn Glu Lys Ile Lys Xaa Ile Arg															
	50				55				60						
Met Asp Met Asp Lys Met Ala Ser Lys Ile Ala Ser Glu Ile Ile Gln															
65			70					75					80		
Leu His Met Gln Thr His Ala Asp Tyr His Asn Ala Leu Asn Ala Leu															
	85						90						95		
Ile Ser Arg Tyr Lys Asp Val Ser Ile Xaa Leu Xaa Asp Thr															
	100						105						110		

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

```
Met Arg Ile Ile Ile Arg Leu Leu Ser Phe Lys Met Asn Ala Phe Leu
1           5           10           15

Lys Leu Ala Leu Ala Ser Leu Met Gly Gly Leu Trp Tyr Ala Phe Asn
          20           25           30

Gly Glu Gly Ser Glu Ile Val Ala Ile Gly Ile Phe Val Leu Ile Leu
          35           40           45

Phe Val Phe Phe Ile Arg Pro Val Ser Phe Gln Asp Pro Glu Lys Arg
          50           55           60

Glu Glu Tyr Ile Glu Arg Leu Lys Lys Asn His Glu Arg Lys Met Ile
65           70           75           80

Leu Gln Asp Lys Gln Lys Glu Glu Gln Met Arg Leu Tyr Gln Ala Lys
          85           90           95

Lys Glu Arg Glu Ser Arg Gln Lys Gln Asp Leu Lys Glu Gln Met Lys
          100          105          110

Lys Tyr Ser
          115
```

(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

```
Val Arg Ser Cys Lys Gln Ile Phe Asp Lys Gly Leu Lys Pro Tyr Tyr
1           5           10           15

Lys His Ser Val Cys Leu Lys Pro Phe Phe Arg Phe Cys Phe Leu Lys
          20           25           30

Ile His Ala Tyr Gln Gln Arg Tyr Arg Ala Phe Ala Leu Thr Leu Phe
          35           40           45
```

Ser Cys Lys Phe Phe Asn Ala Cys Lys Ile Phe Ile Pro Ile Ile Asp
50 55 60

Phe Lys Ile Val Phe Ile Pro Ile Leu Lys His Gln Ala Lys Leu Lys
65 70 75 80

Arg Val Ser Asn Ala Tyr
85

(2) INFORMATION FOR SEQ ID NO:707:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

Met Cys Gly Met Gly Phe Ile Gly Phe Lys Thr Lys Leu Thr Gln Thr
1 5 10 15

Lys Ala Phe Ile Ile Leu Ile Pro Ile Phe Gln Asp Arg Ala Val Lys
20 25 30

Ala Ala Thr Arg Ser Ala Pro Ile Gln Leu Ile Cys
35 40

(2) INFORMATION FOR SEQ ID NO:708:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 560 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...560
 - (D) OTHER INFORMATION: /note= "vacuolating cytotoxin"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

Met Gly Asn Phe Asn Ser Tyr Gly Asp Leu Val Phe Asn Leu Ser His

1		5						10					15				
Ser	Val	Ser	His	Ala	Ile	Ile	Asn	Thr	Gln	Gly	Thr	Ala	Thr	Ile	Met		
			20					25					30				
Ala	Asn	Asn	Asn	Pro	Leu	Ile	Gln	Phe	Asn	Ala	Ser	Ser	Lys	Glu	Val		
		35					40					45					
Gly	Thr	Tyr	Thr	Leu	Ile	Asp	Ser	Ala	Lys	Ala	Ile	Tyr	Tyr	Gly	Tyr		
	50					55					60						
Asn	Asn	Gln	Ile	Thr	Gly	Gly	Ser	Ser	Leu	Asp	Asn	Tyr	Leu	Lys	Leu		
65					70					75					80		
Tyr	Ala	Leu	Ile	Asp	Ile	Asn	Gly	Lys	His	Met	Val	Met	Thr	Asp	Asn		
				85					90					95			
Gly	Leu	Thr	Tyr	Asn	Gly	Gln	Ala	Val	Ser	Val	Lys	Asp	Gly	Gly	Leu		
			100					105					110				
Val	Val	Gly	Phe	Lys	Asp	Ser	Gln	Asn	Gln	Tyr	Ile	Tyr	Thr	Ser	Ile		
		115					120					125					
Leu	Tyr	Asn	Lys	Val	Lys	Ile	Ala	Val	Ser	Asn	Asp	Pro	Ile	Asn	Asn		
	130					135					140						
Pro	Gln	Ala	Pro	Thr	Leu	Lys	Gln	Tyr	Ile	Ala	Gln	Ile	Gln	Gly	Val		
145					150					155					160		
Gln	Ser	Val	Asp	Ser	Ile	Xaa	Gln	Ala	Gly	Gly	Asn	Gln	Ala	Ile	Asn		
				165					170					175			
Trp	Leu	Asn	Lys	Ile	Phe	Glu	Thr	Lys	Gly	Ser	Pro	Leu	Phe	Ala	Pro		
		180						185					190				
Tyr	Tyr	Leu	Glu	Ser	His	Ser	Thr	Lys	Asp	Leu	Thr	Thr	Ile	Ala	Gly		
		195					200					205					
Asp	Ile	Ala	Asn	Thr	Leu	Glu	Val	Ile	Ala	Asn	Pro	Asn	Phe	Lys	Asn		
	210					215					220						
Asp	Ala	Thr	Asn	Ile	Leu	Gln	Ile	Asn	Thr	Tyr	Thr	Gln	Gln	Met	Ser		
225					230					235					240		
Arg	Leu	Ala	Lys	Leu	Ser	Asp	Thr	Ser	Thr	Phe	Ala	Arg	Ser	Asp	Phe		
				245					250					255			
Leu	Glu	Arg	Leu	Glu	Ala	Leu	Lys	Asn	Lys	Arg	Phe	Ala	Asp	Ala	Ile		
			260					265					270				
Pro	Asn	Ala	Met	Asp	Val	Ile	Leu	Lys	Tyr	Ser	Gln	Arg	Asn	Arg	Val		
		275					280					285					
Lys	Asn	Asn	Val	Trp	Ala	Thr	Gly	Val	Gly	Gly	Ala	Ser	Phe	Ile	Ser		
	290					295					300						
Gly	Gly	Thr	Xaa	Thr	Leu	Tyr	Gly	Ile	Asn	Xaa	Gly	Tyr	Asp	Arg	Phe		
305					310					315					320		

Ile	Lys	Gly	Val	Ile	Val	Gly	Gly	Tyr	Ala	Ala	Tyr	Gly	Tyr	Ser	Gly		
				325					330					335			
Phe	His	Ala	Asn	Ile	Thr	Gln	Ser	Gly	Ser	Ser	Asn	Val	Asn	Val	Gly		
			340					345					350				
Val	Tyr	Ser	Arg	Ala	Phe	Ile	Lys	Arg	Ser	Glu	Leu	Thr	Met	Ser	Leu		
		355					360					365					
Asn	Glu	Thr	Trp	Gly	Tyr	Asn	Lys	Thr	Phe	Ile	Asn	Ser	Tyr	Asp	Pro		
	370					375					380						
Leu	Leu	Ser	Ile	Ile	Asn	Gln	Ser	Tyr	Arg	Tyr	Asp	Thr	Trp	Thr	Thr		
385					390					395					400		
Asp	Ala	Lys	Ile	Asn	Tyr	Gly	Tyr	Asp	Phe	Met	Phe	Lys	Asp	Lys	Ser		
				405					410					415			
Val	Ile	Phe	Lys	Pro	Gln	Val	Gly	Leu	Ser	Tyr	Tyr	Tyr	Ile	Gly	Leu		
			420					425					430				
Ser	Gly	Leu	Arg	Gly	Ile	Met	Asp	Asp	Pro	Ile	Tyr	Asn	Gln	Phe	Arg		
		435					440					445					
Ala	Asn	Ala	Asp	Pro	Asn	Lys	Lys	Ser	Val	Leu	Thr	Ile	Asn	Phe	Ala		
	450					455					460						
Leu	Glu	Ser	Arg	His	Tyr	Phe	Asn	Lys	Asn	Ser	Tyr	Tyr	Phe	Val	Ile		
465					470					475					480		
Ala	Asp	Val	Gly	Arg	Asp	Leu	Phe	Ile	Asn	Ser	Met	Gly	Asp	Lys	Met		
				485					490					495			
Val	Arg	Phe	Ile	Gly	Asn	Asn	Thr	Leu	Ser	Tyr	Arg	Asp	Gly	Gly	Arg		
			500					505					510				
Tyr	Asn	Thr	Phe	Ala	Ser	Ile	Ile	Thr	Gly	Gly	Glu	Ile	Arg	Leu	Phe		
		515					520					525					
Lys	Thr	Phe	Tyr	Val	Asn	Ala	Gly	Ile	Gly	Ala	Arg	Phe	Gly	Leu	Asp		
	530					535					540						
Tyr	Lys	Asp	Ile	Asn	Ile	Thr	Gly	Asn	Ile	Gly	Met	Xaa	Xaa	Xaa	Phe		
545					550					555					560		

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

Leu Met Thr Lys Ser Leu Lys Leu Ile Gln Lys Gly Val Lys Asn Leu
1 5 10 15
Tyr Glu Thr Leu Lys Asn Arg Ala Leu Glu His Gln Asp Thr Leu Met
20 25 30
Val Gly Arg Ser His Gly Val Phe Gly Glu Pro Ile Thr Phe Gly Leu
35 40 45
Val Leu Ala Leu Phe Ala Asp Glu Ile Lys Arg His Leu Lys Ala Leu
50 55 60
Asp Leu Thr Met Glu Phe Ile Xaa Val Gly Ala Ile Ser Gly Ala Met
65 70 75 80
Gly Asn Phe Ala His Ala Pro Leu Glu Leu Glu Glu Leu Ala Cys Gly
85 90 95
Phe Leu Gly Leu Lys Thr Ala Asn Ile Ser Asn Gln Val Ile Gln Arg
100 105 110
Asp Arg Tyr Ala Gly Leu His Ala Ile Trp Leu Phe
115 120

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

Leu Ser Asp Ala Ser Lys Arg Ser Leu Asn Pro Thr Leu Met Met Asn
1 5 10 15
Asn Asn Asn Thr Leu Pro Lys Pro Leu Glu Glu Ser Leu Asp Leu Lys
20 25 30
Glu Phe Ile Ala Leu Phe Lys Thr Phe Phe Ala Lys Glu Arg Gly Ser
35 40 45
Ile Ala Leu Glu Asn Asp Leu Lys Gln Ala Phe Thr Tyr Leu Asn Glu
50 55 60

Val	Asp	Ala	Ile	Gly	Leu	Pro	Ala	Pro	Xaa	Lys	Arg	Glu	Arg	Lys	Arg
65					70					75					80
Ser	Tyr	Cys	Cys	Gln	Thr	His	Gln	Ile	Arg	Asp	Ala	Pro	Phe	Arg	
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:711:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

Leu	Pro	Ile	Ile	Leu	Xaa	Val	Ile	Val	Met	Met	Phe	Phe	Ser	Lys	Ile
1				5					10					15	
Val	Gly	Asp	Phe	Ile	Glu	Lys	His	Tyr	Arg	Val	Lys	Thr	Leu	Ala	Phe
			20					25					30		
Val	Phe	Leu	Leu	Val	Val	Gly	Val	Phe	Leu	Phe	Leu	Glu	Gly	Leu	His
		35				40						45			
Leu	His	Ile	Asn	Lys	Asn	Tyr	Leu	Tyr	Ala	Gly	Ile	Gly	Phe	Ala	Leu
	50					55					60				
Leu	Ile	Glu	Cys	Leu	Xaa	Ile	Phe	Ile	Glu	Lys	Lys	Met	Lys	Lys	Ser
65					70					75					80

(2) INFORMATION FOR SEQ ID NO:712:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

Met	Glu	Ser	Asn	Gln	Ser	Leu	Pro	Met	Ala	Leu	Ile	Ser	Cys	Ser	Pro
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...233
- (D) OTHER INFORMATION: /note= "PROBABLE ABC TRANSPORTER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

Met	Asp	Ile	Leu	Lys	Ala	Glu	His	Leu	Asn	Lys	Gln	Ile	Lys	Lys	Thr
1				5					10					15	
Lys	Ile	Val	Ser	Asp	Val	Ser	Leu	Glu	Val	Lys	Ser	Gly	Glu	Val	Val
			20					25					30		
Gly	Leu	Leu	Gly	Pro	Asn	Gly	Ala	Gly	Lys	Thr	Thr	Thr	Phe	Tyr	Met
			35				40					45			
Ile	Cys	Gly	Leu	Leu	Glu	Pro	Ser	Gly	Gly	Ser	Val	Tyr	Leu	Asn	Asp
	50					55					60				
Val	Asp	Leu	Ala	Lys	Tyr	Pro	Leu	His	Lys	Arg	Ser	Asn	Leu	Gly	Ile
65					70					75					80
Gly	Tyr	Leu	Pro	Gln	Glu	Ser	Ser	Ile	Phe	Lys	Glu	Leu	Ser	Val	Glu
				85					90					95	
Glu	Asn	Leu	Ala	Leu	Ala	Gly	Glu	Ser	Thr	Phe	Lys	Asn	Ser	Lys	Glu
			100					105						110	
Ser	Glu	Glu	Lys	Met	Glu	Ser	Leu	Leu	Asp	Ala	Phe	Asn	Ile	Gln	Ala
			115					120				125			
Ile	Arg	Glu	Arg	Lys	Gly	Met	Ser	Leu	Ser	Gly	Gly	Glu	Arg	Arg	Arg
	130					135						140			
Val	Glu	Ile	Ala	Arg	Ala	Leu	Met	Lys	Asn	Pro	Lys	Phe	Val	Leu	Leu
145					150					155					160
Asp	Glu	Pro	Phe	Ala	Gly	Val	Asp	Pro	Ile	Ala	Val	Ile	Asp	Ile	Gln
				165					170					175	
Arg	Ile	Ile	Glu	Ser	Leu	Ile	Gly	Leu	Asn	Ile	Gly	Val	Leu	Ile	Thr
			180					185					190		

Asp His Asn Val Arg Glu Thr Leu Ser Val Cys His Arg Ala Tyr Val
195 200 205

Ile Lys Ser Gly Thr Leu Leu Ala Ala Gly Thr Leu Met Lys Phe Met
210 215 220

Lys Thr Leu Trp Cys Val Ser Ile Ile
225 230

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 265 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

Met Ile Lys Ala Arg Phe Lys Lys Arg Leu Leu Gly Ser Arg Gly Ala
1 5 10 15

Phe Asp Leu Asn Ile Asp Leu Glu Ile Lys Glu Ala Glu Val Val Ala
20 25 30

Leu Leu Gly Glu Ser Gly Ala Gly Lys Ser Thr Ile Leu Arg Ile Leu
35 40 45

Ala Gly Leu Glu Ala Val Ser Ser Gly Tyr Ile Glu Ala Asn His Ser
50 55 60

Val Trp Leu Asp Thr Gln Lys Lys Ile Phe Leu Lys Pro Gln Gln Arg
65 70 75 80

Lys Ile Gly Phe Val Phe Gln Asp Tyr Ala Leu Phe Pro His Leu Asn
85 90 95

Val Tyr Gln Asn Ile Ala Phe Ala His Pro Lys Asp Lys Asn Lys Ile
100 105 110

His Glu Val Leu Arg Leu Met Arg Leu Glu Asn Leu Ser Gln Gln Lys
115 120 125

Ile Pro Lys Leu Ser Gly Gly Gln Ala Gln Arg Val Ala Leu Ala Arg
130 135 140

Ala Leu Ile Ala Ala Lys Asn Leu Leu Leu Leu Asp Glu Pro Leu Asn
145 150 155 160

Ala Leu Asp Asn Ala Leu Lys Asn Glu Val Gln Gln Gly Leu Leu Asp
165 170 175

Phe Ile Lys Arg Glu Asn Leu Ser Val Leu Leu Val Ser His Asp Pro
 180 185 190
 Asn Glu Ile Thr Lys Leu Ala Arg Thr Phe Leu Phe Leu Asn Asn Gly
 195 200 205
 Val Ile Asp Pro Asn Gln Glu Asn Arg Leu Phe Ser Asn Arg Leu Leu
 210 215 220
 Val Lys Pro Leu Phe Glu Asp Glu Asn Tyr Cys His Tyr Glu Val Ile
 225 230 235 240
 Pro Gln Thr Ile Ser Leu Pro Lys Asp Cys Leu Asn Pro Thr Phe Lys
 245 250 255
 Leu Asp Phe Ile Gln Asn Lys Lys Phe
 260 265

(2) INFORMATION FOR SEQ ID NO:716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...158
- (D) OTHER INFORMATION: /note= "HYPOTHETICAL ABC TRANSPORTER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

Met Lys Glu Ile Val Thr Ile Glu Asn Val Ser Phe Asn Tyr His Asn
 1 5 10 15
 Arg Ala Ile Phe Lys Asp Phe Asn Leu Ser Ile Gln Glu Gly Asp Phe
 20 25 30
 Leu Cys Val Leu Gly Glu Ser Gly Ser Gly Lys Ser Thr Leu Leu Gly
 35 40 45
 Leu Ile Leu Gly Leu Leu Lys Pro Ser Leu Gly Ser Val Lys Ile Phe
 50 55 60
 Asn Glu Thr Leu Ser Asn Asn Ala Phe Leu Arg Gln Lys Ile Gly Tyr
 65 70 75 80
 Ile Ala Gln Gly Asn Ser Leu Phe Pro His Leu Asn Ala Leu Gln Asn
 85 90 95

Met Thr Phe Cys Leu Asn Leu Gln Gly Ile Asn Lys Gln Ala Ala Gln
100 105 110

Lys Glu Ala Lys Ala Leu Ala Leu Lys Met Gly Leu Asp Glu Ser Leu
115 120 125

Met Asp Lys Phe Pro Asn Glu Leu Ser Gly Gly Gln Ala Lys Glu Trp
130 135 140

Ala Leu Leu Gly Gly Leu Ser Thr Gly Gln Asn Ser Phe Tyr
145 150 155

(2) INFORMATION FOR SEQ ID NO:717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

Met Ile Phe Pro Glu Arg Phe Gln Asn Ala Phe Leu Gly Leu Ser Glu
1 5 10 15

Leu Phe Tyr Tyr Ala Ser Ser Leu Ser Phe Tyr Thr Ile Leu Ser Leu
20 25 30

Ser Pro Ile Leu Leu Phe Val Phe Ser Leu Phe Val Ser His Tyr Leu
35 40 45

Gln Ala His Ser Gly Glu Met Glu Ala Leu Ile Phe Pro Asn Ala Pro
50 55 60

Lys Leu Ile Gly Ala Ile Lys Asp Phe Leu Glu Asn Phe Lys Lys Thr
65 70 75 80

Asp Met Thr Leu Gly Thr Leu Glu Glu Val Ser Ile Val Val Ala Leu
85 90 95

Val Leu Phe Cys Glu Asn Tyr Arg Ser Ile Ala Ser Lys Ile Phe Asp
100 105 110

Ala Lys Pro Arg Asp Tyr Ala His Phe Lys Gly Lys Glu Ile Phe Leu
115 120 125

Phe Trp Gly Phe Gly Thr Thr Leu Val Phe Leu Phe Ala Leu Pro Leu
130 135 140

Val Val Phe Phe Asp Ile Lys Ile Gln Val Phe Phe Glu Asp Lys Asp

145		150		155		160
Ser Ser Leu Leu His Val Leu Arg Trp Ile Gly Thr Tyr Ala Phe Phe						
	165		170		175	
Leu Ile Leu Phe Thr Ile Pro Thr Asn Lys Val Phe Lys Leu Lys						
	180		185		190	

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 243 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

Met Val Leu Met Ile Phe Thr Ser Ile Leu Lys Ile Ala Leu Lys Val			
1	5	10	15
Leu Ser Glu Arg Lys Lys Asn Arg Tyr Gly Phe Pro Arg Ile Phe Asp			
	20	25	30
Val Ala Asp Ile Glu Gln Glu Glu Arg Glu Val Ile Glu Trp Arg Glu			
	35	40	45
Lys Lys Lys Ala Ser Lys Gln Ser Tyr Lys Gln Asn Leu Gln Ile Asn			
	50	55	60
Lys Ile Ala Asn Asp Leu Lys Arg Asp Lys Ile Val Asp Lys Arg Thr			
65	70	75	80
Ile Leu Ser Val Ile Asp Ala Asp Ile Glu Arg Gly Phe Ile Pro Pro			
	85	90	95
Lys Asp Leu Leu Lys Gln Leu Glu Lys Ile Ser Ala Ser Leu Ser Lys			
	100	105	110
Asp Ile Val Ile Thr Ile Lys Gln Val Glu Lys Leu Glu Leu Asn Tyr			
	115	120	125
Ala Leu Ile Asp Asn Ile Gln His Asn Thr Leu Asp Asp Thr Leu Asp			
	130	135	140
Phe Thr Phe Ile Val Gly Asp Ser Leu Ser Val Gln Ser Leu Tyr Val			
145	150	155	160
Thr Phe Asn Leu Val Ile Asp Ile Asp Arg Pro Met Ser Glu Gln Phe			
	165	170	175

Leu Asn Xaa Ile Gly Lys Leu Gly Ser Phe Glu Ser Arg Glu Gln Ala
 180 185 190
 Leu Glu Trp Val Arg Leu Ser Gln Thr Lys Leu Ile Ile Glu Thr Pro
 195 200 205
 Lys Glu Ala Leu Lys Asn Ala Glu Leu Ser Gln Ile Glu Glu Ile Leu
 210 215 220
 Thr Gly Cys Ile Phe Asn Gly Ala Tyr Arg Leu Gln Asn Asp Leu Lys
 225 230 235 240
 Lys Gly Arg

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...236
- (D) OTHER INFORMATION: /note= "cation efflux system membrane protein czcA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

Val Ser Glu Val Ala Ser Val Gly Gly Phe Val Lys Asp Tyr Glu Val
 1 5 10 15
 Thr Leu Gln Asn Asp Ser Leu Ile Arg Tyr Asn Leu Ser Leu Glu Gln
 20 25 30
 Val Ala Asn Ala Ile Lys Asn Ser Asn Asn Asp Thr Gly Gly Gly Val
 35 40 45
 Ile Leu Glu Asn Gly Phe Glu Lys Ile Ile Arg Ser His Gly Tyr Ile
 50 55 60
 Gln Ser Leu Asn Asp Leu Glu Glu Ile Val Val Lys Lys Glu Gly Ala
 65 70 75 80
 Ile Pro Leu Lys Ile Lys Asp Ile Ala Ser Val Arg Leu Ala Pro Lys
 85 90 95
 Pro Arg Arg Gly Ala Ala Asn Leu Asn Gly Asp Lys Glu Val Val Gly
 100 105 110

Gly Ile Val Met Val Arg Tyr His Ala Asp Thr Tyr Lys Val Leu Lys
 115 120 125
 Ala Ile Lys Glu Lys Ile Ala Thr Leu Gln Ala Ser Asn Pro Asp Val
 130 135 140
 Lys Ile Thr Ser Val Tyr Asp Arg Ser Glu Leu Ile Glu Lys Gly Ile
 145 150 155 160
 Asp Asn Leu Ile His Thr Leu Ile Glu Glu Ser Val Ile Val Leu Val
 165 170 175
 Ile Ile Ala Ile Phe Leu Leu His Phe Arg Ser Ala Leu Val Val Ile
 180 185 190
 Ile Thr Leu Pro Leu Arg Val Cys Ile Ser Phe Leu Leu Met Ser Tyr
 195 200 205
 Phe Asn Ile Glu Ala Ser Ile Met Ser Leu Gly Gly Ile Ala Ile Ala
 210 215 220
 Ile Gly Ala Met Val Asn Ala Ala Ile Val Met Val
 225 230 235

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...175
- (D) OTHER INFORMATION: /note= "KERATIN- TYPE II CYTOSKELETAL-intermediate filament"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

Val Glu Thr Phe Leu Arg Ile Phe Glu Lys Asp Ile Phe Asn Thr Pro
 1 5 10 15
 Tyr Lys Leu Glu Val Ile Asn Ala Thr Glu Gly Gly Ala Arg Ile Lys
 20 25 30
 Gly Thr Lys Glu Met Pro Phe Lys Glu Val Cys Glu Lys Ile Asp Lys
 35 40 45
 Ser Lys Pro Lys Pro Pro Ile Asn Leu Ile Tyr Pro Thr Gln Ser Glu
 50 55 60

Gln	Ala	Lys	Asn	Leu	Lys	Ile	Ala	Lys	Lys	Lys	Cys	Glu	Glu	Ile	Ile	65	70	75	80
Lys	Tyr	Ala	Asn	Glu	Lys	Lys	Thr	Gln	Val	Glu	Glu	Ala	Phe	Leu	Lys	85	90	95	
Val	Ala	Glu	Phe	Leu	Glu	Lys	Val	Glu	Lys	Leu	His	Glu	Lys	Asn	Lys	100	105	110	
Leu	Glu	Glu	Leu	Asp	Phe	Glu	Glu	Leu	Glu	Asn	Leu	Ser	Ala	Glu	Ile	115	120	125	
Asp	Asn	Val	Lys	Glu	Leu	Phe	Asp	Asp	Lys	Arg	Phe	Asn	Ser	Tyr	Phe	130	135	140	
Met	Asp	Ala	Ile	Gln	Ser	Tyr	Ile	Phe	His	Gln	Glu	Leu	His	Ile	Ala	145	150	155	160
Glu	Ile	Val	Cys	Lys	Lys	Thr	Ser	Asn	Glu	Asp	Gly	Ile	Lys	Gly	165	170	175		

(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

Met	Lys	Thr	Pro	Cys	Asn	Ala	Tyr	Phe	Leu	Lys	Thr	Pro	Pro	Lys	Asn	1	5	10	15
Lys	Lys	Arg	Arg	Val	Tyr	Val	Asn	Leu	Ala	Val	Phe	Leu	Phe	Leu	Leu	20	25	30	
Leu	Ala	Ser	Ala	Leu	Trp	Leu	Ile	Pro	Arg	Ser	Ala	Ile	Glu	Xaa	Lys	35	40	45	
Pro	Leu	Val	Val	Ala	Thr	Lys	Pro	Ser	Ser	Glu	Gln	Tyr	Ile	Leu	Gly	50	55	60	
Glu	Ile	Leu	Ser	Leu	Leu	Leu	Glu	Lys	His	His	Ile	Pro	Ile	Lys	Arg	65	70	75	80
Ala	Phe	Gly	Ile	Gly	Gly	Gly	Thr	Met	Asn	Ile	His	Pro	Ala	Leu	Ile	85	90	95	
Arg	Gly	Asp	Phe	Asp	Leu	Tyr	Val	Glu	Tyr	Thr	Gly	Thr	Ala	Trp	Val				

100	105	110
Asn Thr Leu Lys Asn Pro Leu Thr Gln Lys Val Asp Phe Glu Thr Ile		
115	120	125
Lys Lys Arg Tyr Glu Lys Glu Phe Asn Leu Leu Trp Val Gly Leu Leu		
130	135	140
Gly Phe Asn Asn Thr Tyr Ser Leu Ala Ile Ser Lys Glu Asp Ala Gln		
145	150	155
Lys Tyr Ala Ile Glu Thr Phe Ser Asp Leu Ala Phe His Ser Pro Asn		
165	170	175
Phe Asp Phe Gly Ala Glu Xaa Asp Phe Phe Glu Arg Glu Asp Ala Phe		
180	185	190
Lys Gly Leu Ile Lys Ala Tyr Arg Phe His Phe Arg Ser Leu His Glu		
195	200	205
Met Xaa Ile Asn Leu Arg Tyr Lys Ser Phe Glu Ser Leu Ile Arg Xaa		
210	215	220
Thr Leu		
225		

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

Val Met Val Tyr Lys Leu Pro Lys His Gln Gln Asn Lys Val Met Ile		
1	5	10
Leu Gly Leu Gly Leu Ala Met Ile Thr Arg Ile Gly Leu Leu Gly Ser		
20	25	30
Leu Phe Phe Ile Ser His Leu Gln Lys Pro Leu Phe Ala Ile Ala Gly		
35	40	45
Met Ser Phe Ser Trp Arg Asp Val Val Leu Leu Leu Gly Gly Ala Phe		
50	55	60
Leu Ala Phe Lys Ala Leu Val Glu Leu Lys Arg Ala Asp Leu Ser		
65	70	75

(2) INFORMATION FOR SEQ ID NO:723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

Val	Lys	Phe	Ser	Val	Leu	Thr	Leu	Phe	Pro	Gln	Leu	Ile	Leu	Pro	Tyr
1				5					10					15	
Phe	Glu	Asp	Ser	Ile	Leu	Lys	Arg	Ala	Leu	Glu	Lys	Asn	Leu	Phe	Glu
			20					25					30		
Leu	Glu	Val	Leu	Asn	Leu	Arg	Asp	Phe	Ser	Ala	Asn	Lys	Tyr	Gln	Lys
		35					40					45			
Ala	Xaa	Ser	His	Ala	His	Trp	Trp	Gly	Cys	Gly	Ala	Asn	Phe	Arg	Pro
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

Leu	Trp	Arg	Thr	Pro	Lys	Thr	Pro	Leu	Val	Ile	Lys	Pro	Tyr	Leu	Lys
1				5					10					15	
Ser	Met	Ser	Asp	Ser	Glu	Ile	Phe	Ala	Xaa	Xaa	Cys	Val	Gly	Met	Ala
			20					25					30		
Ser	Val	Xaa	Gly	Pro	Val	Leu	Ala	Gly	Tyr	Ala	Ser	Met	Gly	Ile	Pro
		35					40					45			
Leu	Pro	Tyr	Leu	Ile	Ala	Ala	Ser	Phe	Met	Ser	Ala	Pro	Gly	Gly	Leu
	50					55					60				

Leu Phe Ala Lys Thr Ile Tyr Pro Gln Asn Glu Thr Ile Ser Ser His
 65 70 75 80
 Ala Asp Val Ser Ala Glu Glu His Val Asn Ile Ile Glu Ala Xaa Ala
 85 90 95
 Xaa Gly Ala Ser Thr Gly Xaa His Leu Ala Leu His Val Gly Ala Met
 100 105 110
 Leu Leu Ala Phe Val Gly Met Val Ala Leu Val Asn Gly Leu Leu Gly
 115 120 125
 Val Val Gly Gly Phe Leu Gly Met Glu His
 130 135

(2) INFORMATION FOR SEQ ID NO:725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...210
- (D) OTHER INFORMATION: /note= "MEMBRANE-ASSOCIATED HYPOTHETICAL
21.7 KD"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

Met Phe Val Val Phe Ile Glu Gly Phe Gly Leu Ala Ile Ser Leu Cys
 1 5 10 15
 Ala Ala Val Gly Ala Gln Ser Leu Phe Ile Val Glu Arg Gly Met Ala
 20 25 30
 Arg Asn Tyr Val Phe Leu Ile Cys Ala Leu Cys Phe Met Cys Asp Ile
 35 40 45
 Val Leu Met Ser Met Gly Val Phe Gly Val Gly Ala Tyr Phe Ala Lys
 50 55 60
 Asn Leu Tyr Leu Ser Leu Phe Leu Asn Leu Phe Gly Ala Val Phe Thr
 65 70 75 80
 Gly Phe Tyr Ala Phe Leu Ala Leu Lys Thr Leu Phe Gln Thr Phe Lys
 85 90 95
 Lys Lys Gln Val Gln Thr Pro Lys Lys Leu Ser Leu Lys Lys Thr Leu
 100 105 110

Leu Phe Thr Leu Gly Val Thr Leu Leu Asn Pro Gln Val Tyr Leu Glu
 115 120 125
 Met Val Phe Leu Ile Gly Ala Ser Ala Met Ser Phe Asn Leu Val Gln
 130 135 140
 Lys Phe Val Phe Leu Ala Gly Thr Leu Ser Ala Ala Phe Ser Trp Leu
 145 150 155 160
 Leu Leu Leu Cys Thr Met Ser Leu Arg Tyr Gly Ser Lys Leu Leu Asn
 165 170 175
 Asn Gln Lys Ile Phe Met Gly Val Asn Leu Phe Val Thr Ala Ile Met
 180 185 190
 Gly Thr Leu Ser Val Thr Leu Phe Arg Asp Phe Leu Ala Leu Leu Ser
 195 200 205
 Lys Thr
 210

(2) INFORMATION FOR SEQ ID NO:726:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

Val Lys Pro Lys Ser Met Lys Glu Lys Leu Arg Gly Ala Met Val Asn
 1 5 10 15
 Ile Leu Arg Ile Lys Met Ile Glu Ile Ser Glu Trp Leu Gln Lys Leu
 20 25 30
 Asp Asp Ala Leu Asp Lys Val Val Ala Lys Lys Glu Pro Glu Ser Phe
 35 40 45
 Leu Lys Pro Ile Ile Ser Pro Ile Glu Asp Tyr Gln Lys Ser Val Arg
 50 55 60
 Gln Ile Gln Ala Gln Phe Thr Asp Ala Pro Lys Phe Asn Glu Glu Gly
 65 70 75 80
 Ala Tyr Pro Gln Phe Leu Ser Cys Gly Leu Leu Gln Val Arg Gly Lys
 85 90 95
 Asn Gly Ala Asn Met Glu Phe Leu Leu Pro Lys Val Tyr Pro Phe Pro

100					105					110					
Pro	Lys	Ser	Leu	Tyr	Ile	Glu	His	Glu	Lys	Asp	Gly	Gln	Phe	Leu	Arg
		115					120					125			
Glu	Met	Leu	Met	Arg	Leu	Leu	Ser	Ser	Ala	Pro	Leu	Val	Gln	Leu	Glu
	130					135					140				
Val	Ile	Leu	Ile	Asp	Ala	Leu	Ser	Leu	Gly	Gly	Ile	Phe	Asn	Leu	Ala
145					150					155					160
Arg	Arg	Leu	Leu	Asp	Lys	Asn	Asn	Asp	Phe	Ile	Tyr	Gln	Gln	Arg	Ile
				165					170					175	
Leu	Thr	Glu	Ser	Lys	Glu	Ile	Glu	Glu	Ala	Leu	Lys	His	Leu	His	Glu
			180					185					190		
Tyr	Leu	Lys	Val	Asn	Leu	Gln	Glu	Lys	Leu	Ala	Gly	Phe	Arg	Asp	Phe
	195						200					205			
Val	His	Tyr	Asn	Glu	Asn	Ala	Lys	Asp	Ser	Leu	Pro	Leu	Lys	Ala	Leu
	210					215					220				
Phe	Leu	Ser	Gly	Val	Asp	Ala	Leu	Ser	Lys	Asp	Ala	Leu	Tyr	Tyr	Leu
225					230					235					240
Glu	Lys	Ile	Met	Arg	Phe	Gly	Ser	Lys	Asn	Gly	Val	Leu	Ser	Phe	Val
				245					250					255	
Asn	Leu	Glu	Ser	Glu	Lys	Asn	Asn	Gln	Ser	Ala	Glu	Asp	Leu	Lys	Arg
			260					265					270		
Tyr	Ala	Glu	Phe	Phe	Lys	Asp	Arg	Thr	Ser	Phe	Glu	Xaa	Leu	Lys	Tyr
	275						280					285			
Leu	Asn	Val	Glu	Ile	Ile	Ser	Asp								
	290					295									

(2) INFORMATION FOR SEQ ID NO:727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

Val	Leu	Ile	Ser	Val	Met	Ile	Gly	Gln	Asn	Gln	Val	Leu	Gly	Phe	Ile
1				5				10						15	

Gly Thr Asn Phe Lys Gln Glu Leu Val Val Asp Phe Ile Val Pro Ser
 20 25 30
 Ala Glu Ile Asn Ile Gly Asn Gln Val Ile Thr Ser Gly Leu Asp Gly
 35 40 45
 Ile Phe Gly Ala Gly Val Phe Val Gly Glu Val Ser Ser Val Glu Asp
 50 55 60
 His Tyr Thr Tyr Lys Ser Ala Val Leu Lys Asn Ala Phe Leu Ser Glu
 65 70 75 80
 Ala Lys Leu Leu Arg His Val Phe Leu Ser Gly Val Lys Asn
 85 90

(2) INFORMATION FOR SEQ ID NO:728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

Met Glu Ala Gln Leu Arg Phe Thr Gly Val Gly Gly Gln Gly Val Leu
 1 5 10 15
 Leu Ala Gly Glu Ile Leu Ala Glu Ala Lys Ile Val Ser Gly Gly Tyr
 20 25 30
 Gly Thr Lys Thr Ser Thr Tyr Thr Ser Gln Val Arg Gly Gly Pro Thr
 35 40 45
 Lys Val Asp Ile Leu Leu Asp Lys Asp Glu Ile Ile Phe Pro Tyr Ala
 50 55 60
 Lys Glu Gly Glu Ile Asp Phe Met Leu Ser Val Ala Gln Ile Ser Tyr
 65 70 75 80
 Asn Gln Phe

(2) INFORMATION FOR SEQ ID NO:729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

Met	Gln	Ala	Trp	Val	Asp	Lys	Pro	Val	Leu	Leu	Glu	Pro	Asp	Ser	Asn	
1				5					10					15		
Ala	Gln	Tyr	Ala	Ala	Val	Ile	Glu	Ile	Asp	Val	Ala	Glu	Ile	Thr	Glu	
			20					25					30			
Pro	Ile	Leu	Ala	Cys	Pro	Asn	Asp	Pro	Asp	Asp	Val	Ala	Thr	Leu	Ser	
		35					40					45				
Glu	Val	Leu	Ala	Asp	Thr	Thr	Gly	Lys	Arg	Pro	His	Ala	Ile	Asp	Glu	
	50					55					60					
Val	Phe	Ile	Gly	Ser	Cys	Met	Thr	Asn	Ile	Gly	His	Phe	Arg	Ala	Phe	
65				70					75						80	
Gly	Glu	Ile	Val	Lys	Asn	Ala	Pro	Pro	Ser	Gln	Ala	Arg	Leu	Trp	Val	
				85					90					95		
Val	Pro	Pro	Ser	Lys	Met	Asp	Glu	Gln	Glu	Leu	Ile	Asn	Glu	Gly	Tyr	
			100					105					110			
Tyr	Ala	Ile	Phe	Gly	Ala	Ala	Gly	Ala	Arg	Thr	Glu	Val	Pro	Gly	Cys	
		115					120					125				
Ser	Leu	Cys	Met	Gly	Asn	Gln	Ala	Arg	Val	Arg	Asp	Asn	Ala	Val	Val	
	130					135					140					
Phe	Ser	Thr	Ser	Thr	Arg	Asn	Phe	Asp	Asn	Arg	Met	Gly	Arg	Gly	Ala	
145					150				155						160	
Lys	Val	Tyr	Leu	Gly	Ser	Ala	Glu	Leu	Gly	Ala	Ala	Cys	Ala	Leu	Leu	
				165					170					175		
Gly	Arg	Ile	Pro	Thr	Lys	Glu	Glu	Tyr	Met	Asn	Leu	Val	Ser	Glu	Lys	
			180					185					190			
Leu	Glu	Ser	Gln	Lys	Asp	Lys	Ile	Tyr	Arg	Ser						
		195					200									

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

Val	Gly	Asn	Ala	Gly	Val	Ala	Leu	Ala	Gly	Leu	Met	Ser	Asp	Glu	Ile	
1				5					10					15		
Tyr	Leu	Cys	Ala	Leu	Asp	Cys	Ala	Tyr	Ile	Lys	Gly	Phe	Lys	Lys	His	
			20					25					30			
Ala	Gln	Asn	Ser	Tyr	Tyr	Gly	Asp	Glu	Lys	Glu	Ile	Asp	Thr	Ser	Ser	
		35					40					45				
Leu	Ile	Ser	Val	Glu	Gly	Asn	Val	Glu	Gly	Tyr	Glu	Thr	Phe	Ser	Asp	
	50					55					60					
Ser	Leu	Phe	Leu	Leu	Ser	Lys	Glu	Arg	Ile	Glu	Glu	Ala	Leu	His	Tyr	
65					70				75						80	
Tyr	Gln	Pro	Lys	Lys	Val	Tyr	Asn	Leu	Ser	Tyr	Gly	Ala	Lys	Ile	Lys	
			85					90						95		
His	Ala	Val	Ser	Leu	Asn	His	Ser	Gln	Val	Lys	Leu	Lys	Gln	Ile	Asn	
			100					105					110			
Lys	Gln	Asp	Ala	Ile	Val	Arg	Ile	Lys	Ser	Met	Phe	Ser	Pro	Arg	Ser	
		115					120					125				
Asn	His	Ala	Lys	Asp	Leu	Lys	Asn	Leu	Gln	Lys	Asn	Leu	Ile	Arg	Phe	
	130					135					140					
Lys	Glu	Asp	Phe	Phe	Thr	His	Leu	Asn	Thr	Pro	Cys	Lys	Thr	Lys	Gln	
145					150				155						160	
Glu	Ala	Phe	Glu	Trp	Val	Asp	Ser	Leu	Ser	Gly	Phe	Cys	Gln	Thr	Ala	
			165					170						175		
Ser	Ala	Lys	Thr	Pro	Thr	Ile	Gly	Ile	Leu	Phe	Glu	Gly	Ser	Val	Ala	
			180					185					190			
His	Ile	Leu	Gln	Ser	Val	Leu	Ile	Val	Ser	Leu	His	Leu	Lys	Glu	Asn	
	195					200						205				
Glu	Leu	Thr	Leu	Leu	Ser	Asn	Ser	Leu	Lys	Thr	Pro					
	210					215					220					

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

```
Val Met Asn Phe Phe Val Gly Gly Leu Ser Ile Val Cys Asn Val Val
1          5          10          15

Val Ile Thr Tyr Ser Ala Leu His Pro Thr Ala Pro Val Glu Gly Ala
20          25          30

Glu Asp Ile Val Gln Val Ser His His Leu Thr Ser Phe Tyr Gly Pro
35          40          45

Ala Thr Gly Leu Leu Phe Gly Phe Thr Tyr Leu Tyr Ala Ala Ile Asn
50          55          60

His Thr Phe Gly Leu Asp Trp Arg Pro Tyr Ser Trp Tyr Ser Leu Phe
65          70          75          80

Val Ala Ile Asn Thr Val Pro Ala Ala Ile Leu Ser His Tyr Ser Asp
85          90          95

Met Leu Asp Asp His Lys Val Leu Gly Ile Thr Glu Gly Asp Trp Trp
100         105         110

Ala Ile Ile Xaa
115
```

(2) INFORMATION FOR SEQ ID NO:732:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

```
Met Gln Lys Ser Ile Phe Lys Ile Thr Leu Leu Leu Val Phe Leu Phe
1          5          10          15

Leu Arg Asn Ala Val Gly Leu Asp Asp Lys Lys Ala Ala Pro Lys Ser
20          25          30

Val Gln Asn Thr Pro Lys Asn Leu Pro Pro Ile Gln Leu Arg Leu Asp
35          40          45

Gln Ala Tyr Glu Asp Leu Ile Lys Met Leu Asp Asn Met Gly Lys Ser
```


Leu Gly Glu Leu Pro Glu Ile Lys Leu Lys Gln Lys Ala Leu Ile Ile
 20 25 30
 Ser Asp Ser Ile Val Ala Gly Leu His Leu Pro Tyr Leu Leu Glu Arg
 35 40 45
 Leu Asn Ala Leu Glu Val Arg Val Cys Val Ile Glu Ser Gly Glu Lys
 50 55 60
 Tyr Lys Asn Phe His Ser Leu Glu Arg Ile Leu Asn Asn Ala Phe Glu
 65 70 75 80
 Met Gln Leu Asn Arg His Ser Leu Met Ile Ala Leu Gly Gly Gly Val
 85 90 95
 Ile Ser Asp Met Val Gly Phe Ala Ser Ser Ile Tyr Phe Arg Gly Ile
 100 105 110
 Asp Phe Ile Asn Ile Pro Tyr Asp Phe Thr Arg Ser Ser Gly Cys Glu
 115 120 125
 Arg Gly Gly Glu Asn Arg Asp Gln His Ala Leu Trp Gln Glu Pro Asn
 130 135 140
 Arg Ile Val Pro Pro Ala
 145 150

(2) INFORMATION FOR SEQ ID NO:734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

Val Leu Leu Gly Lys His Ser Gly Ala Gly Leu Leu Ser Ala Leu Xaa
 1 5 10 15
 Ala Leu Ser Phe Gly Ser Gly Val Val Ser Ile Gln Ala Leu Glu Cys
 20 25 30
 Glu Ile Thr Ser Asn Asn Lys Pro Leu Glu Leu Val Phe Cys Glu Asn
 35 40 45
 Phe Pro Lys Lys Leu Ser Ala Phe Ala Leu Gly Met Gly Leu Glu Asn
 50 55 60
 Ile Pro Lys Asp Phe Lys Lys Trp Leu Glu Leu Ala Pro Cys Val Leu
 65 70 75 80

Asp Ala Gly Val Phe Tyr His Lys Glu Val Leu Gln Ala Leu Glu Lys
 85 90 95
 Glu Val Ile Leu Thr Pro His Pro Lys Glu Phe Leu Ser Leu Leu Lys
 100 105 110
 Ser Val Gly Ile Asn Ile Ser Met Leu Glu Leu Leu Asp Asn Lys Leu
 115 120 125
 Glu Ile Ala Arg Asp Phe Ser Gln Lys Tyr Pro Lys Val Val Leu Leu
 130 135 140
 Leu Lys Gly Ala Asn Thr Leu Ile Ala His Gln Gly Arg Val Phe Ile
 145 150 155 160
 Asn Asn Leu Gly Ser Val Ala Leu Ala Lys Ala Gly Ser Gly Asp Val
 165 170 175
 Leu Ala Gly Leu Ile Val Ser Leu Leu Ser Gln Asn Tyr Thr Pro Leu
 180 185 190
 Xaa Ala Ala Ile Asn Ala Ser Leu Ala His Ala Leu Ala Gly Leu Xaa
 195 200 205
 Phe Lys Asn Xaa Xaa Ala Leu Thr Pro Xaa Asp Leu Ile Glu Lys Xaa
 210 215 220
 Lys Arg Leu
 225

(2) INFORMATION FOR SEQ ID NO:735:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...187
 - (D) OTHER INFORMATION: /note= "UDP-N-ACETYLMURAMYL-TRIPETIDE SYNTHETASE"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

Met Arg Ile Leu His Tyr Gly Gly Glu Leu Pro Cys Asp Cys Pro Lys
 1 5 10 15
 Arg Ile Ala Gly Leu Asp Phe Ala Leu Lys Ile Leu Thr Asn Ile Thr

20					25					30						
Ser	Asp	His	Leu	Asp	Phe	His	Gln	Asn	Ile	Glu	Asn	Tyr	Arg	Asp	Ala	
35					40					45						
Lys	Asn	Ser	Phe	Phe	Lys	Asp	Glu	Gly	Leu	Lys	Val	Ile	Asn	Arg	Asp	
50					55					60						
Glu	Thr	Asn	Ala	Leu	Phe	Asn	Pro	Ile	Asn	Ala	Arg	Thr	Tyr	Ala	Leu	
65					70					75					80	
Asp	Lys	Lys	Ala	His	Leu	Asn	Val	Gln	Ala	Phe	Ser	Leu	Asn	Pro	Ser	
85					90					95						
Ile	Ser	Ala	Ser	Leu	Cys	Tyr	Gln	His	Asp	Leu	Arg	Asp	Pro	Asn	Leu	
100					105					110						
Lys	Glu	Thr	Ala	Leu	Ile	His	Ser	Pro	Leu	Leu	Gly	Arg	Tyr	Asn	Leu	
115					120					125						
Tyr	Asn	Ile	Leu	Ala	Gly	Val	Leu	Gly	Val	Lys	Leu	Leu	Thr	Gln	Leu	
130					135					140						
Pro	Leu	Glu	Thr	Ile	Ala	Pro	Leu	Leu	Glu	Asn	Phe	Tyr	Gly	Val	Lys	
145					150					155					160	
Gly	Arg	Leu	Glu	Ile	Val	His	Ser	Lys	Pro	Leu	Val	Val	Val	Asp	Phe	
165					170					175						
Ala	His	Thr	Thr	Asp	Gly	Met	Gln	Gln	Val	Phe						
180					185											

(2) INFORMATION FOR SEQ ID NO:736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...198
- (D) OTHER INFORMATION: /note= "PREPROTEIN TRANSLOCASE
SECA SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

Val	Ser	Ile	Lys	Glu	Glu	Ser	Gln	Thr	Leu	Ala	Asp	Ile	Thr	Phe	Gln
1				5					10					15	

Asn	Tyr	Phe	Arg	Met	Phe	Ser	Lys	Leu	Ser	Gly	Met	Thr	Gly	Thr	Ala			
			20					25					30					
Gln	Thr	Glu	Ala	Thr	Glu	Phe	Leu	Glu	Ile	Tyr	Asn	Leu	Glu	Val	Val			
		35					40					45						
Ser	Ile	Pro	Thr	Asn	Leu	Ala	Ile	Lys	Arg	Lys	Asp	Leu	Asn	Asp	Leu			
	50					55					60							
Ile	Tyr	Lys	Ser	Glu	Lys	Glu	Lys	Phe	Asp	Ala	Val	Ile	Leu	Lys	Ile			
65					70				75					80				
Lys	Glu	Leu	His	Asp	Lys	Gly	Gln	Pro	Val	Leu	Val	Gly	Thr	Ala	Ser			
			85					90						95				
Ile	Glu	Lys	Ser	Glu	Thr	Leu	His	Ala	Leu	Leu	Lys	Lys	Glu	Arg	Ile			
			100					105					110					
Pro	His	Thr	Val	Leu	Asn	Ala	Lys	Gln	His	Thr	Lys	Glu	Ala	Glu	Ile			
		115					120					125						
Ile	Lys	Asp	Ala	Gly	Leu	Lys	Gly	Ala	Val	Thr	Ile	Ala	Thr	Asn	Met			
	130					135					140							
Ala	Gly	Arg	Gly	Val	Asp	Ile	Lys	Leu	Thr	Asp	Glu	Val	Lys	Glu	Leu			
145					150					155					160			
Gly	Gly	Leu	Tyr	Ile	Ile	Gly	Thr	Glu	Arg	His	Glu	Ser	Arg	Arg	Ile			
			165					170						175				
Asp	Asn	Gln	Leu	Arg	Gly	Arg	Ser	Gly	Arg	Gln	Gly	Asp	Pro	Gly	Val			
		180						185					190					
Ser	Gln	Phe	Tyr	Leu	Ser													
		195																

(2) INFORMATION FOR SEQ ID NO:737:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...208
 - (D) OTHER INFORMATION: /note= "putative chemoreceptor"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

Val	Val	Ala	Asp	Glu	Val	Arg	Lys	Leu	Ala	Glu	Lys	Thr	Gln	Lys	Ala	1	5	10	15
Thr	Lys	Glu	Ile	Ala	Val	Val	Val	Lys	Ser	Met	Gln	Gln	Glu	Ala	Asn	20	25	30	
Asp	Ile	Gln	Thr	Asn	Thr	His	Asp	Ile	Asn	Ser	Ile	Val	Gly	Ser	Ile	35	40	45	
Lys	Gly	Asp	Val	Glu	Glu	Leu	Lys	Ser	Thr	Val	Lys	Asn	Asn	Met	Ile	50	55	60	
Val	Ala	Gln	Ala	Ala	Lys	Tyr	Thr	Ile	Tyr	Asn	Ile	Asn	Asn	Arg	Val	65	70	75	80
Phe	Cys	Gly	Xaa	Ala	Lys	Leu	Asp	His	Val	Val	Phe	Lys	Asn	Asn	Leu	85	90	95	
Tyr	Gly	Met	Val	Xaa	Leu	Val	Ser	Ile	Pro	Leu	Thr	Leu	Pro	Ala	His	100	105	110	
Lys	Ser	Xaa	Arg	Leu	Gly	Lys	Trp	Tyr	Tyr	Glu	Gly	Ala	Gly	Lys	Glu	115	120	125	
Asn	Phe	Ala	Asn	Thr	Ser	Gly	Tyr	Arg	Ala	Leu	Glu	Ser	His	His	Ala	130	135	140	
Ser	Val	His	Ala	Glu	Ala	Asn	Asp	Leu	Val	Lys	Ala	Val	Gln	Glu	Asp	145	150	155	160
His	Val	Thr	Asp	Ser	Lys	Tyr	Leu	Glu	His	Lys	Val	His	Leu	Met	Glu	165	170	175	
Asp	Ser	Ala	Lys	His	Val	Lys	Glu	Asn	Ile	Asp	Lys	Met	Phe	Tyr	Glu	180	185	190	
Lys	Gln	Asp	Glu	Leu	Asn	Lys	Ile	Ile	Glu	Lys	Ile	Gln	Lys	Gly	Glu	195	200	205	

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

Met	Asn	Thr	Ser	Lys	Lys	Leu	Gly	Asn	Pro	Leu	Leu	Phe	Leu	His	Asp	1	5	10	15
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----	----

20	25	30
Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp		
35	40	45
Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe		
50	55	60
Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser		
65	70	75
Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser		
85	90	95
Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr		
100	105	110
Asp Gly Met Thr Val Arg Glu Leu Ser Arg Trp Cys His Asn His		
115	120	125

(2) INFORMATION FOR SEQ ID NO:740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...79
- (D) OTHER INFORMATION: /note= "Cu++-transporting P-type ATPase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

Val Asn Val Gly Val Pro Phe Ser Tyr Gln Val Ser Ala Thr Phe Gln		
1	5	10
Asn Ser Arg Leu Ser Ser Leu Leu Glu Thr Leu Lys Lys Ser Phe Leu		
20	25	30
Glu Lys Pro Leu Ile Glu Ser Ser Ala Asn Lys Ile Ala Asp Ile Phe		
35	40	45
Ser Lys Ala Val Leu Phe Leu Ala Phe Val Ser Phe Leu Leu Trp Gln		
50	55	60
Phe Gly Leu Gly Gly Asn Phe Glu Lys Ser Phe Asn Gly Val Tyr		
65	70	75

(2) INFORMATION FOR SEQ ID NO:741:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...49
 - (D) OTHER INFORMATION: /note= "antigen [*Entamoeba histolytica*]"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

Met Leu Met Val Asn Gly Tyr Gln Ile Thr Met His Lys Gly Tyr Lys
1 5 10 15

Val Gly Phe Phe Thr Ser Gly Tyr Asn Pro Asp Phe Ala Gln Thr Ile
 20 25 30

Gln Asn Arg Ser Tyr Leu Met Ser Ser Tyr Glu Leu Ser Phe Leu Arg
 35 40 45

Asn

(2) INFORMATION FOR SEQ ID NO:742:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 412 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

Met Val Gln Phe Gln Asn Thr Leu Ile Lys Phe His Ala Leu Ser Phe
1 5 10 15

Lys Asn Ala Asn Leu Ile Tyr Asn Ala Lys Leu Asn Lys Thr Cys Tyr
 20 25 30

Lys Glu Asn Ser Asn Thr Ile Ile Leu Arg Ile Lys Met Leu Thr Gln
 35 40 45

Glu Asp Val Leu Asn Ala Leu Lys Thr Ile Ile Tyr Pro Asn Phe Glu
 50 55 60

Lys Asp Ile Val Ser Phe Gly Phe Val Lys Asn Ile Thr Leu His Asp
 65 70 75 80

Asn Gln Leu Gly Leu Leu Ile Glu Ile Pro Ser Ser Ser Glu Glu Thr
 85 90 95

Ser Ala Ile Leu Arg Glu Asn Ile Ser Lys Ala Met Gln Glu Lys Gly
 100 105 110

Val Lys Ala Leu Asn Leu Asp Ile Lys Thr Pro Pro Lys Pro Gln Ala
 115 120 125

Pro Lys Pro Thr Thr Lys Asn Leu Ala Lys Asn Ile Lys His Val Val
 130 135 140

Met Ile Ser Ser Gly Lys Gly Gly Val Gly Lys Ser Thr Thr Ser Val
 145 150 155 160

Asn Leu Ser Ile Ala Leu Ala Asn Leu Asn Gln Lys Val Gly Leu Leu
 165 170 175

Asp Ala Asp Val Tyr Gly Pro Asn Ile Pro Arg Met Met Gly Leu Gln
 180 185 190

Asn Ala Asp Val Ile Met Asp Pro Ser Gly Lys Lys Leu Ile Pro Leu
 195 200 205

Lys Ala Phe Gly Val Ser Val Met Ser Met Gly Leu Leu Tyr Asp Glu
 210 215 220

Gly Gln Ser Leu Ile Trp Arg Gly Pro Met Leu Met Arg Ala Ile Glu
 225 230 235 240

Gln Met Leu Ser Asp Ile Ile Trp Gly Asp Leu Asp Val Leu Val Val
 245 250 255

Asp Met Pro Pro Arg Asn Arg Arg Cys Ala Ala His Ala Ala Gln Ala
 260 265 270

Val Pro Leu Ser Ala Gly Ile Thr Val Thr Thr Pro Gln Ile Val Ser
 275 280 285

Leu Asp Asp Ala Lys Arg Ser Leu Asp Met Phe Lys Lys Leu His Ile
 290 295 300

Pro Ile Ala Gly Ile Val Glu Asn Met Gly Ser Phe Val Cys Glu His
 305 310 315 320

Cys Lys Lys Glu Ser Glu Ile Phe Gly Ser Asn Ser Met Ser Gly Leu
 325 330 335

Leu Glu Ala Tyr Asn Thr Gln Ile Leu Ala Lys Leu Pro Leu Glu Pro
 340 345 350

Lys Val Arg Leu Gly Gly Asp Lys Gly Glu Pro Ile Val Ile Ser His

355	360	365
Pro Thr Ser Val Ser Ala Lys Ile Phe Glu Lys Met Ala Lys Asp Leu		
370	375	380
Ser Ala Phe Leu Asp Lys Val Glu Arg Glu Lys Leu Ala Asp Asn Lys		
385	390	395
Asp Ile Gln Pro Thr Gln Thr His Ala Tyr Ser His		
405	410	

(2) INFORMATION FOR SEQ ID NO:743:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

Met Gly Val Val Ile Gly Glu Thr Thr Glu Ile Gly Asp Asp Val Thr		
1	5	10
Ile Tyr His Gly Val Thr Leu Gly Gly Thr Gly Lys Phe Lys Gly Lys		
20	25	30
Arg His Pro Thr Leu Gly Asn Arg Val Val Val Gly Ala Gly Ala Lys		
35	40	45
Val Leu Gly Ala Ile Cys Val Gly Asp Asp Val Arg Ile Gly Ala Asn		
50	55	60
Ala Val Val Leu Ser Asp Leu Pro Thr Gly Ser Thr Ala Val Gly Ala		
65	70	75
Lys Ala Lys Thr Ile Thr Lys Asp Arg		
85		

(2) INFORMATION FOR SEQ ID NO:744:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

Met	Leu	Ser	Phe	Ile	Ser	Ala	Phe	Asp	Lys	Arg	Gly	Val	Ser	Ile	Arg
1				5					10					15	
Leu	Leu	Thr	Ala	Leu	Leu	Leu	Leu	Phe	Ser	Leu	Gly	Leu	Ala	Lys	Asp
			20					25					30		
Leu	Glu	Ile	Gln	Thr	Phe	Val	Ala	Lys	Tyr	Leu	Ser	Lys	Asn	Gln	Lys
		35					40					45			
Ile	Gln	Ala	Leu	Gln	Glu	Gln	Ile	Asp	Ala	Leu	Asp	Ser	Gln	Glu	Lys
	50					55					60				
Val	Val	Ser	Lys	Trp	Asp	Asn	Pro	Ile	Leu	Tyr	Leu	Gly	Tyr	Asn	Asn
65					70					75				80	
Ala	Asn	Val	Ser	Asp	Phe	Phe	Arg	Leu	Asp	Ser	Thr	Leu	Met	Gln	Asn
				85					90					95	
Met	Ser	Leu	Gly	Leu	Ser	Gln	Lys	Val	Asp	Leu	Asn	Gly	Lys	Lys	Leu
			100					105					110		
Thr	Gln	Ser	Lys	Met	Ile	Asn	Leu	Glu	Lys	Gln	Lys	Lys	Ile	Leu	Glu
			115				120					125			
Leu	Lys	Lys	Thr	Lys	Gln	Gln	Leu	Val	Ile	Asn	Leu	Met	Ile	Asn	Gly
	130					135					140				
Ile	Glu	Asn	Tyr	Lys	Asn	Gln	Gln	Glu	Ile	Glu	Leu	Leu	Asn	Thr	Ala
145					150					155					160
Ile	Lys	Asn	Leu	Glu	Asn	Thr	Leu	Tyr	Gln	Ala	Asn	His	Ser	Ser	Ser
				165					170					175	
Pro	Asp	Leu	Ile	Glu	Ile	Asp	Lys	Leu	Glu	Asn	Leu	Lys	Ile	Ala	Asn
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

Val Xaa Leu Tyr Leu Ala Leu Thr Leu Ser Leu Gly Ile Ala Met Leu
 1 5 10 15
 Leu Val Glu Met Leu Ile Gly Asn Leu Gly Lys Lys Asp Val Val Ser
 20 25 30
 Asn Tyr Gln Ile Leu Asp Pro Lys Arg Lys Lys Tyr Tyr Pro Phe Thr
 35 40 45
 Ser Phe Phe Ile Leu Gly Gly Pro Leu Ile Leu Ser Phe Tyr Ala Val
 50 55 60
 Val Leu Gly Trp Val Leu Tyr Tyr Leu Phe Val Val Thr Phe Asp Leu
 65 70 75 80
 Pro Lys Asp Leu Xaa Gln Ala Lys Met Gln Phe Xaa Met Leu Gln Asn
 85 90 95
 Gly Ser Leu Ile Trp Pro Val Ile Asp Phe Ser Ala Cys
 100 105

(2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

Val Pro Ala Val Gly Gly Ala Leu Ile Trp Xaa Xaa Ile Xaa Ile Tyr
 1 5 10 15
 Glu Leu Tyr His Gly Xaa Val Asn Glu Xaa Ile Phe Xaa Val Leu Tyr
 20 25 30
 Ser Ile Leu Leu Ile Gly Val Leu Ile Asp Ser Val Ile Lys Pro Ile
 35 40 45
 Leu Ile Val Phe Ile Lys Lys Arg Ile Phe Lys Thr Thr Leu Lys Ile
 50 55 60
 Asn Glu Ile Leu Ile Phe Phe Ser Met Ile Ala Gly Ile Ser Gln Phe
 65 70 75 80
 Gly Phe Trp Gly Ile Ile Val Gly Pro Thr Ile Thr Ala Phe Phe Ile
 85 90 95
 Ala Leu Leu Arg Leu Tyr Glu Asn Tyr Phe Ile Gln Lys Glu Gln Lys
 100 105 110

Thr Cys Glu Cys
115

(2) INFORMATION FOR SEQ ID NO:747:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

Val	Val	Val	Ile	Ile	Leu	Val	Val	Val	Ile	Ile	Gln	Asn	Ser	Ser	Ser	
1				5					10					15		
Leu	Lys	Glu	Glu	Arg	Glu	Gln	Glu	Arg	Ala	Ile	Lys	Pro	Asp	Thr	Lys	
		20					25					30				
Asn	Asn	Ser	Phe	Asn	Glu	Thr	Asn	Pro	Thr	Glu	Glu	Lys	Lys	Leu	Glu	
		35					40					45				
Pro	Thr	Pro	Lys	Leu	Glu	Glu	Lys	His	Lys	Glu	Gln	Asp	Lys	Gln	Gly	
	50					55					60					
Lys	Glu	Ala	Ile	Lys	Glu	Asn	Pro	Asn	Thr	Ile	Tyr	Ile	Ile	Pro	Lys	
65				70					75					80		
Arg	Asp	Ile	Trp	Val	Glu	Val	Ile	Asp	Leu	Asp	Glu	Lys	Lys	Asn	Ser	
			85					90						95		
Phe	Gln	Lys	Val	Phe	Lys	Lys	Ser	Tyr	Pro	Leu	Glu	Ala	Lys	Asn	His	
		100					105						110			
Arg	Leu	Leu	Leu	Arg	Phe	Gly	His	Gly	His	Leu	Ile	Leu	Lys	Asn	Asn	
	115					120						125				
His	Gln	Glu	Gln	Asp	Tyr	Asn	Asp	Ser	Lys	Thr	Arg	Arg	Phe	Leu	Tyr	
	130					135					140					
Glu	Pro	Asn	Lys	Gly	Leu	Thr	Leu	Ile	Asn	Glu	Ala	Gln	Tyr	Lys	Ala	
145				150					155						160	
Leu	Gln	Gln														

(2) INFORMATION FOR SEQ ID NO:748:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...40

(D) OTHER INFORMATION: /note= "HAEMOLYSIN SECRETION ATP-BINDING PROTEIN"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

Met	Asp	Glu	Ile	Tyr	Gln	Ile	Ala	Lys	Asn	Lys	Thr	Leu	Ile	Val	Ile
1				5					10					15	
Ala	His	Arg	Leu	Ser	Thr	Ile	Glu	Arg	Cys	Glu	Val	Ile	Ile	Asp	Met
			20					25						30	
Ser	Gln	His	Lys	Asp	Asn	Leu	Gly								
			35				40								

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

Val	Ala	Gly	Ser	Phe	Ile	Ile	Ala	Leu	Phe	Ser	Val	Leu	Ala	Asp	Gln
1				5					10					15	
Phe	Val	Ser	Val	Phe	Gln	His	Glu	Asn	Ala	Leu	Gln	Arg	Leu	Phe	Ser
			20					25					30		
Gln	Asn	Ala	Thr	Gln	Lys	Gln	Lys	Lys	Lys	Ser	Leu	Cys			
			35				40					45			

(2) INFORMATION FOR SEQ ID NO:750:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

Met	Val	Ala	Leu	Ser	Asn	Ala	Leu	Ser	Arg	Val	Phe	Gly	Ser	Val	Ala	
1				5				10					15			
Gly	Tyr	Lys	Phe	Pro	Ser	Phe	Ile	Gln	Lys	Ser	Ile	Asn	Ala	Leu	Tyr	
			20					25				30				
Val	Lys	Ile	Phe	Lys	Ile	Asp	Leu	Ser	Glu	Phe	Glu	Pro	Leu	Glu	Asn	
		35					40					45				
Tyr	Lys	Ser	Leu	Asn	Ala	Leu	Phe	Met	Arg	Ser	Leu	Lys	Lys	Glu	Arg	
	50					55					60					
Pro	Phe	Asp	Lys	Ala	Pro	Ile	Phe	Ala	Leu	Arg	Leu	Ala	Met	Ala	Leu	
65					70				75						80	
Ile	Thr	Glu	Cys	Ala	Phe	Leu	Asp	Asn	Asp	Ser	Ala	Leu	Gln	Ile	Lys	
				85					90					95		
Gly	Met	Pro	Tyr	Lys	Ala	His	Glu	Leu	Val	Gly	Glu	Ile	Asn	Pro	Leu	
			100					105					110			
Ser	Pro	Leu	Phe	Ser	Met											
			115													

(2) INFORMATION FOR SEQ ID NO:751:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

Met	Ala	Val	Leu	Lys	Lys	Met	Ile	Gly	Leu	Val	Ala	Val	Leu	Ser	Val	
1				5				10					15			
Leu	Leu	Ala	Arg	Asp	Asn	Pro	Phe	Glu	Pro	Glu	Ile	Asn	Ser	Lys	Asn	
			20					25					30			

Leu Gln Gly Gly Phe Ser Gly Ile Tyr Asp Asp Tyr Leu Lys Glu Ile
 35 40 45
 His Val Asp Leu Pro Thr Ser Ala Arg Ile Leu Lys Lys Ile Thr Leu
 50 55 60
 Thr Tyr Gln Asp Ile Asp Gly Ser Ile His Ser Lys Val Val Gly Ile
 65 70 75 80
 Asp Lys Ser Ile Asp Trp His Tyr Pro Leu Lys Leu Ser Gln His Thr
 85 90 95
 Leu Asn Gln Asp Ala Phe Glu Lys Arg Tyr Gln Ile Gln Asp Phe Asp
 100 105 110
 Phe Leu Met Ala Asn Asn Thr Met Ile Leu Arg Ser Pro Tyr Lys Ile
 115 120 125
 Leu Arg Ser Phe Val Leu Val Asn Pro Tyr Arg Ile Val Leu Asp Thr
 130 135 140
 Gln Lys Gly Pro Leu Asp Ile Tyr Gln Asn Met Asp Leu Asn Gln Lys
 145 150 155 160
 Phe Phe Ser His Ile Lys Val Gly Thr His Lys Asp Tyr Tyr Arg Ile
 165 170 175
 Thr Leu Ile Leu Asp Gly Lys Tyr Arg Tyr Leu Leu Glu Glu Lys Asn
 180 185 190
 Gly Ala Tyr Glu Leu Lys Leu Lys
 195 200

(2) INFORMATION FOR SEQ ID NO:752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

Met Gly Gly Phe Thr Ser Ile Trp His Trp Val Ile Val Leu Leu Val
 1 5 10 15
 Ile Val Leu Leu Phe Gly Ala Lys Lys Ile Pro Glu Leu Ala Lys Gly
 20 25 30
 Leu Gly Ser Gly Ile Lys Asn Phe Lys Lys Ala Val Lys Asp Asp Glu

	35		40		45										
Glu	Glu	Ala	Lys	Asn	Glu	Leu	Lys	Thr	Leu	Asp	Ala	Gln	Ala	Thr	Gln
	50					55						60			
Thr	Lys	Val	His	Glu	Thr	Ser	Glu	Ile	Lys	Ser	Lys	Gln	Glu	Ser	
65					70					75					

(2) INFORMATION FOR SEQ ID NO:753:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

Leu	Thr	Thr	Lys	Ala	Cys	Trp	Leu	Leu	Arg	Val	Cys	Cys	Tyr	Arg	Ser
1			5						10					15	
Leu	Asn	Ile	Thr	Ile	Lys	Asp	Arg	Thr	Met	Lys	Thr	Asn	Gly	His	Phe
		20						25					30		
Lys	Asp	Phe	Ala	Trp	Lys	Lys	Cys	Phe	Leu	Gly	Ala	Ser	Val	Val	Ala
	35						40					45			
Leu	Leu	Val	Gly	Cys	Ser	Pro	His	Ile	Ile	Glu	Thr	Asn	Glu	Val	Ala
	50					55					60				
Leu	Lys	Leu	Asn	Tyr	His	Pro	Ala	Ser	Glu	Lys	Val	Gln	Ala	Leu	Asp
65				70						75				80	
Glu	Lys	Ile	Leu	Leu	Leu	Arg	Pro	Ala	Phe	Gln	Tyr	Ser	Xaa	Asn	Ile
			85						90					95	
Cys															

(2) INFORMATION FOR SEQ ID NO:754:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

[illegible]

(2) INFORMATION FOR SEQ ID NO:755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

Val Arg Leu Asn Ala Ala Val Val Val Asp Gly Lys Tyr Lys Ile Ala
1 5 10 15
Leu Glu Asp Gly Ala Asn Ala Leu Glu Tyr Glu Pro Leu Ser Asp Glu
20 25 30
Xaa Xaa Lys Lys Ile Asn Xaa Leu Val Lys Gln Ala Ile Gly Asp Asn

35		40		45
Gln Asn Arg Gly Asp Asp Val Ala Val Ser Asn Phe Glu Phe Asn Pro				
50		55		60
Met Val Pro Met Ile Asp Asn Ala Thr Leu Ser Glu Lys Ile Ile Tyr				
65		70		75
Lys Thr Gln Lys Ile Leu Gly Leu Phe Met Phe Leu Ile Lys Val Tyr				
		85		90
Leu Val Phe Ile Val Leu Phe Ile Phe Tyr Lys Lys Val Ile Val Pro				
		100		105
Phe Ser Glu Arg Met Leu Glu Val Val Pro Asp Glu Asp Lys Glu Val				
		115		120
Lys Ser Met Phe Glu Glu Met Asn Glu Glu Glu Asp Glu Leu Asn Lys				
		130		135
Leu Gly Asp Leu Arg Lys Lys Val Glu Asp Gln Leu Gly Leu Asn Ala				
145		150		155
Ser Phe Ser Glu Glu Glu Val Arg Tyr Glu Ile Ile Leu Glu Lys Ile				
		165		170
Arg Gly Thr Leu Lys Glu Arg Pro Asp Glu Ile Ala Thr Leu Phe Lys				
		180		185
Leu Leu Ile Lys Asp Glu Ile Ser Ser Asp Ser Ala Lys Gly				
		195		200
				205

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

Val Cys Phe Ile Leu Pro Phe Cys Leu Gly Val Leu Gly Thr Gln Ile			
1	5	10	15
Phe Lys Gln Glu Thr Pro Arg Gln Leu Pro Ile Val Val Val Asp Leu			
	20	25	30
Asp Lys Thr Thr Thr Ser His Gln Val Ala Phe Glu Leu Gly Ala Thr			
35	40	45	

Ser Ala Val Glu Ile Lys Tyr Gln Val Thr Ser Leu Ser Glu Ala Lys
50 55 60

Arg Phe Leu Asn Ser Ala Glu Val Tyr Gly Ala Leu Ile Leu Pro Lys
65 70 75 80

Asp Leu Glu Arg Lys Ile Lys Met Gly Arg Lys Val Xaa Phe Ala Leu
85 90 95

Leu Leu

(2) INFORMATION FOR SEQ ID NO:757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

Met Lys Gly Leu Trp Leu Val Ile Ser Leu Val Phe Val Gly Phe Leu
1 5 10 15

Trp Ala Asn Glu Ser Tyr Val Phe Asn Asn Ser Lys Gly Arg Leu Thr
20 25 30

Glu Lys Ser Val Ala Phe Ile Glu Gly Val Ser Lys Glu Leu Tyr Leu
35 40 45

Lys Thr Gly Val Arg Phe Ala Ile Asp Met Thr Asp Phe Glu Lys Asn
50 55 60

Pro Ile Ala Leu Ala Asn Lys Lys Glu Arg Gln Ser Tyr Gln Glu Gly
65 70 75 80

Phe Leu Lys Gln Leu Lys Pro Pro Phe Val Val Phe Phe Phe Tyr His
85 90 95

Asp Ala Gln Lys Ile Glu Leu Val Ala Asn Pro Lys Asp Leu Leu Asp
100 105 110

Thr Asp Lys Ile Phe Phe Glu Lys Ile Ala Pro Leu Leu Pro Thr Asn
115 120 125

Ala Lys Glu Tyr Thr Pro Gln Arg Ile Ser Ala Met Leu Ile Asn Gly
130 135 140

Tyr Ser Val Ala Val Asp Ala Leu Ala Glu Lys Tyr His Val Asn Ile
145 150 155 160

Thr Gln Asn Phe Ser Ala Pro Lys Gly Val Thr Phe Val Lys Val Val
165 170 175

Ile Tyr Ile Leu Leu Leu Thr Leu Leu Gly Ala Phe Leu Gly Leu Tyr
180 185 190

Phe Phe Lys Lys Ser
195

(2) INFORMATION FOR SEQ ID NO:758:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

Leu Val Gln Ile Val Val Val Phe Tyr Gly Leu Pro Ala Leu Gly Val
1 5 10 15

Tyr Met Asp Pro Ile Pro Ala Gly Ile Ile Ala Phe Ser Phe Asn Val
20 25 30

Gly Ala Tyr Ala Ser Glu Thr Leu Arg Ala Ser Phe Leu Ser Val Pro
35 40 45

Lys Asp Gln Trp Asp Ser Ser Leu Ser Leu Gly Leu Asn Tyr Leu Gln
50 55 60

Thr Phe Trp His Val Ile Phe Phe Gln Ala Leu Lys Val Ala Thr Pro
65 70 75 80

Ser Leu Ser Asn Thr Phe Ile Ser Leu Phe Lys Glu Thr Ser Leu Ala
85 90 95

Ser Val Val Thr Ile Ala Glu Xaa Phe Arg Ile Ala Gln Gln Lys Xaa
100 105 110

Asn Val Ser Tyr Asp Phe Xaa Pro Ile Tyr Leu Glu Xaa Ala Leu Ile
115 120 125

Tyr Trp Leu Phe Cys Leu Val Leu Glu Val Ile Gln Lys Arg Val Glu
130 135 140

Lys Ile Leu Asn
145

(2) INFORMATION FOR SEQ ID NO:759:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

```

Met Cys Ser Lys Lys Ile Arg Asn Leu Ile Leu Cys Phe Gly Phe Ile
1           5           10           15
Leu Ser Leu Cys Ala Glu Glu Asn Ile Thr Lys Glu Asn Met Thr Glu
          20           25           30
Thr Asn Thr Thr Glu Glu Asn Thr Pro Lys Asp Ala Pro Ile Leu Leu
          35           40           45
Glu Glu Lys Arg Ala Gln Thr Leu Glu Leu Lys Glu Glu Asn Glu Val
          50           55           60
Ala Lys Lys Ile
65
  
```

(2) INFORMATION FOR SEQ ID NO:760:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

```

Val Val Ala Asp Glu Val Arg Asn Leu Ala Gly Arg Thr Gln Lys Ser
1           5           10           15
Leu Ala Glu Ile Asn Ser Thr Ile Met Val Ile Val Gln Glu Ile Asn
          20           25           30
Asp Val Ser Ser Gln Met Asn Leu Asn Ser Gln Lys Met Glu Arg Leu
          35           40           45
Ser Asp Met Ser Lys Ser Val Gln Glu Thr Tyr Glu Lys Met Ser Ser
          50           55           60
  
```

Asn	Leu	Ser	Ser	Val	Val	Leu	Asp	Ser	Asn	Gln	Ser	Met	Asp	Asp	Tyr
65					70					75					80
Ala	Lys	Ser	Gly	His	Gln	Ile	Glu	Ala	Met	Val	Ser	Asp	Phe	Ala	Glu
				85					90					95	
Val	Glu	Lys	Val	Ala	Ser	Lys	Thr	Leu	Ala	Asp	Ser	Ser	Asp	Ile	Leu
			100					105					110		
Asn	Ile	Ala	Thr	His	Val	Ser	Gly	Thr	Thr	Met	Asn	Leu	Xaa	Lys	Gln
		115					120					125			
Val	Asn	Leu	Phe	Lys	Thr										

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

Val	Leu	Lys	Thr	Leu	Ser	Ile	Arg	Leu	Val	Ile	Leu	Leu	Asn	Cys	Ser
1				5					10					15	
Leu	Ala	Thr	Asn	Ala	Cys	Ser	Gly	Val	Gln	Lys	Leu	Arg	Asp	Glu	Ser
			20					25					30		
His	Arg	Tyr	Ala	Ile	Asn	Phe	His	Arg	Ser	Thr	Lys	Leu	Lys	Asn	Met
		35					40					45			
Lys	Gln	Ile	Ala	Leu	Leu	Lys	Glu	Lys	Gly	Ile	Gly	Glu	Ala	Ser	Val
		50				55				60					
Lys	Lys	Leu	Leu	Asp	Tyr	Phe	Gly	Ser	Phe	Glu	Ala	Ile	Glu	Lys	Ala
65				70					75					80	
Ser	Asp	Gln	Glu	Lys	Asn	Ala	Val	Leu	Lys	Lys	Arg	Lys			
				85					90						

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...73
 - (D) OTHER INFORMATION: /note= "SULFATE TRANSPORT ATP-BINDING"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

```

Val Gly Ile Ile Arg Gly Ile Ile His Arg Pro Glu Leu Ile Leu Leu
1           5           10           15
Asp Glu Pro Phe Ser Ala Leu Asp Ser Leu Asn Arg Lys Asn Leu Gln
20           25           30
Asp Leu Ile Lys Glu Ile His Gln Asn Ser Cys Ala Thr Phe Ile Met
35           40           45
Val Thr His Asp Glu Asn Glu Ala Gln Lys Leu Ala Thr Lys Thr Leu
50           55           60
Glu Ile Lys Ala Leu Lys Gln Glu Gln
65           70

```

(2) INFORMATION FOR SEQ ID NO:763:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 268 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

```

Val Ile Phe Ile Ala Thr Ala Asn Asn Ile Asp Arg Ile Pro Ala Pro
1           5           10           15
Leu Arg Asp Arg Met Glu Phe Ile Ser Val Ser Ser Tyr Thr Pro Ser
20           25           30
Glu Lys Glu Glu Ile Ala Lys Asn Tyr Leu Ile Pro Gln Glu Leu Glu
35           40           45
Lys His Ala Leu Lys Pro Ser Glu Val Asp Ile Ser His Glu Cys Leu
50           55           60

```

Lys Leu Ile Ile Glu Lys Tyr Thr Arg Glu Ala Gly Val Arg Asp Leu
 65 70 75 80
 Arg Arg Gln Ile Ala Thr Ile Met Arg Lys Ala Ala Leu Lys Tyr Leu
 85 90 95
 Glu Asp Asn Pro His Lys Lys Gly Arg Thr Lys Lys Ser Glu Asp Lys
 100 105 110
 Asp Lys Lys Gly Gly Asn Glu Glu Asn Glu Lys Arg Gly Glu Ser Lys
 115 120 125
 Asp Phe Cys Val Ser Ile Thr Pro Asp Asn Leu Lys Glu Tyr Leu Glu
 130 135 140
 Arg Met Val Phe Glu Ile Xaa Pro Ile Asp Glu Glu Asn Lys Ile Gly
 145 150 155 160
 Ile Val Asn Gly Leu Ala Trp Thr Pro Val Gly Gly Asp Val Leu Lys
 165 170 175
 Ile Glu Ala Val Lys Ile Arg Gly Lys Gly Glu Leu Lys Leu Thr Gly
 180 185 190
 Ser Leu Gly Asp Val Met Lys Glu Ser Ala Ile Ile Ala Phe Ser Val
 195 200 205
 Val Lys Val Leu Leu Asp Asn Glu Thr Leu Lys Val Pro Lys Ile Pro
 210 215 220
 Ser Glu Thr Asp Ala Glu Asn Xaa Lys Lys Lys Lys Val Leu Lys Val
 225 230 235 240
 Xaa Asn Ala Tyr Asp Leu His Leu His Val Pro Lys Gly Leu Arg Leu
 245 250 255
 Lys Thr Ala Arg Ala Leu Gly Ser Leu Trp Arg Ala
 260 265

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

Met Glu Xaa Xaa Lys Lys Phe Val Ala Leu Gly Leu Leu Ser Ala Val

1		5		10		15									
Leu	Ser	Ser	Ser	Leu	Leu	Ala	Glu	Gly	Asp	Gly	Val	Tyr	Ile	Gly	Thr
			20					25					30		
Asn	Tyr	Gln	Leu	Gly	Gln	Ala	Arg	Leu	Asn	Ser	Asn	Ile	Tyr	Asn	Thr
		35					40					45			
Gly	Asp	Cys	Thr	Gly	Ser	Val	Val	Gly	Cys	Pro	Pro	Gly	Leu	Thr	Ala
	50					55					60				
Asn	Lys	His	Asn	Pro	Gly	Gly	Thr	Asn	Ile	Asn	Trp	His	Ser	Lys	Tyr
65					70					75					80
Ala	Asn	Gly	Ala	Leu	Asn	Gly	Phe	Gly	Leu	Asn	Val	Gly	Tyr	Lys	Lys
				85					90					95	
Phe	Phe	Gln	Phe	Lys	Ser	Leu	Asp	Met	Thr	Ser	Lys	Trp	Phe	Gly	Phe
			100					105					110		
Arg	Val	Tyr	Gly	Leu	Phe	Asp	Tyr	Gly	His	Ala	Asp	Leu	Gly	Lys	Gln
		115					120					125			
Val	Tyr	Ala	Pro	Asn	Lys	Ile	Gln	Leu	Asp	Met	Val	Ser	Trp	Gly	Val
	130					135					140				
Gly	Ser	Xaa	Leu	Leu	Ala	Asp	Ile	Ile	Asp	Xaa	Arg	Gln	Arg	Phe	Phe
145					150				155						160
Trp	Tyr	Phe	Trp	Trp	Gly	Arg	Tyr	Arg	Arg						
			165					170							

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

Met	Asn	Tyr	Asp	Asn	Tyr	Trp	Asp	Glu	Asp	Lys	Pro	Glu	Leu	Asn	Ile
1				5				10					15		
Thr	Pro	Leu	Val	Asp	Val	Met	Leu	Val	Leu	Leu	Ala	Ile	Leu	Met	Val
		20					25					30			
Thr	Thr	Pro	Thr	Leu	Thr	Tyr	Lys	Glu	Glu	Ile	Ala	Leu	Pro	Ser	Gly
	35					40					45				

Ser Lys Thr Ala Arg Ala Thr Gln Asp Lys Val Ile Glu Ile Arg Met
50 55 60

Asp Lys Asp Ala Lys Ile Tyr Ile Asp Ser Gln Thr Tyr Glu Tyr Xaa
65 70 75 80

Ser Phe Pro Asp Thr Phe Asn Leu Leu Ser Lys Lys Tyr Asp Lys Asp
85 90 95

Thr Arg Val Ser Ile Arg Ala Asp Lys Arg Leu Thr Tyr Asp Lys Val
100 105 110

Ile Tyr Leu Leu Lys Thr Ile Lys Glu Ala Gly Phe Leu Lys Val Ser
115 120 125

Leu Ile Thr Ser Pro
130

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

Met Pro Pro Thr Xaa Pro Gln Ala Ser Ile Leu Arg Leu Thr Leu Lys
1 5 10 15

Asn Pro Leu Xaa Xaa Leu Ser Arg Tyr Ser Leu Cys Leu Leu Lys Lys
20 25 30

Thr Arg Leu Gln Thr Thr Ser Asn Ser Ala Pro Lys Ala Cys Leu Ile
35 40 45

Ala Gly Leu Leu Lys Lys Ser Lys Pro Phe Ile Leu Asn Thr Leu Lys
50 55 60

Ile Arg Ser Leu Leu Lys Pro
65 70

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

```

Met Gly Cys Ser Phe Ile Phe Lys Lys Val Arg Val Tyr Ser Lys Met
1           5           10           15

Leu Val Ala Leu Gly Leu Ser Ser Val Leu Ile Gly Cys Ala Met Asn
          20           25           30

Pro Ser Ala Glu Thr Lys Lys Pro Asn Asp Ala Lys Asn Gln Gln Pro
          35           40           45

Val Gln Thr His Glu Arg Met Thr Thr Ser Ser Glu His Val Thr Pro
          50           55           60

Leu Asp Phe Asn Tyr Pro Val His Ile Val Gln Ala Pro Gln Asn His
65           70           75           80

His Val Val Gly Ile Leu Met Pro Arg Ile Gln Val Ser Asp Asn Leu
          85           90           95

Lys Pro Tyr Ile Asp Lys Phe Gln Asp Ala Leu Ile Asn Gln Ile Gln
          100          105          110

Thr Ile Phe Glu Lys Arg Gly Tyr Gln Val Leu Arg Phe Gln Asp Glu
          115          120          125

Lys Ala Leu Asn Val Gln Asp Lys Lys Lys Ile Phe Ser Val Leu Asp
          130          135          140

Leu Lys Gly
145

```

(2) INFORMATION FOR SEQ ID NO:768:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

```

Met Asp Arg Lys Leu Leu Arg Leu Tyr Gln Pro Leu Asn Ala Tyr Ser
1           5           10           15

```

Tyr	Asn	Ser	Asp	Ser	Leu	Phe	Leu	Tyr	Asp	Phe	Ser	Arg	Pro	Phe	Ile			
			20					25					30					
Lys	Asn	Ser	Gly	Ala	Ile	Leu	Asp	Ile	Gly	Ser	Gly	Cys	Gly	Val	Leu			
		35					40					45						
Gly	Leu	Leu	Cys	Ala	Arg	Asp	Asn	Pro	Leu	Ala	Ser	Val	His	Leu	Val			
		50				55					60							
Glu	Lys	Asp	Ser	Lys	Met	Ala	Phe	Cys	Ser	Gln	Lys	Asn	Ala	Leu	Lys			
		65			70				75					80				
Phe	Pro	Asn	Ala	Gln	Val	Phe	Glu	Ser	Asp	Phe	Leu	Asp	Phe	Asn	Pro			
			85					90						95				
Pro	Ile	Leu	Tyr	Asp	Ala	Ile	Val	Cys	Asn	Pro	Pro	Phe	Tyr	Ala	Leu			
			100					105					110					
Gly	Ser	Ile	Lys	Ser	Gln	Ile	Lys	Gly	His	Ala	Arg	His	Gln	Ser	Glu			
		115					120					125						
Leu	Asp	Phe	Ala	Ser	Leu	Val	Ala	Lys	Val	Lys	Lys	Cys	Leu	Lys	Pro			
		130					135					140						

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

Met	Leu	Ser	Ala	Leu	Val	Met	Leu	Pro	Phe	Met	Glu	Val	Phe	Tyr	Tyr			
1				5				10					15					
Phe	Asn	Phe	Pro	Leu	Trp	Leu	Asn	Leu	Phe	Leu	Gly	Gln	Thr	Ile	Gly			
			20				25						30					
Ala	Val	Ile	Phe	Phe	Lys	Leu	Asp	Lys	Leu	Ile	Phe	Ser	Lys	Lys				
		35				40					45							

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

Val Val Ile Ile Val Leu Val Gln Ile Ile Gln Ser Ala Gly Asp Tyr
85 90 95

Val Val Lys Arg Leu Arg Lys Asn Lys Tyr
100 105

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 527 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...527

(D) OTHER INFORMATION: /note= "stringent response-like protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

Met Asn Glu Ile Asp Lys Ser Val Asp Ile Gly Phe Leu Arg Ile Leu
1 5 10 15

Asp Val Ile Lys Lys Val Lys Thr Pro Lys Gly Gly Ile Glu Val Leu
20 25 30

Arg Thr Leu Ile Asp Phe Thr Pro Lys Ile Glu Asn Ala Leu Asn Leu
35 40 45

Ala Thr Lys Ser His Lys Gly Gln Tyr Arg Lys Ser Gly Glu Pro Tyr
50 55 60

Ile Val His Pro Ile Cys Val Ala Ser Val Val Ala Phe Cys Gly Gly
65 70 75 80

Asp Glu Ala Met Val Cys Ala Ala Leu Leu His Asp Val Val Glu Asp
85 90 95

Thr Pro Cys Glu Ile Glu Thr Ile Glu Arg Glu Phe Gly Gln Asp Val
100 105 110

Ala Asn Leu Val Asp Ala Leu Thr Lys Ile Thr Glu Ile Arg Lys Glu
115 120 125

Glu Leu Gly Val Ser Ser Gln Asp Pro Arg Met Val Val Ser Ala Leu
130 135 140

Thr Phe Arg Lys Ile Leu Ile Ser Ala Ile Gln Asp Pro Arg Ala Leu
145 150 155 160

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:

```

Met Asn Thr Ile Ile Arg Tyr Ala Ser Leu Trp Gly Leu Cys Ile Thr
1           5           10           15
Leu Thr Leu Ala Gln Thr Pro Ser Lys Thr Pro Asp Glu Ile Lys Gln
          20           25           30
Ile Leu Asn Asn Tyr Ser His Lys Asn Leu Lys Leu Ile Asp Xaa Pro
          35           40           45
Thr Ser Ser Leu Xaa Ala Thr Pro Gly Phe Xaa Pro Ser Pro Lys Glu
          50           55           60
Thr Ala Thr Thr Ile Asn Gln Glu Ile Ala Lys Tyr His Glu Lys Ser
65           70           75           80
Asp Lys Ala Ala Leu Gly Leu Tyr Glu Leu Leu Lys Gly Ala Thr Thr
          85           90           95
Asn Leu Ser Leu Gln Ala Gln Glu Leu Ser Val Lys Gln Ala Met Glu
          100          105          110
Glu Pro His His Arg Gln Ser Asp Val Phe Ala Tyr Phe Glu Arg Glu
          115          120          125
Leu

```

(2) INFORMATION FOR SEQ ID NO:771:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

```

Met Val Leu Phe Leu Ser Ile Phe Lys Lys Ser Phe Asn Asp Phe Leu
1           5           10           15
Ser Ala Arg Met Leu Leu Ile Asn Leu Gly Pro Ile Leu Leu Ser Leu
          20           25           30

```

Ala	Phe	Phe	Gly	Ala	Ile	Phe	Tyr	Tyr	Asn	Gly	Gly	Ser	Ile	Val	Asn	
		35					40					45				
Tyr	Cys	Gln	Thr	Leu	Leu	Pro	Gln	Ser	Leu	Asn	Asp	Tyr	Ala	His	Ser	
	50					55					60					
Gln	Gly	Phe	Phe	Ala	Gly	Val	Phe	Ala	Trp	Val	Phe	Lys	Ala	Leu	Val	
65					70					75					80	
Tyr	Phe	Leu	Ile	Phe	Trp	Ile	Val	Ile	Leu	Leu	Ser	Leu	Val	Ile	Asn	
			85						90					95		
Ile	Phe	Ala	Ser	Ile	Phe	Tyr	Thr	Pro	Leu	Val	Val	Ser	Tyr	Leu	His	
			100					105					110			
Gln	Lys	Tyr	Tyr	Pro	His	Val	Val	Leu	Glu	Glu	Phe	Gly	Ser	Ile	Leu	
		115					120					125				
Phe	Ser	Ile	Lys	Tyr	Phe	Leu	Lys	Ser	Leu	Thr	Phe	Met	Leu	Leu	Phe	
	130					135					140					
Leu	Ala	Val	Leu	Thr	Pro	Leu	Tyr	Phe	Ile	Pro	Phe	Ile	Gly	Val	Phe	
145					150					155					160	
Gly	Val	Phe	Phe	Ser	Ile	Val	Pro	His	Phe	His	Phe	Phe	Lys	Asn	Thr	
				165					170					175		
Met	Ser	Leu	Asp	Ile	Ala	Ser	Met	Ile	Phe	Asn	His	Gln	Ser	Tyr	Gln	
			180					185					190			
Asn	Leu	Leu	Lys	Gln	His	Arg	Leu	Lys	His	Tyr	Arg	Phe	Ser	Phe	Phe	
		195					200					205				
Cys	Tyr	Leu	Phe	Ser	Leu	Ile	Pro	Phe	Phe	Asn	Phe	Phe	Ala	Thr	Leu	
	210					215					220					
Leu	Gln	Thr	Leu	Lys	Leu	Thr	His	Tyr	Ile	Phe	Ile	Phe	Lys	Glu	Lys	
225					230					235					240	
Glu	Cys															

(2) INFORMATION FOR SEQ ID NO:772:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION: 1...97
 (D) OTHER INFORMATION: /note= "flagellar protein fliS"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

Met	Gln	Tyr	Ala	Asn	Ala	Tyr	Gln	Ala	Tyr	Gln	His	Asn	Arg	Val	Ser
1				5				10						15	
Val	Glu	Ser	Pro	Ala	Lys	Leu	Ile	Glu	Met	Leu	Tyr	Glu	Gly	Ile	Leu
			20					25					30		
Arg	Phe	Ser	Ser	Gln	Ala	Lys	Arg	Cys	Ile	Glu	Asn	Glu	Asp	Ile	Glu
		35					40					45			
Lys	Lys	Ile	Tyr	Tyr	Ile	Asn	Arg	Val	Thr	Asp	Ile	Phe	Thr	Glu	Leu
	50					55					60				
Leu	Asn	Ile	Leu	Asp	Tyr	Glu	Lys	Gly	Gly	Xaa	Val	Ala	Val	Tyr	Leu
65					70					75					80
Thr	Gly	Leu	Tyr	Thr	His	Gln	Ile	Lys	Val	Leu	Thr	Gln	Ala	Asn	Val
				85					90					95	

Glu

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 143 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

Met	Met	Phe	Asp	Asn	Thr	Leu	Ile	Asn	Leu	Phe	Glu	Thr	Ala	Pro	Leu
1				5				10						15	
Leu	Thr	Ser	Leu	Leu	Ala	Gly	Ile	Leu	Thr	Phe	Leu	Ser	Pro	Cys	Val
			20					25					30		
Leu	Pro	Leu	Ile	Pro	Ala	Tyr	Met	Ser	Tyr	Ile	Ser	Gln	Ile	Ser	Leu
	35						40					45			
Glu	Asp	Ile	Lys	Asp	Gly	Lys	Ala	Lys	Arg	Val	Ser	Val	Phe	Leu	Lys
	50					55					60				
Ser	Leu	Met	Phe	Val	Val	Gly	Phe	Ser	Leu	Val	Phe	Leu	Gly	Val	Gly
65					70				75					80	

Met	Ser	Met	Ala	Lys	Leu	Ile	His	Ser	Phe	Ser	Phe	Ser	Trp	Val	Asn	
				85					90					95		
Tyr	Ile	Ala	Gly	Gly	Ile	Val	Ile	Leu	Phe	Gly	Leu	His	Phe	Leu	Gly	
			100					105					110			
Val	Phe	Arg	Phe	Ala	Phe	Leu	Tyr	Lys	Thr	Gln	Ser	Val	Gly	Leu	Ala	
		115					120					125				
Ser	Lys	Ser	Asn	Ser	Met	Gln	Arg	Phe	Thr	Pro	Phe	Phe	Leu	Ala		
	130					135					140					

(2) INFORMATION FOR SEQ ID NO:774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

Met	Pro	Val	Ile	Arg	Val	Leu	Val	Met	Leu	Ala	Thr	Met	Met	Met	Lys	
1				5					10					15		
Leu	Val	Lys	Thr	Ala	Lys	Glu	Lys	Lys	Val	Phe	Lys	Asn	Val	Gly	Ile	
			20					25					30			
Ser	Ile	Met	Gly	Ile	Ala	Phe	Trp	Glu	Ala	Ile	Lys	Asp	Ser	Ile	Lys	
		35					40					45				
Lys	Gln	Ile	Lys	Lys	Ser	Asp	Trp	Ile	Cys	Gly	Asn	Val	Lys	Thr	Ala	
	50					55					60					
Asp	Asp	Tyr	Leu	Lys	Thr	His	Pro	Asn	Ser	Trp	Phe	Asn	Ser	Ala	Ile	
65					70					75					80	
Gly	Val	Thr	Ala	Ile	Thr	Ala	Met	Leu	Met	Asn	Val	Cys	Phe	Ala	Asp	
			85					90						95		
Asp	Gln	Ser	Lys	Lys	Glu	Val	Ala	Gln	Ala	Gln	Lys	Glu	Ala	Glu	Asn	
		100						105					110			
Ala	Arg	Asp	Arg	Ala	Asn	Lys	Ser	Gly	Ile	Glu	Leu	Glu	Gln	Glu	Glu	
		115					120					125				
Gln	Lys	Thr	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Glu	Gln	Glu	Lys	Gln	Lys	
	130					135					140					
Thr	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Glu	Gln	Glu	Lys	Gln	Lys	Thr	Glu	
145					150				155						160	

Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln Ile Lys
165 170 175

Val Glu Gln Glu Gln Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Asn
180 185 190

Asn Thr Gln Lys Asp Leu Val Asn Lys Ala Glu Gln Asn Cys Gln Glu
195 200 205

Asn His Asn Gln Phe Phe Ile Lys Asn
210 215

(2) INFORMATION FOR SEQ ID NO:775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...84
- (D) OTHER INFORMATION: /note= "Plasmodium falciparum gametocyte specific antigen"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

Val Leu Val Val Gly Lys Pro Asn Glu Ser Tyr Ala Asp Thr His Ala
1 5 10 15

Arg Ile Glu His Phe Ile Lys Leu Val Asp Phe Lys Gly Glu Ile Val
20 25 30

Phe Ile Asn Glu Asp Asn Ser Ser Val Glu Ala Tyr Glu Asn Leu Glu
35 40 45

His Leu Gly Lys Lys Asn Lys Arg Ile Ala Thr Lys Asp Gly Arg Leu
50 55 60

Asp Ser Leu Ser Ala Cys Arg Ile Leu Glu Arg Tyr Cys Gln Gln Val
65 70 75 80

Leu Lys Lys Gly

(2) INFORMATION FOR SEQ ID NO:776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

Met	Val	Ile	Ser	Gly	His	Phe	Thr	Thr	Tyr	Ser	Tyr	Ile	Glu	Pro	Phe
1				5					10					15	
Ile	Ile	Gln	Ile	Ser	Gln	Phe	Ser	Pro	Asp	Ile	Thr	Thr	Leu	Met	Leu
			20					25					30		
Phe	Val	Phe	Gly	Leu	Ala	Gly	Val	Val	Gly	Ser	Phe	Leu	Phe	Gly	Arg
		35					40					45			
Leu	Tyr	Ala	Lys	Asn	Ser	Arg	Lys	Phe	Ile	Ala	Phe	Ala	Met	Val	Leu
	50					55					60				
Val	Ile	Cys	Pro	Gln	Pro	Leu	Ala	Phe	Cys	Val					
65					70				75						

(2) INFORMATION FOR SEQ ID NO:777:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777

Met	Arg	Ile	Leu	Ile	Leu	Lys	Asn	Lys	Pro	Pro	Thr	Leu	Arg	Ser	Lys
1				5					10					15	
Ala	Leu	Thr	Arg	Ser	Trp	Gly	Ile	Asn	Phe	Ser	Leu	Lys	Asn	Thr	Leu
			20					25					30		
Ala	Tyr	Ala	Phe	Met	Gly	Phe	Phe	Asp	Tyr	Ala	His	Ala	Asn	Ser	Ile
		35					40					45			
Lys	Leu	Lys	Asn	Pro	Asn	Tyr	Asn	Ser	Glu	Ala	Ala	Gln	Val	Ala	Ser
	50					55					60				
Gln	Ile	Leu	Gly	Lys	Gln	Glu	Ile	Asn	Arg	Leu	Thr	Asn	Ile	Ala	Asp
65					70				75					80	

Pro Arg Thr Phe Glu Pro Asn Met Leu Thr Tyr Gly Gly Ala Met Asp
85 90 95

Val Met Val Asn Val Ile Asn Asn Gly Ile Met Ser Leu Gly Ala Phe
100 105 110

Gly Gly Ile Gln Leu Ala Gly Asn Ser Trp Leu Met Ala Xaa Pro Ser
115 120 125

Phe Glu Gly Ile Leu Gly Glu Gln Ala Leu Val Ser Arg Lys Pro Leu
130 135 140

Leu Ser Asn Phe Tyr Ser Met Trp Gly Leu Ala
145 150 155

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

Met Lys Ser Thr Arg Ile Gly Ser Lys Ile Val Met Met Val Cys Ala
1 5 10 15

Val Val Ile Val Ile Ser Ala Val Met Gly Val Ile Ile Ser Tyr Lys
20 25 30

Val Glu Ser Val Leu Gln Ser Gln Ala Thr Glu Leu Leu Gln Lys Lys
35 40 45

Ala Gln Leu Val Ser Phe Lys Ile Gln Gly Ile Met Lys Arg Ile Phe
50 55 60

Met Gly Ala Asn Thr Leu Glu Arg Phe Leu Ser Asp Glu Asn Gly Ala
65 70 75 80

Ile Asn Asp Thr Leu Lys Arg Arg Met Leu Ser Glu Phe Leu Leu Ala
85 90 95

Asn Pro His Val Leu Leu Val Ser Ala Ile Tyr Thr Asn Asn Asn Glu
100 105 110

Arg Met Ile Thr Ala Met Asn Met Asp Ser Lys Ile Ala Tyr Pro Asn
115 120 125

Thr Ala Leu Asn Glu Asn Met Thr Xaa Pro Ile His Ser Leu Lys Ser

130		135		140
Ile Thr Arg Ser Xaa Pro Tyr Tyr Lys Glu Val Asn Xaa Xaa Lys Ile				
145		150		155
				160
Tyr Xaa Xaa Xaa Ile Thr Leu Pro Leu Xaa Xaa Lys Asn Xaa Asn Xaa				
	165		170	175
Ile Xaa Xaa Leu Asn Phe Xaa Leu Asn Ile Asp Xaa Phe Leu Tyr Xaa				
	180		185	190

(2) INFORMATION FOR SEQ ID NO:779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

Met Asn Val Lys Lys Lys Glu Lys Pro Gln Ser Gly Lys Ile Asp Arg		
1	5	10
		15
Val Asp Cys Leu Glu Lys Leu Gly Lys Glu Asn Thr Thr Phe Leu Ser		
	20	25
		30
Ser Ile Ala Met Gly Ser Ile Gly Gln Leu Ala Ile Pro Ile Pro Gly		
	35	40
		45
Val Gly Val Leu Ile Gly Gly Phe Val Gly Gly Val Met Ser Lys Thr		
	50	55
		60
Phe Tyr Asp Val Ser Leu Thr Ile Phe Lys Glu Ala Lys Leu Ala Arg		
65	70	75
		80
Gln Arg Arg Ile Glu Ile Glu Lys Glu Cys Arg Glu Ser Ile Arg Gln		
	85	90
		95
Leu Glu Met Tyr Gln Asn Gln Phe Asn Glu Val Phe Glu Arg Tyr Phe		
	100	105
		110
His Gly Thr Ile Lys Phe Phe Asn Glu Ser Phe Asp Glu Leu Glu Arg		
	115	120
		125
Ala Leu Cys Ala Gly Asp Ala Asp Leu Ala Ile Ala Val Asn Asn Lys		
	130	135
		140
Ile Gln Glu Gly Met Gly Gln Glu Leu Leu Phe Asp Asn Lys Gln Glu		
145	150	155
		160

Cys Trp Glu Phe Ile Thr Ser Arg Lys Glu Gly
 165 170

(2) INFORMATION FOR SEQ ID NO:780:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

Met	Trp	Pro	Xaa	Lys	Leu	Phe	Leu	Lys	Pro	Leu	Lys	Glu	Thr	Ser	Leu	1	5	10	15
Ala	Leu	Val	Gly	Val	Ala	Lys	Asn	Ile	Lys	Ile	Val	Ala	Leu	Lys	Ala	20	25	30	
Gly	Leu	Lys	Arg	Ala	Tyr	Leu	Pro	Asn	Arg	Ser	Leu	Ile	Phe	Phe	Leu	35	40	45	
Ile	Lys	Arg	Tyr	Leu	Arg	Phe	Asp	Lys	Ser	Gln	Pro	Phe	Ile	Ser	Ile	50	55	60	
Thr	Ala	Leu	Leu	Ala	Phe	Phe	Gly	Val	Ala	Val	Gly	Val	Met	Val	Leu	65	70	75	80
Ile	Val	Ala	Met	Ala	Ile	Met	Asn	Gly	Met	Ser	Lys	Glu	Phe	Glu	Lys	85	90	95	
Lys	Leu	Phe	Val	Met	Asn	Tyr	Pro	Leu	Thr	Leu	Tyr	Thr	Thr	Ser	Pro	100	105	110	
Tyr	Gly	Ile	Ser	Glu	Glu	Val	Val	Gln	Ala	Leu	Glu	Lys	Lys	Phe	Pro	115	120	125	
Asn	Leu	Pro	Phe	Ser	Xaa	Pro	Ile	Cys	Lys	Pro	Lys	Ala	130	135	140				

(2) INFORMATION FOR SEQ ID NO:781:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

Met Val Ser Leu Leu Gly Ala Leu Lys Arg Thr Pro Cys Thr Asn Arg
1 5 10 15
Phe Tyr Leu Lys Ala Leu Leu Phe Ala Ile Phe Tyr His Ala Val Asn
20 25 30
Asn Phe Leu Thr Gln Cys Pro Pro His Gln Val Arg Glu Phe Phe Ser
35 40 45
Ser Arg His Ala Gln Gly Trp Lys Arg Glu Thr Leu Pro Cys Ala Leu
50 55 60
Ser Phe Gln Asn Ala Leu
65 70

(2) INFORMATION FOR SEQ ID NO:782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

Val His His Leu Xaa Arg Leu Leu Asp Ser Gly Ser Glu Arg Cys Ile
1 5 10 15
Gly Cys Gly Leu Cys Glu Lys Ile Cys Thr Ser Asn Cys Ile Arg Ile
20 25 30
Ile Thr His Lys Gly Glu Asp Asn Arg Lys Lys Ile Asp Ser Tyr Thr
35 40 45
Ile Asn Leu Gly Arg Cys Ile Tyr Cys Gly Leu Cys Ala Glu Val Cys
50 55 60
Pro Glu Leu Ala Ile Val Met Gly Asn Arg Phe Glu Asn Ala Ser Thr
65 70 75 80
Gln Arg Ser Gln Tyr Gly Ser Lys Ser Glu Phe Leu Thr Ser Glu Gln
85 90 95
Asp Ala Lys Asn Cys Ser His Ala Glu Phe Leu Gly Phe Gly Ala Val
100 105 110

Ser Pro Asn Tyr Asn Glu Arg Met Gln Ala Thr Pro Leu Asp Tyr Val
115 120 125

Gln Glu Pro Ser Lys Glu Glu Ser Lys Glu Glu Phe Xaa Thr Ser Pro
130 135 140

Glu Ser His Lys Gly Asp Glu Asn Val
145 150

(2) INFORMATION FOR SEQ ID NO:783:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

Met Ala Ile Trp Gly Trp Cys Phe Leu Phe Leu Ser Ser Leu Met Trp
1 5 10 15

Gly Ser Ser Met His Glu Leu Val Leu Arg Ser Gln Ala Leu Gly Phe
20 25 30

Glu Thr Arg Leu Val Gln Cys Asp Leu Ser Phe Ser Tyr Glu Arg Phe
35 40 45

Ile Ser Lys Thr Lys Arg Ser Leu Ala Val Leu Glu Glu Phe Asp Trp
50 55 60

Leu Asn Ser Gly Phe Asp Phe Ser Arg Leu Asn Val Glu Asn Asp Thr
65 70 75 80

Leu Glu Leu Leu Lys Ala Leu Tyr Phe Lys Leu Glu Lys Leu Glu Ser
85 90 95

Leu Leu Leu Lys Glu Asn Leu Leu Glu Leu Glu Gln Lys Asp Arg Ile
100 105 110

Ile Ala Leu Gly His Gly Leu Val Cys Leu Lys Lys Gln Ser Leu Ile
115 120 125

Ala Pro Gln Thr Tyr Tyr Gly Arg Cys Val Leu Glu Gly Lys Ile Leu
130 135 140

Ala Phe Phe Gly Val Ala Arg Asp Lys Asp Phe Leu Glu Ile Thr Arg
145 150 155 160

Met His Ala Leu Asp Ile Lys Arg Tyr Asp Ser Phe Ile Val Asp Ser

Glu Arg Lys Gly Leu Lys Leu
180

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

Met Pro Glu Asn Ser Lys Leu Gln Pro Ala Lys Leu Gly Lys Asn Phe
1 5 10 15

Asp Pro Val Asp His Ser Asn Arg Asn Phe Phe Phe Ser Leu Ile Leu
20 25 30

Ser Val Leu Leu His Trp Leu Ile Tyr Phe Leu Phe Glu His Arg Glu
35 40 45

Asp Phe Phe Pro Ser Lys Pro Lys Leu Val Lys Leu Asn Pro Glu Asn
50 55 60

Leu Leu Val
65

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

Met Ala Tyr Lys Tyr Asp Arg Asp Leu Glu Phe Leu Lys Gln Leu Glu
1 5 10 15

Ser Ser Asp Leu Leu Asp Leu Phe Glu Val Leu Val Phe Gly Lys Asp

20					25					30						
Gly	Glu	Lys	Arg	His	Asn	Glu	Lys	Leu	Thr	Ser	Ser	Ile	Glu	Tyr	Lys	
35					40					45						
Arg	His	Gly	Asp	Asp	Tyr	Ala	Lys	Tyr	Ala	Glu	Arg	Ile	Ala	Glu	Glu	
50					55					60						
Leu	Gln	Tyr	Tyr	Gly	Ser	Asn	Ser	Phe	Ala	Ser	Phe	Ile	Lys	Gly	Glu	
65					70					75					80	
Gly	Val	Leu	Tyr	Lys	Glu	Ile	Leu	Cys	Asp	Val	Cys	Asp	Lys	Leu	Lys	
85					90					95						
Val	Asn	Tyr	Asn	Lys	Lys	Thr	Glu	Thr	Thr	Leu	Ile	Glu	Gln	Asn	Met	
100					105					110						
Leu	Ser	Lys	Ile	Leu	Glu	Arg	Ser	Leu	Glu	Glu	Met	Asp	Asp	Glu	Glu	
115					120					125						
Val	Lys	Glu	Met	Cys	Asp	Glu	Leu	Ser	Ile	Lys	Asn	Thr	Asp	Asn	Leu	
130					135					140						
Asn	Arg	Gln	Ala	Leu	Ser	Ala	Ala	Thr	Leu	Thr	Leu	Phe	Lys	Met	Gly	
145					150					155					160	
Gly	Phe	Lys	Ser	Tyr	Gln	Leu	Ala	Val	Ile	Val	Ala	Asn	Ala	Val	Ala	
165					170					175						
Lys	Thr	Ile	Leu	Gly	Arg	Gly	Leu	Ser	Leu	Ala	Gly	Asn	Gln	Val	Leu	
180					185					190						
Thr	Arg	Thr	Leu	Ser	Phe	Leu	Thr	Gly	Pro	Val	Gly	Trp	Ile	Ile	Thr	
195					200					205						
Gly	Val	Trp	Thr	Ala	Ile	Asp	Ile	Ala	Gly	Pro	Ala	Tyr	Arg	Val	Thr	
210					215					220						
Ile	Pro	Ala	Cys	Ile	Val	Val	Ala	Thr	Leu	Arg	Leu	Lys	Thr	Gln	Gln	
225					230					235					240	
Ala	Asn	Glu	Asp	Lys	Lys	Ser	Leu	Gln	Ile	Glu	Ser	Val				
245					250											

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

Val Phe Leu Val Gln Ser Trp Ala Leu Ser Leu Lys Ile Asp Ser Leu
1 5 10 15
Phe Ser Leu Phe Ser Val Gly Lys Ile Pro Ser Gly Ser Lys Asp Pro
 20 25 30
Phe Ala Leu Arg Arg Leu Ser Phe Gly Leu Leu Lys Ile Ile Ala His
 35 40 45
Tyr Gly Leu Glu Phe Asp Leu Lys Ala Asp Leu Lys Asn Leu Phe Glu
 50 55 60
Lys Val Gly Val Tyr Gln Ser Phe Asp Leu Glu Val Leu Glu Lys Phe
65 70 75 80
Leu Leu Glu Arg Phe His Asn Leu Ile Asp Cys Asn Leu Ser Ile Ile
 85 90 95
Arg Ser Val Leu Asn Thr Asn Glu Arg Asp Ile Val Lys Ile Ile Gln
 100 105 110
Lys Val Lys Ala Leu Lys Arg Phe Leu Asp Asn Pro Lys Asn Ala Gln
 115 120 125
Lys Lys Glu Leu Leu Phe Ser Ala Phe Lys Arg Leu Ala Asn Ile Asn
 130 135 140
Lys Asp Arg Asn Pro Asn Glu Ser Ser Gly Phe Ser Thr Ser Leu Phe
145 150 155 160
Lys Glu Leu Gln Glu His Ala Leu Phe Glu Ala Phe Asn
 165 170

(2) INFORMATION FOR SEQ ID NO:787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

Met Ser Leu Ala Pro Ser Val Met Ala Gly Phe Leu Phe Cys Ala Gly
1 5 10 15
Ser Cys Ser Leu Arg Phe Pro Asn Tyr Ser Lys Ile Ile Ser Ile Asp
 20 25 30

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

Leu	Leu	Leu	Phe	Ile	Val	Val	Ile	Thr	Ser	Leu	Val	Lys	Asn	Thr	Ile	
1				5					10						15	
Pro	Asn	Ile	Trp	Leu	Thr	Lys	Ile	Leu	Tyr	Met	Ala	Ile	Leu	Leu	Cys	
			20					25					30			
Ala	Ile	Ala	His	Ser	Val	Gly	Xaa	Ile	Leu	Arg	Trp	Tyr	Val	Ser	Gly	
		35					40					45				
His	Ser	Pro	Trp	Ser	Asn	Ala	Tyr	Glu	Ser	Met	Phe	Tyr	Ile	Ala	Trp	
	50					55					60					
Ala	Ser	Val	Ile	Ala	Gly	Phe	Val	Leu	Arg	Xaa	Lys	Leu	Ala	Leu	Ser	
65					70					75					80	
Ala	Ser	Ser	Phe	Leu	Ala	Gly	Ile	Ala	Leu	Phe	Val	Ala	His	Leu	Gly	
				85					90					95		
Phe	Met	Asp	Pro	Gln	Ile	Gly	Pro	Leu	Val	Pro	Val	Leu	Lys	Ser	Tyr	
			100					105					110			
Trp	Leu	Asn	Ile	His	Val	Ser	Val	Ile	Thr	Ala	Ser	Tyr	Gly	Phe	Leu	
		115					120					125				
Gly	Leu	Cys	Phe	Val	Leu	Gly	Ile	Leu	Ser	Leu	Val	Leu	Phe	Ile	Leu	
	130					135					140					
Arg	Lys	Gln	Gly	Arg	Phe	Asn	Leu	Asp	Lys	Thr	Ile	Leu	Ser	Ile	Ser	
145					150					155					160	
Ala	Ile	Asn	Glu	Met	Ser	Met	Ile	Leu	Gly	Leu	Phe	Met	Leu	Thr	Ala	
			165						170					175		
Gly	Asn	Phe	Leu	Gly	Gly	Val	Trp	Ala	Asn	Glu	Ser	Trp	Gly	Arg	Tyr	
		180						185					190			
Trp	Gly	Trp	Asp	Pro	Lys	Glu	Thr	Trp	Ala	Leu	Ile	Ser	Ile	Cys	Val	
		195					200					205				
Tyr	Ala	Leu	Ile	Leu	His	Leu	Arg	Phe	Leu	Gly	Ser	Gln	Asn	Trp	Pro	
	210					215					220					
Phe	Ile	Leu	Ala	Ser	Ser	Ser	Val	Leu	Gly	Phe	Tyr	Ser	Val	Leu	Met	
225					230					235					240	
Thr	Leu	Phe	Trp	Arg	Glu	Leu	Leu	Pro	Phe	Trp	Leu	Ala	Gln	Leu	Cys	
			245						250					255		
Arg	Arg	Xaa	Ser	Phe	Ala	Asp	Pro	Tyr	Phe	Phe	Ile	Leu	Phe	Gly	Ser	
		260						265					270			
Asp	Thr	Phe	Arg	Ser	Arg	Ile	Leu	Ala	Tyr	Phe	Lys	Arg	His	Leu	Ser	
	275						280					285				

Leu Pro Lys Leu Val
290

(2) INFORMATION FOR SEQ ID NO:789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...194
- (D) OTHER INFORMATION: /note= "GLUTATHIONE-REGULATED POTASSIUM-EFFLUX SYSTEM PROTEIN"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

Val	Ile	Val	Cys	Ser	Ala	Ala	Gly	Leu	Ser	His	Phe	Phe	Gly	Phe	Ser	
1				5				10					15			
Met	Ser	Leu	Gly	Ala	Phe	Ile	Val	Gly	Met	Ala	Ile	Ser	Lys	Ser	Arg	
		20						25					30			
Tyr	Lys	Ile	Asn	Val	Gln	Glu	Glu	Phe	Ala	Gln	Leu	Lys	Asn	Leu	Phe	
		35					40					45				
Leu	Ala	Leu	Phe	Phe	Ile	Thr	Ile	Gly	Met	Gln	Ile	Asn	Val	Ser	Phe	
	50					55					60					
Phe	Met	Glu	Lys	Phe	Phe	Val	Val	Ile	Phe	Leu	Leu	Ile	Leu	Val	Met	
65					70				75					80		
Ser	Phe	Lys	Thr	Phe	Ile	Ile	Tyr	Ala	Leu	Leu	Arg	Phe	Phe	Arg	Asp	
			85					90						95		
Ala	Lys	Thr	Ala	Ile	Lys	Thr	Ala	Leu	Ser	Leu	Ala	Gln	Ile	Gly	Glu	
		100						105					110			
Phe	Ser	Phe	Val	Ile	Phe	Leu	Asn	Ser	Gly	Ser	His	Gln	Leu	Phe	Asn	
	115						120					125				
Leu	Gln	Glu	Lys	Lys	Gly	Ile	Leu	Gly	Phe	Leu	His	Gln	Lys	Asn	Ile	
	130					135					140					
Leu	Asn	Ile	Ala	Gln	Asn	Asp	Ile	His	Gln	Leu	Leu	Ile	Leu	Met	Val	
145					150					155				160		
Val	Phe	Ser	Met	Leu	Ala	Thr	Pro	Phe	Ile	Leu	Lys	Tyr	Leu	Glu	Ser	
			165					170						175		

Ile Ala Gln Phe Ile Leu His Gln Lys Ser Gln Glu Asn Glu Pro Ala
180 185 190

Lys Lys

(2) INFORMATION FOR SEQ ID NO:790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

Met Phe Tyr Leu Ile Asn Thr Gly Val Pro His Leu Val Gly Phe Val
1 5 10 15

Lys Asn Lys Gly Leu Leu Asn Ser Leu Asn Thr Leu Glu Leu Arg Ala
20 25 30

Leu Arg His Glu Phe Asn Ala Asn Ile Asn Ile Ala Phe Ile Glu Asn
35 40 45

Lys Glu Thr Ile Phe Leu Gln Thr Tyr Glu Arg Gly Val Glu Asp Phe
50 55 60

Thr Leu Ala Cys Gly Thr Gly Met Ala Ala Val Phe Ile Ala Ala Arg
65 70 75 80

Leu Phe His Asn Thr Pro Lys Lys Ala Thr Leu Ile Pro Lys Ser Asn
85 90 95

Glu Phe Leu Glu Leu Ser Leu Lys Asn Asp Gly Ile Phe Tyr Lys Gly
100 105 110

Val Ala Arg Tyr Ile Gly Met Ser Val Leu Gly Met Gly Val Phe Lys
115 120 125

Asn Gly Cys Phe
130

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...213
 - (D) OTHER INFORMATION: /note= "hypothetical abc transporter
n tesA region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

```

Met Ile Lys Ala Ile Asp Ile Ser His Asp Phe Glu Lys Pro Leu Tyr
1           5           10           15

Asn Gly Val Asn Leu Arg Ile Lys Pro Lys Glu Ser Met Glu Ile Leu
20           25           30

Gly Val Ser Gly Ser Gly Lys Ser Thr Leu Ile Ser His Leu Ala Thr
35           40           45

Met Leu Lys Pro Asp Ser Gly Thr Val Ser Leu Leu Glu His Gln Asp
50           55           60

Ile Tyr Ala Leu Asn Ser Lys Lys Leu Leu Glu Leu Arg Arg Leu Lys
65           70           75           80

Val Gly Ile Val Phe Gln Ser His Tyr Leu Phe Lys Gly Phe Ser Ala
85           90           95

Leu Glu Asn Leu Gln Val Ala Ser Ile Leu Ala Lys Gln Glu Ile Asn
100          105          110

His Ser Leu Leu Glu Gln Leu Gly Ile Ala His Thr Leu Lys Gln Gly
115          120          125

Val Gly Glu Leu Ser Gly Gly Gln Gln Gln Arg Leu Ser Ile Ala Arg
130          135          140

Val Leu Ser Lys Lys Pro Gln Ile Ile Ile Ala Asp Glu Pro Thr Gly
145          150          155          160

Asn Leu Asp Thr Thr Ser Ala Asn Gln Val Ile Ser Met Leu Gln Asn
165          170          175

Tyr Ile Thr Glu Asn Glu Gly Ala Leu Val Leu Ala Thr His Asp Glu
180          185          190

His Leu Ala Phe Thr Cys Ser Gln Val Tyr Arg Leu Glu Lys Glu Ser
195          200          205

Leu Ile Lys Glu Lys
210

```

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

```
Met Leu Asp Lys Arg Ile Lys Thr Leu Leu Leu Phe Phe Gly Leu Asn
1           5           10           15
Met Val Cys Leu Ser Val Ser Phe Thr Asn Lys Pro His Leu Cys Phe
          20           25           30
Trp Phe Leu Val Leu Gly Cys Tyr Leu Val Tyr Glu Trp Gln Lys
          35           40           45
```

(2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

```
Val Glu Met Ile His Thr Gln Asp Tyr Ile Lys Met Glu Glu Ala Ala
1           5           10           15
Thr Glu Ala Ile Lys Arg Lys Glu Ser Ser Ile Tyr Leu Gly Met Asp
          20           25           30
Ile Leu Lys Asn Gly Ala Asp Ala Leu Ile Ser Ala Gly His Ser Gly
          35           40           45
Ala Thr Met Gly Leu Ala Thr Leu Arg Leu Gly Arg Ile Lys Gly Val
          50           55           60
Glu Arg Pro Ala Ile Cys Thr Leu Met Pro Ser Val Gly Lys Arg Pro
          65           70           75           80
Ser Val Leu Leu Asp Ala Gly Ala Asn Thr Asp Cys Lys Pro Glu Tyr
```

85

90

95

Leu Ile Asp Phe Ala Leu Met Gly Tyr Glu Tyr Ala Lys Ser Val Leu
 100 105 110

His Tyr Asp Ser Pro Lys Val Gly Leu Leu Ser Asn Gly Glu Glu Asp
 115 120 125

Ile Lys Gly Gly Ile Arg Ser Leu Lys Lys Arg Ile Lys Cys
 130 135 140

(2) INFORMATION FOR SEQ ID NO:794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

Met Lys Thr Ile Lys Asn Gly Ile Met Ile Gly Thr Leu Gly Ala Leu
 1 5 10 15

Leu Leu Ser Gly Cys Ser Ser Phe Asp Ala Gln Arg Phe Ala Cys Leu
 20 25 30

Pro Lys Asp His Ser Ser Lys Asp Ala Ser Thr Lys Lys Glu Ala Gln
 35 40 45

Tyr Ile Pro Lys Gly Phe Phe Asp Pro Tyr Ser Ser Asn Leu Asn His
 50 55 60

Trp Asp Ser Thr Phe
 65

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

Met Leu Glu Ile Lys Asn Leu Asn Cys Val Leu Asn Ser His Phe Ser
1 5 10 15
Leu Gln Asn Ile Asn Ile Ser Leu Ser Tyr Ser Glu Arg Val Ala Ile
 20 25 30
Val Gly Glu Ser Gly Ser Gly Lys Ser Ser Ile Ala Asn Leu Val Met
 35 40 45
Arg Leu Asn Pro Arg Phe Lys Ser His Asn Gly Glu Ile Leu Phe Glu
 50 55 60
Thr Thr Asn Leu Leu Lys Glu Ser Glu Ala Phe Xaa Gln His Leu Arg
65 70 75 80
Gly Asn Ile Ile Ala Tyr Ile Ala Gln Asp Pro Leu Ser Ser Leu Asn
 85 90 95
Pro Leu His Lys Ile Gly Lys Gln Met Ser Glu Ala Tyr Phe Leu His
 100 105 110
His Lys Asn Ala Ser Gln Val Ser Leu Asn Glu Gln Val Leu Asn Val
 115 120 125
Met Lys Gln Val Gln Leu Asp Glu Asn Phe Trp Asn Val Ser Leu Met
 130 135 140

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...190
- (D) OTHER INFORMATION: /note= "E.coli mreD gene Rod shape-determining protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

Met Glu Leu Ile Leu Gly Ser Gln Ser Ser Ala Arg Ala Asn Leu Leu
1 5 10 15
Lys Glu His Gly Ile Lys Phe Glu Gln Lys Ala Leu Tyr Phe Asp Glu
 20 25 30

Glu	Ser	Leu	Lys	Thr	Thr	Asp	Pro	Arg	Glu	Phe	Val	Tyr	Leu	Ala	Cys			
		35					40					45						
Lys	Gly	Lys	Leu	Glu	Lys	Ala	Lys	Glu	Leu	Leu	Ala	Asn	Asn	Cys	Ala			
	50					55					60							
Ile	Val	Val	Ala	Asp	Ser	Val	Val	Ser	Val	Gly	Asn	Arg	Met	Gln	Arg			
65					70					75					80			
Lys	Ala	Lys	Asn	Lys	Arg	Glu	Ala	Leu	Glu	Phe	Leu	Lys	Arg	Gln	Asn			
			85						90					95				
Gly	Asn	Glu	Ile	Glu	Val	Leu	Thr	Cys	Ser	Ala	Leu	Ile	Ser	Pro	Val			
			100					105					110					
Leu	Glu	Trp	Leu	Asp	Leu	Ser	Val	Phe	Arg	Ala	Arg	Leu	Lys	Ala	Phe			
		115					120					125						
Asp	Cys	Ser	Glu	Ile	Glu	Lys	Tyr	Leu	Glu	Ser	Gly	Leu	Trp	Gln	Gly			
	130					135					140							
Ser	Ala	Gly	Cys	Val	Arg	Leu	Glu	Asp	Phe	His	Lys	Pro	Tyr	Ile	Lys			
145					150					155					160			
Ser	Ser	Ser	Lys	Asn	Leu	Ser	Val	Gly	Leu	Gly	Leu	Asn	Val	Glu	Gly			
			165					170						175				
Leu	Leu	Gly	Ala	Leu	Lys	Leu	Gly	Val	Lys	Leu	Ser	Leu	Leu					
		180					185						190					

(2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

Met	Asn	Tyr	Lys	Val	Ala	Ser	Ala	Arg	Asn	Ile	Ala	Thr	Leu	Leu	Phe			
1				5					10					15				
Leu	Phe	Phe	Ser	Gln	Ser	Glu	Ala	Phe	Asp	Leu	Gly	Lys	Ile	Ala	Lys			
			20					25					30					
Ile	Lys	Ala	Gly	Ala	Glu	Ser	Phe	Ser	Lys	Val	Gly	Phe	Asn	Asn	Lys			
		35					40					45						
Pro	Ile	Asn	Xaa	Asn	Lys	Gly	Ile	Tyr	Pro	Thr	Glu	Thr	Phe	Met	Thr			
		50				55					60							

Ile Asn Gly Leu His Ala Gly Gly Phe Tyr Gly Ala Leu Ala Gln Lys
 65 70 75 80

Arg Tyr Gly

(2) INFORMATION FOR SEQ ID NO:798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

Met	Leu	Ile	Leu	Gly	His	Pro	Leu	Ile	Pro	Ser	Ala	Arg	Phe	Val	Phe	1	5	10	15
Ile	Lys	Asn	Thr	Asp	Ala	Ile	His	Ser	Ser	Ala	Asn	Asn	Asp	Ile	Val	20	25	30	
Cys	Phe	Glu	Ala	Asn	Pro	Lys	Asn	Leu	Glu	Leu	Ala	Gln	Tyr	Cys	Cys	35	40	45	
Glu	Asn	Gly	Val	His	Phe	Ser	Val	Ile	Phe	Leu	Ser	His	Lys	Ile	Glu	50	55	60	
Thr	Asp	Thr	Phe	Phe	Leu	Phe	Asn	Ala	Phe	Lys	Pro	Leu	Tyr	Cys	Ile	65	70	75	80
Phe	Lys	Asp	Ile	Lys	Gln	Ala	Ile	Leu	Ala	Gln	Gln	His	Ala	Thr	Asn	85	90	95	
Tyr	Leu	Leu	Asp	Ser	Lys	Ile	Leu	Phe	Ser	Met	Asp	Phe	Asn	Asp	Thr	100	105	110	
Glu	Ser	Trp	Glu	Ile	Cys	Ala	Lys	Asn	Gln	Ile	Asp	Gly	Val	Ile	Ser	115	120	125	
Lys	Asp	Ser	Leu	Leu	Leu	Lys										130	135		

(2) INFORMATION FOR SEQ ID NO:799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:

Met	Lys	Lys	Arg	Leu	Asn	Ile	Gly	Leu	Val	Gly	Leu	Gly	Cys	Val	Gly	
1				5					10					15		
Ser	Thr	Val	Ala	Lys	Ile	Leu	Gln	Glu	Asn	Gln	Glu	Ile	Ile	Lys	Asp	
			20					25					30			
Arg	Ala	Gly	Val	Glu	Ile	Lys	Ile	Lys	Lys	Ala	Val	Val	Arg	Asp	Val	
			35					40				45				
Lys	Lys	His	Lys	Gly	Tyr	Ala	Phe	Glu	Ile	Ser	Asp	Asp	Leu	Glu	Ser	
	50					55					60					
Val	Ile	Glu	Asp	Lys	Gly	Ile	Asp	Ile	Val	Val	Glu	Leu	Met	Gly	Gly	
65					70				75					80		
Val	Glu	Ala	Pro	Tyr	Leu	Leu	Ala	Lys	Lys	Thr	Leu	Ala	Lys	Gln	Lys	
				85					90					95		
Ala	Phe	Val	Thr	Ala	Asn	Lys	Ala	Met	Leu	Ala	Tyr	His	Arg	Tyr	Glu	
			100					105					110			
Leu	Glu	Gln	Ile	Ala	Lys	Asn	Thr	Pro	Ile	Gly	Phe	Glu	Ala	Ser	Val	
		115					120					125				
Cys	Gly	Gly	Ile	Pro	Ile	Ile	Lys	Ala	Leu	Lys	Asp	Gly	Leu	Ser	Ala	
	130					135					140					
Asn	His	Ile	Leu	Ser	Phe	Lys	Gly	Ile	Leu	Asn	Gly	Thr	Ser	Asn	Tyr	
145					150					155					160	
Ile	Leu	Ser	Gln	Met	Phe	Lys	Asn	Gln	Ala	Ser	Phe	Lys	Asp	Ala	Leu	
				165					170					175		
Lys	Asp	Ala	Gln	His	Leu	Gly	Tyr	Ala	Glu	Leu	Asn	Pro	Glu	Phe	Asp	
		180						185					190			
Ile	Lys	Gly	Ile	Asp	Ala	Ala	His	Lys	Leu	Leu	Ile	Leu	Ala	Ser	Leu	
	195						200					205				
Ala	Tyr	Gly	Ile	Asp	Ala	Lys	Leu	Glu	Glu	Ile	Leu	Ile	Glu	Gly	Ile	
	210					215					220					
Glu	Lys	Ile	Glu	Pro	Asp	Asp	Met	Glu	Phe	Ala	Lys	Glu	Phe	Gly	Tyr	
225					230					235					240	
Ser	Ile	Lys	Leu	Leu	Gly	Ile	Ala	Lys	Lys	His	Gln	Gly	Leu	His		
				245					250					255		

(2) INFORMATION FOR SEQ ID NO:800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

Met	Gln	Glu	Lys	Arg	Leu	Lys	Ala	Ile	Gln	Asn	Lys	Ile	Ala	Ser	Trp	
1				5					10					15		
Ile	Lys	Glu	Ile	Glu	Ser	Gly	Phe	Ile	Asp	Ala	Leu	Phe	Ser	Lys	Ile	
			20					25					30			
Gly	Pro	Ser	Lys	Met	Leu	Arg	Ser	Lys	Leu	Met	Leu	Ala	Leu	Leu	Asp	
			35				40					45				
Glu	Lys	Thr	Asp	Ala	Ile	Leu	Leu	Asp	Lys	Ala	Leu	Asn	Leu	Cys	Ala	
			50			55					60					
Ile	Val	Glu	Met	Ile	Gln	Thr	Ala	Ser	Leu	Leu	His	Asp	Asp	Val	Ile	
65					70					75					80	
Asp	Lys	Ala	Thr	Met	Arg	Arg	Lys	Leu	Pro	Ser	Ile	Asn	Ala	Leu	Phe	
				85					90					95		
Gly	Asn	Phe	Asn	Ala	Val	Met	Leu	Gly	Asp	Val	Phe	Tyr	Ser	Lys	Ala	
			100					105					110			
Phe	Phe	Glu	Leu	Ser	Lys	Met	Gly	Glu	Ser	Ile	Ala	Gln	Ala	Leu	Ser	
			115				120					125				
Asn	Ala	Val	Leu	Arg	Leu	Ser	Arg	Gly	Glu	Ile	Glu	Asp	Val	Phe	Val	
			130			135					140					
Gly	Glu	Cys	Phe	Asn	Ser	Asp	Lys	Gln	Lys	Tyr	Trp	Arg	Ile	Leu	Glu	
145					150					155					160	
Asp	Lys	Thr	Ala	His	Phe	Ile	Glu	Ala	Ser	Leu	Lys	Ser	Met	Ala	Ile	
				165					170					175		
Leu	Leu	Asn	Lys	Asp	Ala	Lys	Met	Tyr	Ala	Asp	Phe	Gly	Leu	His	Phe	
			180					185					190			
Gly	Met	Ala	Phe	Gln	Ile	Ile	Asp	Asp	Leu	Leu	Asp	Ile	Thr	Gln	Asp	
			195				200					205				
Ala	Asn	Thr	Leu	Gly	Lys	Pro	Asn	Phe	Ser	Asp	Phe	Lys	Glu	Gly	Lys	
			210			215					220					

Thr Thr Leu Pro Tyr Leu Leu Leu Tyr Glu Lys Leu Asn Gln His Glu
 225 230 235 240

Gln Gly Phe

(2) INFORMATION FOR SEQ ID NO:801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

Met	Leu	Gly	Lys	Lys	Asn	Glu	Glu	Val	Leu	Ile	Asp	Glu	Asn	Leu	Val	1	5	10	15
Gly	Gly	Val	Ile	Ala	Leu	Asp	Arg	Leu	Ala	Lys	Leu	Asn	Lys	Ala	Asn	20	25	30	
Arg	Thr	Phe	Lys	Arg	Ala	Phe	Tyr	Leu	Ser	Met	Val	Leu	Asn	Val	Ala	35	40	45	
Ala	Val	Thr	Ser	Ile	Val	Met	Met	Met	Pro	Leu	Lys	Lys	Thr	Asp	Ile	50	55	60	
Phe	Val	Tyr	Gly	Ile	Asp	Arg	Tyr	Thr	Gly	Glu	Phe	Lys	Ile	Val	Lys	65	70	75	80
Arg	Ser	Asp	Ala	Arg	Gln	Ile	Val	Asn	Ser	Glu	Ala	Val	Val	Asp	Ser	85	90	95	
Ala	Thr	Ser	Lys	Phe	Val	Ser	Leu	Leu	Phe	Gly	Tyr	Ser	Lys	Asn	Ser	100	105	110	
Leu	Arg	Asp	Arg	Lys	Asp	Gln	Leu	Met	Gln	Tyr	Cys	Asp	Val	Ser	Phe	115	120	125	
Gln	Thr	Gln	Ala	Met	Arg	Met	Phe	Asn	Glu	Asn	Ile	Arg	Gln	Phe	Val	130	135	140	
Asp	Lys	Val	Arg	Ala	Glu	Ala	Ile	Ile	Ser	Ser	Asn	Ile	Gln	Arg	Glu	145	150	155	160
Lys	Val	Lys	Asn	Ser	Pro	Leu	Thr	Arg	Leu	Thr	Phe	Phe	Ile	Thr	Ile	165	170	175	
Lys	Ile	Thr	Pro	Asp	Thr	Met	Glu	Asn	Tyr	Glu	Tyr	Ile	Thr	Lys	Lys	180	185	190	

Gln Val Thr Ile Tyr Tyr Asp Phe Ala Arg Gly Asn Ser Ser Gln Glu
195 200 205

Asn Leu Ile Ile Asn Pro Phe Gly Phe Lys Val Phe Asp Ile Gln Ile
210 215 220

Thr Asp Leu Gln Asn Glu Gln Thr Val Ser Glu Ile Leu Arg Lys Ile
225 230 235 240

Lys Glu Val Glu Ser Lys Asn Lys Ala Leu Asn Lys
245 250

(2) INFORMATION FOR SEQ ID NO:802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

Met Arg Ala Ile Ala Ile Val Leu Ala Arg Ser Ser Ser Lys Arg Ile
1 5 10 15

Lys Asn Lys Asn Met Ile Asp Phe Phe Asn Lys Pro Met Leu Ala Tyr
20 25 30

Pro Ile Glu Thr Ala Leu Asn Ser Lys Leu Phe Glu Lys Val Phe Ile
35 40 45

Ser Ser Asp Ser Met Glu Tyr Val Asn Leu Ala Lys Asn Tyr Gly Ala
50 55 60

Ser Phe Leu Asn Leu Arg Pro Lys Asn Leu Ala Asp Asp Arg Ala Thr
65 70 75 80

Thr Leu Glu Val Met Ala Tyr His Met Lys Glu Leu Glu Leu Lys Asp
85 90 95

Glu Asp Ile Ala Cys Cys Leu Tyr Gly Val Ser Val Phe Leu Gln Glu
100 105 110

Lys His Leu Gln Asn Ala Phe Glu Thr Leu Lys Gln Asn Gln Asn Thr
115 120 125

Asp Tyr Val Phe Thr Cys Ser Pro Phe Ser Ala Ser Pro Ile Val Leu
130 135 140

Leu Ala Leu Lys Thr Ala Phe Lys Trp Leu Leu Lys Ser Ile Gln Thr
145 150 155 160 165

Arg Ala Arg Lys Ile
165

(2) INFORMATION FOR SEQ ID NO:803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...171
- (D) OTHER INFORMATION: /note= "Cell division inhibitor"

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:803:

Met	Ser	Asn	Gln	Ala	Ser	His	Leu	Asp	Asn	Phe	Met	Asn	Ala	Lys	Asn	
1				5					10					15		
Pro	Lys	Ser	Phe	Phe	Asp	Asn	Lys	Gly	Asn	Thr	Lys	Phe	Ile	Ala	Ile	
			20					25					30			
Thr	Ser	Gly	Lys	Gly	Gly	Val	Gly	Lys	Ser	Asn	Ile	Ser	Ala	Asn	Leu	
		35					40					45				
Ala	Tyr	Ser	Leu	Tyr	Lys	Lys	Gly	Tyr	Lys	Val	Gly	Val	Phe	Asp	Ala	
	50					55					60					
Asn	Ile	Gly	Leu	Ala	Asn	Leu	Asp	Val	Ile	Phe	Gly	Val	Lys	Thr	Gln	
65					70					75					80	
Lys	Asn	Ile	Leu	His	Asp	Leu	Lys	Gly	Glu	Asp	Lys	Leu	Lys	Glu	Ile	
				85					90					95		
Ile	Cys	Glu	Ile	Glu	Pro	Gly	Leu	Cys	Leu	Ile	Pro	Gly	Asp	Ser	Gly	
		100					105						110			
Glu	Glu	Ile	Leu	Lys	Tyr	Ile	Ser	Glu	Ala	Glu	Asp	Phe	Asp	Ser	Phe	
		115					120					125				
Leu	Asp	Glu	Glu	Gly	Val	Leu	Ser	Ala	Leu	Ile	Tyr	Ile	Leu	Ile	Asn	
	130					135					140					
Thr	Phe	Ser	Lys	Asn	Leu	Gly	Pro	Leu	Ser	Gln	Thr	Phe	Leu	Asn	Phe	
145					150					155					160	
Gln	Ser	Phe	Leu	Phe	Ile	Phe	Ile	Gln	Ser	Pro						
			165							170						

(2) INFORMATION FOR SEQ ID NO:804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

Met	Gln	His	Leu	Val	Leu	Ile	Gly	Phe	Met	Gly	Ser	Gly	Lys	Ser	Ser
1				5					10					15	
Leu	Ala	Gln	Glu	Leu	Gly	Leu	Ala	Leu	Lys	Leu	Glu	Val	Leu	Asp	Thr
			20				25						30		
Asp	Met	Ile	Ile	Ser	Glu	Arg	Val	Gly	Leu	Ser	Val	Arg	Gly	Ile	Phe
		35					40					45			
Glu	Glu	Leu	Gly	Glu	Asp	Asn	Phe	Arg	Met	Phe	Glu	Lys	Ile		
		50				55					60				

(2) INFORMATION FOR SEQ ID NO:805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

Met	Ser	Ile	Lys	Glu	Asn	Leu	Glu	Gln	Val	Arg	Asn	Glu	Phe	Lys	Ser
1					5				10					15	
Asp	Glu	Lys	Leu	Leu	Glu	Gly	Ala	Phe	Arg	Leu	Glu	Lys	Phe	Phe	Lys
			20					25					30		
Arg	Tyr	Lys	Trp	Val	Leu	Leu	Phe	Ile	Val	Val	Ala	Phe	Ile	Ala	Tyr
		35					40					45			
Leu	Gly	Asp	Thr	Lys	Leu	Gln	Asp	Tyr	Lys	His	Glu	Gln	Thr	Arg	Glu
		50				55					60				

Arg Ile Thr Gln Ile Tyr Asn Glu Val Leu Glu Ser Pro Asn Asn Ile
 65 70 75 80
 Ala Leu Gln Lys Arg Leu Lys Glu Val Ala Pro Glu Leu Tyr Asp Leu
 85 90 95
 Tyr Gln Phe Ala Arg Ala Ser Glu Arg Asn Asp Ala Asn Glu Phe Lys
 100 105 110
 Arg Leu Ser Gln Ser Ser Asn Glu Ile Val Lys Ala Phe Ala Lys Tyr
 115 120 125
 Ser Tyr Ala Ser Leu Ser Arg Asp Lys Asn Leu Leu Glu Lys Ser Pro
 130 135 140
 Ile Leu Lys Glu Met Ser Ala Leu Gln Glu Val Asn Leu Leu Tyr Glu
 145 150 155 160
 Glu Asn Ser Lys Asp Ala Ile Lys Lys Ala His Gln Ser Leu Ser Thr
 165 170 175
 Ile Pro Leu Ser Ser Ser Leu Tyr Ala Ile Ile Ser Val Leu Lys His
 180 185 190
 Tyr Gly Met Leu Glu Asp Ile
 195

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

Met Asp Ala Leu Glu Ile Thr Gln Lys Leu Ile Ser Tyr Pro Thr Ile
 1 5 10 15
 Thr Pro Lys Glu Cys Gly Ile Phe Glu Tyr Ile Lys Ser Leu Phe Pro
 20 25 30
 Ala Phe Lys Thr Leu Glu Cys Glu Lys Asn Gly Val Lys Asn Leu Phe
 35 40 45
 Leu Tyr Arg Ile Phe Asn Pro Leu Lys Lys His Ala Glu Lys Glu His
 50 55 60
 Ala Lys Glu Lys His Val Lys Glu Asn Val Xaa Pro Leu His Phe Cys

65		70		75		80									
Xaa	Ala	Gly	His	Ile	Xaa	Val	Val	Pro	Pro	Gly	Xaa	Xaa	Xaa	Xaa	Xaa
				85					90					95	
Asp	Ser	Phe	Xaa	Xaa	Ile	Ile	Lys	Glu	Gly	Phe	Leu	Tyr	Gly	Arg	Gly
			100					105					110		
Ala	Gln	Asp	Met	Lys	Gly	Gly	Val	Gly	Xaa	Phe	Xaa	Arg	Cys	Xaa	Xaa
		115					120					125			
Lys	Phe														
	130														

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

Val	His	Phe	Asn	Gln	Val	Val	Leu	Pro	Lys	Gly	Val	Gly	Ala	Ile	Leu
1				5					10					15	
Val	Ala	Pro	Lys	Gly	Pro	Gly	Ser	Ala	Leu	Arg	Glu	Glu	Tyr	Leu	Lys
			20					25					30		
Asn	Arg	Gly	Leu	Tyr	His	Leu	Ile	Ala	Ile	Glu	Gln	Glu	Ser	Ser	Ile
		35					40					45			
His	Asn	Ala	Lys	Ala	Val	Ala	Leu	Ser	Tyr	Ala	Lys	Ala	Met	Gly	Gly
	50					55				60					
Gly	Arg	Met	Gly	Val	Leu	Glu	Thr	Ser	Phe	Lys	Glu	Glu	Cys	Glu	Ser
65					70				75					80	
Asp	Leu	Phe	Gly	Glu	Gln	Ala	Val	Leu	Cys	Gly	Gly	Leu	Glu	Val	Asp
			85					90					95		
Arg	Lys	Asn	Gly	Val											
			100												

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

Met	Lys	Lys	Phe	Phe	Ser	Gln	Ser	Leu	Leu	Ala	Leu	Ile	Ile	Ser	Met
1				5				10						15	
Asn	Ala	Val	Ser	Gly	Met	Asp	Gly	Asn	Gly	Val	Phe	Leu	Gly	Ala	Gly
			20					25					30		
Tyr	Leu	Gln	Gly	Gln	Ala	Gln	Met	His	Ala	Asp	Ile	Asn	Ser	Gln	Lys
		35					40					45			
Gln	Ala	Thr	Asn	Ala	Thr	Ile	Lys	Gly	Phe	Asp	Ala	Leu	Leu	Gly	Tyr
	50					55					60				
Gln	Phe	Phe	Phe	Glu	Lys	His	Phe	Gly	Leu	Arg	Leu	Tyr	Gly	Val	Phe
65					70					75					80

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...447

(D) OTHER INFORMATION: /note= "penicillin binding protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

Met	Leu	Lys	Lys	Ile	Phe	Tyr	Gly	Phe	Ile	Val	Leu	Phe	Leu	Ile	Ile
1				5				10						15	
Val	Gly	Leu	Leu	Ala	Val	Leu	Val	Ala	Gln	Val	Trp	Val	Thr	Thr	Asp
			20					25					30		
Lys	Asp	Ile	Ala	Lys	Ile	Lys	Asp	Tyr	Arg	Pro	Ser	Val	Ala	Ser	Gln
		35					40					45			
Ile	Leu	Asp	Arg	Lys	Gly	Arg	Leu	Ile	Ala	Asn	Ile	Tyr	Asp	Lys	Glu

50						55						60					
Phe	Arg	Phe	Tyr	Ala	Arg	Phe	Glu	Glu	Ile	Pro	Pro	Arg	Phe	Val	Glu		
65					70					75					80		
Ser	Leu	Leu	Ala	Val	Glu	Asp	Thr	Leu	Phe	Phe	Glu	His	Gly	Gly	Ile		
			85						90					95			
Asn	Leu	Asp	Ala	Val	Met	Arg	Ala	Met	Ile	Lys	Asn	Ala	Lys	Ser	Gly		
			100					105					110				
Arg	Tyr	Thr	Glu	Gly	Gly	Ser	Thr	Leu	Thr	Gln	Gln	Leu	Val	Lys	Asn		
		115					120						125				
Met	Val	Leu	Thr	Arg	Glu	Lys	Thr	Leu	Thr	Arg	Lys	Leu	Lys	Glu	Ala		
	130					135					140						
Ile	Ile	Ser	Ile	Arg	Ile	Glu	Lys	Val	Leu	Ser	Lys	Glu	Glu	Ile	Leu		
145					150					155					160		
Glu	Arg	Tyr	Leu	Asn	Gln	Thr	Phe	Phe	Gly	His	Gly	Tyr	Tyr	Gly	Val		
				165					170					175			
Lys	Thr	Ala	Ser	Leu	Gly	Tyr	Phe	Lys	Lys	Pro	Leu	Asp	Lys	Leu	Thr		
			180					185					190				
Leu	Lys	Glu	Ile	Thr	Met	Leu	Val	Ala	Leu	Pro	Arg	Ala	Pro	Ser	Phe		
		195					200					205					
Tyr	Asp	Pro	Thr	Lys	Asn	Leu	Glu	Phe	Ser	Leu	Ser	Arg	Ala	Asn	Asp		
	210					215						220					
Ile	Leu	Arg	Arg	Leu	Tyr	Ser	Leu	Gly	Xaa	Ile	Ser	Ser	Asn	Glu	Leu		
225					230					235					240		
Lys	Ser	Ala	Leu	Asn	Glu	Val	Pro	Ile	Val	Tyr	Asn	Gln	Thr	Ser	Thr		
				245					250					255			
Gln	Asn	Ile	Ala	Pro	Tyr	Val	Val	Asp	Glu	Val	Leu	Lys	Gln	Leu	Asp		
			260					265					270				
Gln	Leu	Asp	Gly	Leu	Lys	Thr	Gln	Gly	Tyr	Thr	Ile	Lys	Leu	Thr	Ile		
		275					280					285					
Asp	Leu	Asp	Tyr	Gln	Arg	Leu	Ala	Leu	Glu	Ser	Leu	Arg	Phe	Gly	His		
	290					295					300						
Gln	Lys	Ile	Leu	Glu	Lys	Ile	Ala	Lys	Glu	Lys	Pro	Lys	Thr	Asn	Ala		
305					310					315					320		
Ser	Asn	Asp	Lys	Asp	Glu	Asp	Asn	Leu	Asn	Ala	Ser	Met	Ile	Val	Thr		
				325					330					335			
Glu	Thr	Ser	Thr	Gly	Lys	Ile	Leu	Ala	Leu	Val	Gly	Gly	Ile	Asp	Tyr		
			340					345					350				
Lys	Lys	Ser	Ala	Phe	Asn	Arg	Ala	Thr	Gln	Ala	Lys	Arg	Gln	Phe	Gly		
		355					360					365					

Ser Ala Ile Lys Pro Phe Val Tyr Gln Ile Ala Phe Asp Asn Gly Tyr
 370 375 380
 Ser Thr Thr Ser Lys Ile Pro Asp Thr Ala Arg Asn Phe Glu Asn Gly
 385 390 395 400
 Asn Tyr Ser Lys Asn Ser Val Gln Asn His Ala Trp His Pro Ser Asn
 405 410 415
 Tyr Xaa Arg Lys Phe Leu Gly Leu Val Thr Leu Gln Glu Ala Leu Ser
 420 425 430
 His Ser Leu Asn Leu Ala Thr Ile Asn Leu Ala Ile Ala Trp Leu
 435 440 445

(2) INFORMATION FOR SEQ ID NO:810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

Met Asn Asp Thr Thr Glu His His Gly Ser Asn Pro Leu Asn Ala Pro
 1 5 10 15
 Pro Pro Ser Asn Ser Gln Ser Asn Asp Leu Leu Asn Leu Leu Asp Ser
 20 25 30
 Leu Tyr Pro Lys Gly Ser Leu Gly Glu Gln Arg Phe His Glu Ala Leu
 35 40 45
 Lys Asn Gln Glu Glu Leu Lys Asn Ile Leu Ile Glu Ile Glu Lys Leu
 50 55 60
 Pro Gln Glu Lys Arg Tyr Glu Leu Leu Met Gln Ile Gly Gln Ala Lys
 65 70 75 80
 Gln Arg Ile Met Glu Ala Tyr Ala His Ser Phe Leu Gly Tyr Ile Gly
 85 90 95
 Gly Leu Glu His Leu Leu Gly Leu Cys Met Gly Gly Ile Phe Val Leu
 100 105 110
 Phe Ala Ile Tyr Phe Val Phe Leu Arg Thr Ser Lys Asn Thr Glu Leu
 115 120 125
 Val Glu Ser Leu Lys Thr Lys Leu Lys Leu Gln Tyr Phe Tyr Tyr Ala

130		135		140
Phe Gly Val Gly Ala Val Leu Phe Phe Gly Leu Glu Thr Ile Arg Ser				
145		150		155
				160
Ile Tyr Glu Leu Tyr Ile Leu Gly Ile Gly Ser Thr Asn Asp Lys Val				
	165		170	175
Leu Phe Val Leu Lys Asn Ile Cys Phe Ile Gly Met Gly Tyr Leu Ile				
	180		185	190
Tyr Lys Val Ile Lys Val Ile Gly Ile Lys Asn Phe Ile Asn Gly Leu				
	195		200	205
Phe Ala Ser Lys Lys Gln Gly Gly Ala Glu				
	210		215	

(2) INFORMATION FOR SEQ ID NO:811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

Met Met Asp Lys Val Gly Phe Lys Ser Gln Gly Ile Phe Val Met Asp			
1	5	10	15
Ala Ser Lys Arg Asp Gly Arg Leu Asn Ala Tyr Phe Gly Gly Leu Gly			
	20	25	30
Lys Asn Lys Arg Val Val Leu Phe Asp Thr Leu Ile Ser Lys Val Gly			
	35	40	45
Thr Glu Xaa Leu Leu Ala Ile Leu Gly His Glu Leu Gly His Phe Lys			
	50	55	60
Asn Lys Asp Leu Leu Lys Asn Leu Gly Ile Met Gly Gly Leu Leu Ala			
65	70	75	80
Leu Val Phe Ala Leu Ile Ala His Leu Pro Pro Leu Val Phe Glu Gly			
	85	90	95
Phe Asn Val Ser Gln Thr Pro Ala Ser Leu Ile Thr Ile Leu Leu Leu			
	100	105	110
Phe Leu Pro Val Phe Ser Phe Tyr Ala Met Pro Leu Ile Gly Phe Phe			
	115	120	125

Ser	Arg	Lys	Asn	Glu	Tyr	Asn	Ala	Asp	Lys	Phe	Gly	Ala	Ser	Leu	Ser
130						135					140				
Ser	Lys	Glu	Thr	Leu	Ala	Lys	Ala	Leu	Val	Ser	Ile	Val	Asn	Glu	Asn
145					150					155					160
Lys	Ala	Phe	Pro	Tyr	Ser	His	Pro	Phe	Tyr	Val	Phe	Leu	His	Phe	Thr
				165					170					175	
His	Pro	Pro	Leu	Leu	Glu	Arg	Leu	Lys	Ala	Leu	Asp	Tyr	Glu	Ile	Glu
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

Met	Ile	Leu	Ser	Ile	Glu	Ser	Ser	Cys	Asp	Asp	Ser	Ser	Leu	Ala	Leu
1				5					10					15	
Thr	Arg	Ile	Glu	Asp	Ala	Lys	Leu	Ile	Ala	His	Phe	Lys	Ile	Ser	Gln
			20					25					30		
Glu	Lys	His	His	Ser	Ser	Tyr	Gly	Gly	Val	Val	Pro	Glu	Ile	Ala	Ser
		35					40					45			
Arg	Leu	His	Ala	Glu	Asn	Leu	Pro	Leu	Leu	Leu	Glu	Arg	Val	Lys	Ile
	50					55					60				
Ser	Leu	Asn	Lys	Asp	Phe	Ser	Lys	Ile	Lys	Ala	Ile	Ala	Ile	Thr	Asn
65				70						75					80
Gln	Pro	Gly	Leu	Ser	Val	Thr	Leu	Ile	Glu	Gly	Leu	Met	Met	Ala	Lys
				85					90					95	
Ala	Leu	Ser	Leu	Ser	Leu	Asn	Leu	Pro	Leu	Ile	Leu	Glu	Asp	His	Leu
			100					105					110		
Arg	Gly	His	Val	Tyr	Ser	Leu	Phe	Ile	Asn	Glu	Lys	Gln	Thr	Arg	Met
		115					120					125			
Pro	Leu	Ser	Val	Leu	Leu	Val	Ser	Gly	Gly	His	Ser	Leu	Ile	Leu	Glu
	130					135						140			
Ala	Arg	Asp	Tyr	Glu	Asp	Ile	Lys	Ile	Val	Ala	Thr	Ser	Leu	Asp	Asp
145					150					155					160

Ser Phe Gly Glu Ser Phe Asp Lys Val Ser Lys Met Leu Asp Leu Gly
 165 170 175
 Tyr Pro Gly Gly Pro Ile Val Glu Lys Leu Ala Leu Asp Tyr Ala His
 180 185 190
 Pro Asn Glu Pro Leu Met Phe Pro Ile Pro Leu Lys Asn Ser Pro Asn
 195 200 205
 Leu Ala Phe Ser Phe Ser Gly Leu Lys Asn Ala Val Arg Leu Glu Val
 210 215 220
 Glu Lys Asn Ala His Asn Leu Asn Asp Glu Val Lys Gln Lys Ile Gly
 225 230 235 240
 Tyr His Phe Gln Ser Ala Ala Ile Glu His Leu Ile Gln Gln Thr Lys
 245 250 255
 Arg Tyr Phe Lys Ile Lys Arg Pro Lys Ile Phe Gly Ile Val Gly Gly
 260 265 270
 Ala Ser Gln Asn Leu Ala Leu Arg Lys Ala Phe Glu Asp Leu Cys Ala
 275 280 285
 Glu Phe Asp Cys Glu Leu Val Leu Ala Pro Leu Glu Phe Cys Ser Asp
 290 295 300
 Asn Ala Ala Met Ile Gly Arg Ser Ser Leu Glu Ala Tyr Gln Lys Lys
 305 310 315 320
 Arg Phe Ile Pro Leu Glu Lys Ala Asp Ile Ser Pro Arg Thr Leu Leu
 325 330 335
 Lys Asn Phe Glu
 340

(2) INFORMATION FOR SEQ ID NO:813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

Met Asn Ile Tyr Gln Lys Asn Leu Gln Ala Leu Phe Lys Lys Asp Pro
 1 5 10 15
 Leu Leu Phe Ala Lys Leu Lys Ala Ile Lys Glu Asn Lys Lys Tyr Glu

Ala Gln Lys Gly Tyr Leu Tyr Gly Ser Gly Ser Ala Thr Ser Lys Glu
35 40 45

Ala Ser Lys Gln Lys Ala Leu Ala Asp Leu Val Ala Ser Ile Ser Val
50 55 60

Val Val Asn Ser Gln Ile His Ile Gln Lys Ser Arg Val Asp Asn Lys
65 70 75 80

Leu Lys Ser Ser Asp Ser Gln Thr Ile Asn Leu Lys Thr Asp Asp Leu
85 90 95

Glu Leu Asn Asn Val Glu Ile Val Asn Gln Glu Ala Gln Lys Gly Ile
100 105 110

Tyr Tyr Thr Arg Val Arg Asn Gln Ser Lys Leu Val Phe Ala Gly Phe
115 120 125

Lys Gly
130

(2) INFORMATION FOR SEQ ID NO:815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815

Met Lys Ile Gln Thr Ile Ser Thr Leu Val Leu Thr Ile Ile Met Val
1 5 10 15

Ile Gln Lys Met Ile Val Gly Lys Ile Ser Pro His Lys Thr Ala Glu
20 25 30

Glu Phe Thr Asn Leu Met Leu Asn Met Ile Ala Val Leu Asp Ser Gln
35 40 45

Ser Trp Gly Asp Ala Ile Leu Asn Ala Pro Phe Glu Phe Thr Asn Ser
50 55 60

Pro Thr Asp Cys Asp Asn Asp Pro Ser Lys Cys Val Asn Pro Gly Thr
65 70 75 80

Asn Gly Leu Val Asn Ser Lys Val Asp Gln Lys Tyr Val Leu Asn Lys
85 90 95

Gln Asp Ile Val Asn Lys Phe Lys Asn Lys Ala Asp Leu Asp Val Ile
100 105 110

Val	Leu	Lys	Asp	Ser	Gly	Val	Val	Gly	Xaa	Xaa	Asn	Gly	Tyr	Gly	Asn
		115					120					125			
Asp	Gly	Glu	Tyr	Gly	Thr	Leu	Gly	Val	Xaa	Ala	Tyr	Ala	Leu	Gly	Ser
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:816:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

Val	Val	Ile	Arg	Leu	Val	Leu	Asn	Met	Leu	Thr	Cys	Gln	Ile	Ser	Tyr
1				5					10					15	
Ile	Arg	Ile	Ser	Tyr	Leu	Val	Ser	Val	Ser	Asp	Phe	Val	Ile	Cys	Lys
			20				25						30		
Glu	Arg	Phe	Met	Asp	Glu	Ile	Lys	Thr	Leu	Leu	Val	Asp	Phe	Phe	Pro
		35					40					45			
Gln	Ala	Lys	His	Phe	Gly	Ile	Ile	Leu	Ile	Lys	Ala	Ile	Val	Val	Phe
	50					55					60				
Cys	Ile	Gly	Phe	Tyr	Phe	Ser	Phe	Phe	Leu	Arg	Asn	Lys	Thr	Met	Lys
65					70				75					80	
Leu	Leu	Ser	Lys	Lys	Asp	Glu	Ile	Leu	Ala	Asn	Phe	Val	Ala	Gln	Val
			85						90					95	
Thr	Phe	Ile	Leu	Ile	Leu	Ile	Ile	Thr	Thr	Ile	Ile	Ala	Leu	Ser	Thr
			100					105					110		
Leu	Gly	Val	Gln	Thr	Thr	Ser	Ile	Ile	Thr	Val	Leu	Gly	Thr	Val	Gly
	115						120					125			
Ile	Ala	Val	Ala	Leu	Ala	Leu	Lys	Asp	Tyr	Leu	Ser	Ser	Ile	Ala	Gly
	130					135					140				
Gly	Ile	Ile	Leu	Ile	Ile	Leu	His	Pro	Phe	Lys	Lys	Gly	Asp	Ile	Ile
145				150					155					160	
Glu	Ile	Ser	Gly	Leu	Glu	Gly	Lys	Val	Glu	Ala	Leu	Asn	Phe	Phe	Asn
			165					170					175		
Thr	Ser	Leu	Arg	Leu	His	Asp	Gly	Arg	Leu	Ala	Val	Leu	Pro	Asn	Arg

180	185	190
Ser Val Ala Asn Ser Asn Ile Ile Asn Ser Asn Asn Thr Ala Cys Arg		
195	200	205
Arg Ile Glu Trp Val Cys Gly Val Gly Tyr Gly Ser Asp Ile Glu Leu		
210	215	220
Val His Lys Thr Ile Lys Asp Val Ile Asp Gly Met Glu Lys Ile Asp		
225	230	235
Lys Asn Met Pro Thr Phe Ile Gly Ile Thr Asp Phe Gly Gln Ser Ser		
245	250	255
Leu Asn Phe Thr Ile Arg Val Trp Ala Lys Ile Glu Asp Gly Ile Phe		
260	265	270
Asn Val Arg Ser Glu Leu Ile Glu Arg Ile Lys Asn Ala Leu Asp Ala		
275	280	285
Asn Arg Ile Glu Ile Pro Phe Asn Lys Leu Asp Ile Ser Ile Asn Lys		
290	295	300
Gln Asp Ser Ser Lys		
305		

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

Met	Lys	Asn	Phe	Ser	Pro	Leu	Tyr	Cys	Leu	Lys	Xaa	Leu	Lys	Lys	Arg
1				5					10					15	
His	Leu	Ile	Ala	Leu	Ser	Leu	Pro	Leu	Leu	Ser	Tyr	Ala	Asn	Gly	Phe
			20					25					30		
Lys	Ile	Gln	Glu	Gln	Ser	Leu	Asn	Gly	Thr	Ala	Leu	Gly	Ser	Ala	Tyr
		35					40					45			
Val	Ala	Gly	Ala	Arg	Gly	Ala	Asp	Ala	Ser	Phe	Tyr	Asn	Pro	Ala	Asn
	50					55						60			
Met	Gly	Phe	Thr	Asn	Asp	Trp	Gly	Glu	Asn	Arg	Ser	Glu	Phe	Glu	Met
65					70					75				80	

Thr Thr Thr Val Ile Asn Ile Pro Thr Phe Ser Phe Lys Val Pro Thr
 85 90 95
 Thr Asn Gln Xaa Leu Tyr Ser Val Thr Ser Leu Glu Ile Asp Lys Ser
 100 105 110
 Gln Gln Asn Ile Leu Gly Ile Ile Asn Thr Ile Gly Leu Gly Asn Ile
 115 120 125
 Leu Lys Ala Leu Gly Asn Thr Ala Ala Thr Asn Gly Leu Ser Gln Ala
 130 135 140
 Ile Asn Arg Val Gln Gly Leu Met Asn Leu Thr Asn Gln Lys Val Val
 145 150 155 160
 Thr Leu Ala Ser

(2) INFORMATION FOR SEQ ID NO:818:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

Met Cys Leu Ala Ile Pro Ser Lys Val Ile Ala Ile Asn Asp Asn Val
 1 5 10 15
 Ala Leu Leu Glu Thr Leu Gly Val Gln Arg Glu Ala Ser Leu Asp Leu
 20 25 30
 Met Gly Glu Ser Val Lys Val Gly Asp Tyr Val Leu Leu His Ile Gly
 35 40 45
 Tyr Val Met Ser Lys Asp
 50

(2) INFORMATION FOR SEQ ID NO:819:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 202 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

Met	Lys	Tyr	Leu	Trp	Leu	Phe	Leu	Ile	Tyr	Ala	Ile	Gly	Leu	Phe	Ala	
1			5					10					15			
Thr	Asp	Lys	Thr	Leu	Asp	Ile	Ile	Lys	Thr	Ile	Gln	Lys	Leu	Pro	Lys	
			20					25					30			
Ile	Glu	Val	Arg	Tyr	Ser	Ile	Asp	Asn	Asp	Ala	Asn	Tyr	Ala	Leu	Lys	
		35					40					45				
Leu	His	Glu	Val	Leu	Ala	Asn	Asp	Leu	Lys	Thr	Ser	Gln	His	Phe	Asp	
	50					55					60					
Val	Ser	Gln	Asn	Lys	Glu	Gln	Gly	Ala	Ile	Asn	Tyr	Ala	Glu	Leu	Lys	
65				70						75					80	
Asp	Lys	Lys	Val	His	Leu	Val	Ala	Leu	Val	Ser	Val	Ala	Val	Glu	Asn	
			85					90						95		
Gly	Asn	Lys	Ile	Ser	Arg	Leu	Lys	Leu	Tyr	Asp	Val	Asp	Thr	Gly	Thr	
			100					105						110		
Leu	Lys	Lys	Thr	Phe	Asp	Tyr	Pro	Ile	Val	Ser	Leu	Asp	Leu	Tyr	Pro	
		115					120					125				
Phe	Ala	Ala	His	Asn	Met	Ala	Ile	Val	Val	Asn	Asp	Tyr	Leu	Lys	Ala	
	130					135					140					
Pro	Ser	Ile	Ala	Trp	Met	Lys	Arg	Leu	Ile	Val	Phe	Ser	Lys	Tyr	Ile	
145					150					155					160	
Gly	Pro	Gly	Ile	Thr	Asn	Ile	Ala	Leu	Ala	Asn	Tyr	Thr	Met	Arg	Tyr	
			165					170						175		
Gln	Lys	Glu	Ile	Ile	Lys	Asn	Asn	Arg	Leu	Asn	Ile	Phe	Pro	Lys	Trp	
			180					185						190		
Ala	Asn	Ala	Glu	Gln	Thr	Glu	Phe	Tyr	Tyr							
		195					200									

(2) INFORMATION FOR SEQ ID NO:820:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

Met	Leu	Ser	Ser	Asn	Asp	Leu	Phe	Met	Val	Val	Leu	Gly	Ala	Ile	Leu
1				5					10					15	
Leu	Val	Leu	Val	Cys	Leu	Val	Gly	Tyr	Leu	Tyr	Leu	Lys	Glu	Lys	Glu
			20				25						30		
Phe	Tyr	His	Lys	Met	Arg	Arg	Leu	Glu	Lys	Thr	Leu	Asp	Glu	Ser	Tyr
		35					40					45			
Gln	Glu	Asn	Tyr	Leu	Tyr	Ser	Lys	Arg	Leu	Arg	Glu	Leu	Glu	Gly	Arg
	50					55					60				
Leu	Glu	Gly	Leu	Ser	Leu	Glu	Lys	Ser	Ala	Lys	Glu	Asp	Ser	Ser	Leu
65					70					75					80
Lys	Thr	Thr	Leu	Ser	His	Leu	Tyr	Asn	Gln	Leu	Gln	Glu	Ile	Gln	Lys
				85				90						95	
Ser	Met	Asp	Lys	Glu	Arg	Asp	Tyr	Leu	Glu	Glu	Lys	Ile	Ile	Xaa	Xaa
			100					105					110		
Lys	Thr	Xaa	Xaa	Lys	Thr	Trp	Gly	Ile	Met	Pro	Leu	Ala	Met	Lys	Ser
		115					120					125			
Thr	Glu	Lys	Gln	Val	Leu	Lys	Met	Tyr	Gln	Glu	Gly	Tyr	Ser	Val	Asp
	130					135					140				
Ser	Ile	Ser	Lys	Glu	Phe	Lys	Val	Ser	Lys	Gly	Glu	Val	Glu	Phe	Ile
145					150					155					160
Leu	Asn	Met	Ala	Gly	Leu	Lys	Trp								
				165											

(2) INFORMATION FOR SEQ ID NO:821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...186
- (D) OTHER INFORMATION: /note= "cation efflux system membrane protein czcA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

- [illegible]

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

Val Ala Leu Val Phe Asp Ser Leu Ile Glu Asn Lys Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

Met Lys Lys Ile Gly Leu Ser Leu Cys Leu Val Leu Ser Leu Gly Phe
1 5 10 15

Leu Lys Ala His Glu Val Ser Ala Glu Glu Ile Ala Asp Ile Phe Tyr
20 25 30

Lys Leu Asn Ala Lys Glu Pro Lys Met Lys Ile Asn His Thr Lys Gly
35 40 45

Phe Cys Ala Lys Gly Val Phe Leu Pro Asn Pro Gln Ala Arg Glu Asp
50 55 60

Leu Glu Val Pro Leu Leu Asn Glu Lys Glu Ile Pro Ala Ser Val Arg
65 70 75 80

Tyr Ser Leu Gly Gly Val Val Asp Trp Thr Ile Lys Ala Arg Leu Gly
85 90 95

Glu Trp Arg

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

```

Val Ile Lys Pro His Ser Val Gly Leu Val Arg Ile Gly Ile Cys Leu
1           5           10           15
Ser Leu Glu Val Gly Tyr Glu Leu Gln Val Arg Thr Arg Ser Gly Leu
          20           25           30
Ala Leu Asn His Gln Val Met Val Leu Asn Xaa Pro Gly Thr Val Asp
          35           40           45
Asn Asp Tyr Arg Gly Glu Ile Lys Val Ile Leu Ala Asn Leu Ser Asp
          50           55           60
Lys Asp Phe Lys Val Gln Val
65           70

```

(2) INFORMATION FOR SEQ ID NO:827:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

```

Met Glu Phe Tyr Gln Val Tyr Asp Pro Leu Gly His Ile Trp Leu Ser
1           5           10           15
Ala Leu Val Ala Leu Ser Pro Ile Ala Leu Phe Phe Ile Ser Leu Ile
          20           25           30
Val Phe Lys Leu Lys Gly Tyr Ser Ala Gly Phe Leu Ser Leu Ala Leu
          35           40           45
Ser Ile Leu Ile Ala Leu Phe Val Tyr Lys Met Pro Val Gln Met Val
          50           55           60
Ser Ala Ser Phe Phe Tyr Gly Phe Leu Tyr Gly Leu Trp Pro Ile Ala
65           70           75           80
Trp Ile Val Ile Ala Ala Ile Phe Leu Tyr Asn Leu Ser Val Lys Ser

```

	85		90		95
Gly Tyr Phe Glu Ile Leu Lys Glu Ser Ile Leu Ser Leu Thr Pro Asp					
	100		105		110
His Arg Ile Leu Val Ile Leu Ile Gly Phe Cys Phe Gly Ser Phe Leu					
	115		120		125
Xaa Gly Ala Xaa Gly Phe Gly Gly Pro Val Ala Ile Thr Ala Ala Ile					
	130		135		140
Leu Val Ala Leu Gly					
145					

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

Met Glu Ile Ile Leu Leu Ile Val Ala Ala Val Val Leu Phe Tyr Phe			
1	5	10	15
Tyr Asn Thr Leu Lys Glu Tyr Leu Lys Asn Pro Leu Asn Pro Lys Thr			
	20	25	30
Lys Thr Glu Glu Tyr Asp Leu Lys Asn Asp Pro Tyr Leu Leu Val Gln			
	35	40	45
Ser Ser Pro Leu Asp Lys Phe Lys Gln Thr Gln Ile Gly Ala Tyr Met			
	50	55	60
Arg Leu Leu Lys Phe Leu Asp Ile Gln Lys Asn Ala Leu Asp Asn Ala			
	65	70	75
Leu Arg Thr Leu Phe Ile His Glu Leu Glu Gln Pro Leu Asn Ser Glu			
	85	90	95
Gln Gln Asn Leu Ala Lys Glu Leu Leu Asn Glu Pro Val Asp Lys Lys			
	100	105	110
Glu Asn Phe Glu Ser Leu Cys Gln Glu Ile Ala Asp His Thr His Gly			
	115	120	125
Glu Tyr Thr Lys Arg Leu Lys Leu Val Glu Phe Leu Met Leu Leu Ala			
	130	135	140

Tyr Ala Asp Gly Ile Leu Asp Ser Lys Glu Lys Glu Leu Phe Leu Asp
 145 150 155 160
 Val Gly Ala Phe Leu Gln Ile Asp Asn Gln Asp Phe Asn Glu Leu Tyr
 165 170 175
 Asp Asn Phe Glu His Phe Asn Ser Ile Glu Ile Pro Met Ser Leu Glu
 180 185 190
 Glu Ala Lys Asn Leu Phe Glu Ile Gln Thr His Thr Thr Met Gln Asp
 195 200 205
 Leu Glu Lys Lys Ala Leu Asp Leu Ser Ala Pro Tyr Tyr His Lys Met
 210 215 220
 Asn Asp Asn Lys Arg Tyr Ser Glu Gln Asp Phe Ile Ser Leu Lys Lys
 225 230 235 240
 Ile Ala Leu Ala Ser Gln Leu Leu Glu Asn Asp Leu Lys Asp Ser
 245 250 255

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...106
- (D) OTHER INFORMATION: /note= "HYPOTHETICAL 23.3 KD PROTEIN-
INTEGRAL MEMBRANE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

Met Glu Val Glu His Gly Lys Ile Glu Thr Thr Leu Ser Leu Gly Ala
 1 5 10 15
 Ser His Leu Glu Val Ile Lys Met Met Leu Leu Glu Ser Leu Pro Ser
 20 25 30
 Leu Val Asn Asn Ile Thr Ile Thr Leu Ile Ser Leu Ile Gly Tyr Ser
 35 40 45
 Ala Lys Ala Gly Ala Leu Gly Ala Gly Gly Leu Gly Asp Leu Ala Ile
 50 55 60
 Arg Ile Gly Tyr Gln Ser Tyr Arg Gly Asp Val Leu Phe Tyr Ala Val
 65 70 75 80

Val	Val	Lys	Ile	Ser	Asp	Arg	Leu	His	Asn	Met	Leu	Thr	Leu	Asp	Ala	
				165					170					175		
Leu	Pro	His	Asp	Lys	Gln	Val	Arg	Ile	Ser	Lys	Glu	Thr	Leu	Ala	Val	
			180					185					190			
Tyr	Ala	Pro	Ile	Ala	Ser	Arg	Leu	Gly	Met	Ser	Ser	Ile	Lys	Asn	Glu	
		195					200					205				
Leu	Glu	Asp	Lys	Ser	Phe	Tyr	Tyr	Ile	Tyr	Pro	Glu	Glu	Tyr	Lys	Asn	
	210					215					220					
Ile	Lys	Glu	Tyr	Leu	His	Lys	Asn	Lys	Gln	Ser	Leu	Leu	Leu	Lys	Leu	
225					230					235					240	
Asn	Ala	Phe	Ala	Ser	Lys	Leu	Glu	Lys	Lys	Leu	Phe	Asp	Ser	Gly	Phe	
				245					250					255		
Ser	His	Ser	Asp	Phe	Lys	Leu	Val	Thr	Arg	Val	Lys	Arg	Pro	Tyr	Ser	
			260					265					270			
Ile	Tyr	Leu	Lys	Met	Gln	Arg	Lys	Gly	Ala	Val	Asn	Ile	Asp	Glu	Ile	
	275						280					285				
Leu	Asp	Leu	Leu	Ala	Ile	Arg	Ile	Leu	Leu	Lys	Asn	Pro	Ile	Asp	Cys	
	290					295					300					
Tyr	Lys	Val	Leu	Gly	Ile	Ile	His	Leu	Asn	Phe	Lys	Pro	Ile	Val	Ser	
305					310					315					320	
Arg	Phe	Lys	Asp	Tyr	Ile	Ala	Leu	Pro	Lys	Glu	Asn	Gly	Tyr	Lys	Thr	
				325					330					335		
Ile	His	Thr	Thr	Ile	Phe	Asp	Glu	Ser	Ser	Val	Tyr	Glu	Val	Gln	Ile	
			340					345					350			
Arg	Thr	Phe	Asp	Met	His	Met	Gly	Ala	Glu	Tyr	Gly	Asn	Ser	Ala	His	
		355					360					365				
Trp	Lys	Tyr	Lys	Ala	Gly	Gly	Val	Asp	His	Glu	Glu	His	His	Glu	Gly	
	370					375					380					
Met	Arg	Trp	Leu	Gln	Asn	Phe	Lys	Tyr	His	Asp	Ser	Asp	Leu	Lys	Asn	
385					390					395					400	
Asp	Pro	Lys	Glu	Phe	Tyr	Glu	Leu	Ala	Lys	Asn	Asp	Leu	Tyr	Arg	Glu	
				405					410					415		
Asp	Ile	Val	Val	Phe	Ser	Pro	His	Gly	Asp	Thr	Tyr	Thr	Leu	Pro	Val	
			420					425					430			
Gly	Ala	Ile	Ala	Leu	Asp	Phe	Ala	Tyr	Met	Val	His	Ser	Asp	Leu	Gly	
		435					440					445				
Asp	Lys	Ala	Thr	Asp	Ala	Tyr	Ile	Asn	Ser	Lys	Lys	Ala	Leu	Leu	Asn	
	450					455					460					

Gln Glu Leu Arg Ser Gly Asp Val Val Lys Ile Ile Lys Gly Asp Lys
 465 470 475 480

Val Ile Pro Arg Phe Ile Trp Met Asp Gln Leu Lys Thr Ser Lys Ala
 485 490 495

Lys Asn His Leu Arg Ile Gln Arg Arg Asn Arg Leu Lys Glu Ile Asp
 500 505 510

Thr Lys Ser Met Ile Asn Ile Leu Ala Thr Phe Phe Trp Ala Leu
 515 520 525

(2) INFORMATION FOR SEQ ID NO:831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

Val Val Val Val Glu Asn Ile Lys Asp Ala Val Pro Leu Ala Gln Ser
 1 5 10 15

Leu Ile Xaa Gly Gly Ile Pro Ile Ile Glu Val Thr Leu Arg Ser Asn
 20 25 30

Cys Ala Leu Glu Ala Ile Glu Leu Ile Ala Lys Asn Val Pro Lys Met
 35 40 45

Arg Val Gly Ala Gly Thr Ile Leu Asn Leu Thr Gln Leu Glu Gln Ala
 50 55 60

Gln Asn Arg Gly Ala Glu Phe Leu Ile Ser Pro Gly Leu Thr Ile Lys
 65 70 75 80

Leu Leu Glu His Ala Lys Lys Lys Asp Met Pro Leu Ile Pro Gly Val
 85 90 95

Ser Ser Ser Ser Glu Val Met Gln Ala Leu Glu Leu Gly Tyr Asn Ala
 100 105 110

Leu Lys Phe Phe Pro Ala Glu Tyr Cys Gly Gly Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...110

(D) OTHER INFORMATION: /note= "UDP-N-ACETYLMURAMOYLALANYL-D-
GLUTAMATE--2 & 6-DIAMINOPIMELATE LIGASE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

Val	Glu	Lys	Ile	Lys	Pro	Tyr	Ala	Pro	Lys	Asp	Ser	Pro	Leu	Ile	Asp
1				5					10					15	
Tyr	Ser	Ser	Leu	Val	Arg	Asn	Val	Gln	Ser	Thr	Leu	Lys	Gly	Thr	Ser
			20					25					30		
Phe	Glu	Thr	Leu	Ile	Asn	Gly	Val	Trp	Glu	Ser	Phe	Glu	Thr	Lys	Val
		35					40					45			
Leu	Gly	Glu	Phe	Asn	Ala	Tyr	Asn	Ile	Ala	Ser	Ala	Ile	Leu	Thr	Ala
	50					55					60				
Lys	His	Leu	Gly	Leu	Glu	Thr	Glu	Arg	Ile	Lys	Arg	Leu	Val	Phe	Glu
65					70					75				80	
Leu	Lys	Pro	Ile	Asn	His	Arg	Leu	Gln	Leu	Leu	Glu	Ala	Asn	Gln	Lys
			85					90						95	
Ile	Ile	Ile	Asp	Asp	Asn	Phe	Asn	Gly	Asn	Leu	Lys	Gly	Met		
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

Met	Lys	Arg	Ile	Leu	Val	Ser	Leu	Ala	Val	Leu	Ser	His	Ser	Ala	His
1				5					10					15	

Ala	Val	Lys	Thr	His	Asn	Leu	Glu	Arg	Val	Glu	Ala	Ser	Gly	Val	Ala		
			20					25					30				
Asn	Asp	Lys	Glu	Ala	Pro	Leu	Ser	Trp	Arg	Ser	Lys	Glu	Val	Arg	Asn		
		35					40					45					
Tyr	Met	Gly	Ser	Arg	Thr	Val	Ile	Ser	Asn	Lys	Gln	Leu	Thr	Lys	Ser		
	50					55					60						
Ala	Asn	Gln	Ser	Ile	Glu	Glu	Ala	Leu	Gln	Asn	Val	Pro	Gly	Val	His		
65					70					75					80		
Ile	Arg	Asn	Ser	Thr	Gly	Ile	Gly	Ala	Val	Pro	Ser	Ile	Ser	Ile	Arg		
				85					90					95			
Gly	Phe	Gly	Ala	Gly	Gly	Pro	Gly	His	Ser	Asn	Thr	Gly	Met	Ile	Leu		
			100					105					110				
Val	Asn	Gly	Ile	Pro	Ile	Tyr	Val	Ala	Pro	Tyr	Val	Glu	Ile	Gly	Thr		
		115					120					125					
Val	Ile	Phe	Pro	Val	Thr	Phe	Gln	Ser	Val	Asp	Arg	Ile	Ser	Val	Thr		
	130					135					140						
Lys	Gly	Gly	Glu	Ser	Val	Arg	Tyr	Gly	Pro	Asn	Ala	Phe	Gly	Gly	Val		
145					150					155					160		
Ile	Asn	Ile	Ile	Thr	Lys	Gly	Ile	Pro	Thr	Asn	Trp	Glu	Ser	Gln	Val		
				165					170					175			
Ser	Glu	Arg	Thr	Thr	Phe	Trp	Gly	Lys	Ser	Glu	Asn	Gly	Gly	Phe	Phe		
			180					185					190				
Asn	Gln	Asn	Ser	Lys	Asn	Ile	Asp	Lys	Ser	Leu	Val	Asn	Asn	Met	Leu		
		195					200					205					
Phe	Asn	Thr	Tyr	Leu	Arg	Thr	Gly	Gly	Met	Met	Asn	Lys	His	Phe	Gly		
	210					215					220						
Ile	Gln	Ala	Gln	Val	Asn	Trp	Leu	Lys	Gly	Gln	Gly	Phe	Arg	Tyr	Asn		
225					230					235					240		
Ser	Pro	Thr	Asp	Ile	Gln	Asn	Tyr	Met	Leu	Asp	Ser	Leu	Tyr	Gln	Ile		
				245					250					255			
Asn	Asp	Ser	Asn	Lys	Ile	Thr	Ala	Phe	Phe	Gln	Tyr	Tyr	Ser	Tyr	Phe		
			260					265					270				
Leu	Thr	Asp	Pro	Gly	Ser	Leu	Gly	Ile	Ala	Ala	Tyr	Asn	Gln	Asn	Arg		
		275					280					285					
Phe	Gln	Asn	Asn	Arg	Pro	Asn	Asn	Asp	Lys	Ser	Gly	Arg	Ala	Lys	Arg		
	290					295					300						
Trp	Gly	Ala	Val	Tyr	Gln	Asn	Phe	Phe	Gly	Asp	Thr	Asp	Arg	Val	Gly		
305					310					315					320		

Gly Gly Phe His Phe
325

(2) INFORMATION FOR SEQ ID NO:834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

Leu	Arg	Ser	Ile	Ser	Arg	Ile	Lys	Met	Leu	Ser	Val	Tyr	Glu	Lys	Gly	
1				5					10					15		
Asn	Ala	Leu	Asp	Lys	Arg	Val	Leu	Glu	Glu	Trp	Leu	Leu	Ser	Glu	Asp	
			20					25					30			
Ile	Leu	Met	Glu	Asn	Ala	Ala	Met	Ala	Leu	Glu	Arg	Ala	Val	Leu	Gln	
		35					40					45				
Asn	Ala	Ser	Leu	Gly	Ala	Lys	Val	Ile	Ile	Leu	Cys	Gly	Ser	Gly	Asp	
	50					55					60					
Asn	Gly	Gly	Asp	Gly	Tyr	Thr	Leu	Ala	Arg	Arg	Leu	Val	Gly	Arg	Phe	
65					70				75						80	
Lys	Thr	Leu	Val	Phe	Glu	Met	Lys	Leu	Ala	Lys	Ser	Pro	Met	Cys	Gln	
			85						90					95		
Leu	Gln	Lys	Glu	Arg	Ala	Lys	Lys	Val	Gly	Val	Val	Ile	Lys	Ala	Trp	
		100						105					110			
Glu	Glu	Lys	Asn	Glu	Asp	Leu	Glu	Cys	Asp	Val	Leu	Val	Asp	Cys	Val	
	115						120					125				
Val	Gly	Ser	Ala	Phe	Lys	Gly	Gly	Leu	Glu	Pro	Phe	Leu	Asp	Phe	Glu	
	130					135					140					
Ser	Leu	Ser	Gln	Lys	Ala	Arg	Phe	Lys	Ile	Ala	Cys	Asp	Ile	Pro	Ser	
145				150					155					160		
Gly	Ile	Asp	Ser	Lys	Gly	Arg	Val	Asp	Lys	Arg	Ala	Phe	Lys	Xaa	Gly	
			165					170						175		
Tyr	Arg	Leu	Ser	Ala	Trp	Ala	Leu	Phe	Lys	Ser	Cys	Leu	Leu	Ser	Xaa	
		180					185						190			
Lys	Xaa	Lys	Xaa	Tyr	Ile	Xaa	Xaa	Leu	Lys	Xaa	Xaa	His	Leu	Xaa	Val	
	195					200						205				

Phe Asn Gln Ile Tyr Glu Ile Pro Thr Xaa Thr Phe Leu Leu Glu Lys
 210 215 220
 Xaa Asp Leu Lys Leu Pro Leu Arg Asp Arg Lys Lys Arg Ser Gln Arg
 225 230 235 240
 Arg Leu Arg Ala Cys Ala Cys Ala Phe Gly Gln Ala
 245 250

(2) INFORMATION FOR SEQ ID NO:835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...597
- (D) OTHER INFORMATION: /note= "heat shock protein C62.5 -
chaperone-ATPase activity"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

Met Ser Asn Gln Glu Tyr Thr Phe Gln Thr Glu Ile Asn Gln Leu Leu
 1 5 10 15
 Asp Leu Met Ile His Ser Leu Tyr Ser Asn Lys Glu Ile Phe Leu Arg
 20 25 30
 Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu Asp Lys Leu Asn Tyr Leu
 35 40 45
 Met Leu Thr Asp Glu Lys Leu Lys Gly Leu Asn Thr Thr Pro Ser Ile
 50 55 60
 His Leu Ser Phe Asp Ser Gln Lys Lys Thr Leu Thr Ile Lys Asp Asn
 65 70 75 80
 Gly Ile Gly Met Asp Lys Ser Asp Leu Ile Glu His Leu Gly Thr Ile
 85 90 95
 Ala Lys Ser Gly Thr Lys Ser Phe Leu Ser Ala Leu Ser Gly Asp Lys
 100 105 110
 Lys Lys Asp Ser Ala Leu Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser
 115 120 125
 Ala Phe Met Val Ala Ser Lys Ile Val Val Gln Thr Lys Lys Val Thr

130	135	140
Ser His Gln Ala Tyr 145	Ala Trp Val Ser Asp 150	Gly Lys Gly Lys Phe Glu 155 160
Ile Ser Glu Cys Val 165	Lys Glu Glu Gln 170	Gly Thr Glu Ile Thr Leu Phe 175
Leu Lys Glu Glu Asp 180	Ser His Phe Ala Ser Arg 185	Trp Glu Ile Asp Ser 190
Val Val Lys Lys Tyr 195	Ser Glu His Ile Pro Phe 200	Pro Ile Phe Leu Thr 205
Tyr Thr Asp Thr Lys 210	Phe Glu Gly Glu Gly Asp 215	Asn Lys Lys Glu Val 220
Lys Glu Glu Lys Cys 225	Asp Gln Ile Asn Gln Ala Ser 230 235	Ala Leu Trp Lys 240
Met Asn Lys Ser Glu 245	Leu Lys Glu Lys Asp Tyr Lys 250	Asp Phe Tyr Gln 255
Ser Phe Ala His Asp 260	Asn Ser Glu Pro Leu Ser Tyr 265	Ile His Asn Lys 270
Val Glu Gly Ser Leu 275	Glu Tyr Thr Thr Leu Phe Tyr 280	Ile Pro Ser Lys 285
Ala Pro Phe Asp Leu 290	Phe Arg Val Asp Tyr Lys Ser 295 300	Gly Val Lys Leu
Tyr Val Lys Arg Val 305	Phe Ile Thr Asp Asp Asp 310 315	Lys Glu Leu Leu Pro 320
Ser Tyr Leu Arg Phe 325	Val Lys Gly Val Ile Asp Ser 330	Glu Asp Leu Pro 335
Leu Asn Val Ser Arg 340	Glu Ile Leu Gln Gln Asn Lys 345	Ile Leu Ala Asn 350
Ile Arg Ser Ala Ser 355	Val Lys Lys Ile Leu Ser 360	Glu Ile Glu Arg Leu 365
Ser Lys Asp Asn Lys 370	Asn Tyr His Lys Phe Tyr 375	Glu Pro Phe Gly Lys 380
Val Leu Lys Glu Gly 385	Leu Tyr Gly Asp Phe Glu 390 395	Asn Lys Glu Lys Leu 400
Leu Glu Leu Leu Arg 405	Phe Tyr Ser Lys Asp Lys 410	Gly Glu Trp Ile Ser 415
Leu Lys Glu Tyr Lys 420	Glu Asn Leu Lys Glu Asn 425	Gln Lys Ser Ile Tyr 430
Tyr Leu Leu Gly Glu 435	Asn Leu Asp Leu Leu Lys 440	Ala Ser Pro Leu Leu 445

Glu Lys Tyr Ala Gln Lys Gly Tyr Asp Val Leu Leu Leu Ser Asp Glu
 450 455 460
 Ile Asp Ala Phe Val Met Pro Gly Val Asn Glu Tyr Asp Lys Thr Pro
 465 470 475 480
 Phe Arg Asp Ala Ser His Ser Glu Ser Leu Lys Glu Leu Gly Leu Ala
 485 490 495
 Glu Ile His Asp Glu Val Lys Asp Gln Phe Lys Asp Leu Ile Lys Ala
 500 505 510
 Phe Glu Glu Asn Leu Lys Asp Glu Ile Lys Gly Val Glu Leu Ser Gly
 515 520 525
 His Leu Thr Ser Ala Val Ala Leu Ile Gly Asp Glu Pro Asn Ala Met
 530 535 540
 Met Ala Asn Trp Met Arg Gln Met Gly Gln Ser Val Pro Glu Ser Lys
 545 550 555 560
 Lys Thr Leu Glu Leu Asn Pro Asn His Ala Ile Leu Gln Lys Leu Leu
 565 570 575
 Lys Cys Glu Asp Lys Glu Gln Leu Ser Ala Phe Ile Trp Leu Leu Tyr
 580 585 590
 Asp Gly Arg Ser Phe
 595

(2) INFORMATION FOR SEQ ID NO:836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

Val Asn Leu Gly Ala Tyr Tyr Thr Pro Pro Tyr Leu Val Asp Cys Ala
 1 5 10 15
 Tyr Lys Leu Leu Lys Lys His Val Gly Ile Glu Asn Tyr Thr Leu Leu
 20 25 30
 Asp Thr Ala Cys Gly Asn Lys Glu Phe Leu Lys Leu His His Pro Lys
 35 40 45
 Lys Ile Gly Ala Asp Ile Asp Pro Lys Cys Asp Ala Leu Ile Ile Asn

50	55	60
Ala Leu Ala Asn Pro Lys Arg Glu Asn Tyr Gly Ile Ser Gln Asp Glu		
65	70	75 80
Pro Leu Ile Ile Val Gly Asn Pro Pro Tyr Asn Asp Arg Thr Ser Phe		
	85	90 95
Ile Lys Gln Asp Ile Lys Asn Lys Asp Phe Ile Phe Glu Ile Asp Asn		
	100	105 110
Asp Leu Lys Ser Arg Asp Leu Gly Ile Ser Phe Leu Lys Ser Phe Ala		
	115	120 125
Ile Leu Lys Pro Ala Phe Ile Cys Val Leu His Pro Leu Ser Tyr Leu		
	130	135 140
Ile Lys Glu Ala Asn Phe Lys Gln Phe Lys Ala Ile		
145	150	155

(2) INFORMATION FOR SEQ ID NO:837:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...157
 - (D) OTHER INFORMATION: /note= "PHOSPHOLIPASE A1"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

Met Lys Ser Ile Leu Leu Phe Ile Ile Phe Val Val Cys Gln Leu Glu		
1	5	10 15
Gly Lys Lys Phe Ser Gln Asp Asn Phe Lys Val Asp Tyr Asn Tyr Tyr		
	20	25 30
Leu Arg Lys Gln Asp Leu His Ile Ile Lys Thr Gln Asn Asp Leu Ser		
	35	40 45
Asn Ala Trp Tyr Leu Pro Pro Gln Lys Ala Pro Lys Glu His Ser Trp		
	50	55 60
Val Asp Phe Ala Lys Lys Tyr Leu Asn Met Met Asp Tyr Leu Gly Thr		
65	70	75 80
Tyr Phe Leu Pro Phe Tyr His Ser Phe Thr Pro Ile Phe Gln Trp Tyr		

	85		90		95
His Pro Asn Ile Asn Pro Tyr Lys Arg Asn Glu Phe Lys Phe Gln Ile					
	100		105		110
Ser Phe Arg Val Pro Val Phe Arg His Ile Leu Trp Thr Lys Gly Thr					
	115		120		125
Leu Tyr Leu Asp Tyr Thr Gln Thr Asn Trp Phe Gln Ile Tyr Asn Asp					
	130		135		140
Pro Gln Ser Ala Pro Met Arg Met Ile Lys Phe His Ala					
	145		150		155

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

Met Gly Leu Met Gly Val Ser Gln Gly Leu Pro Asn Thr Thr Ser Lys					
1	5		10		15
Phe Gly Ile Glu Phe Asp Ser Leu Ala Asp Val Val Ala Phe Gly Val					
	20		25		30
Ala Pro Ser Leu Ile Thr Tyr Phe Tyr Val Gly Tyr Asn Phe Gly Arg					
	35		40		45
Ile Gly Met Ala Val Ser Ala Leu Phe Val Ile Phe Gly Ala Ile Arg					
	50		55		60
Leu Ala Arg Phe Asn Ile Ser Thr Asn Thr Ser Asp Pro Tyr Ser Phe					
	65		70		75
Ile Gly Ile Pro Ile Pro Ala Ala Ala Val Leu Val Val Leu Cys Val					
	85		90		95
Leu Leu Asp Asn Lys Tyr His Phe Leu Glu Gly Asn Thr Glu Lys Leu					
	100		105		110
Phe Leu Gly Phe Ile Val Leu Leu Gly Val Leu Met Val Ser Asn Ile					
	115		120		125
Arg Tyr Pro Asn Phe Lys Lys Val Lys Trp Asn Leu Lys Leu Phe Ile					
	130		135		140

Leu Val Leu Ile Phe Leu Ser Leu Val Phe Val Arg Pro Leu Glu Ala
 145 150 155 160
 Leu Ser Val Phe Met Gly Leu Tyr Leu Ile Tyr Gly Ile Ile Arg Trp
 165 170 175
 Ile Phe Leu Met Val Lys Ile Thr Phe Asn Lys Asn Lys Ser Ala
 180 185 190

(2) INFORMATION FOR SEQ ID NO:839:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

Met Ile Gly Val Tyr Pro Asn Tyr Ser Lys Lys Gln Leu Lys Arg Pro
 1 5 10 15
 Leu Val Ile Phe Val Ser Arg Glu Leu Ala Leu Ala Asn Gly Ile Leu
 20 25 30
 Thr Asp Ala Tyr Asp Ile Glu Ala Asn Leu Tyr Met Asn Ala Arg Ile
 35 40 45
 Val Met Xaa Asn Asn Lys Arg Lys His Tyr Glu Gln Arg Val Asn Leu
 50 55 60
 His Phe Xaa Arg Ser Leu Gly Xaa Val Phe Asp His Arg Ser Asn His
 65 70 75 80
 Val Leu Cys Asp Glu Lys Asp Leu Leu Arg
 85 90

(2) INFORMATION FOR SEQ ID NO:840:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

Val	Lys	Ile	Thr	Ile	Met	Ile	Lys	Asp	Phe	Asn	His	Tyr	Cys	Arg	Lys	
				5					10					15		
Ile	Thr	Arg	Gly	Phe	Val	Lys	Ile	Pro	Thr	Lys	Lys	Gln	Gly	Ala	Lys	
				20					25					30		
Lys	Met	Lys	Lys	Ala	Gly	Phe	Leu	Phe	Leu	Ala	Ala	Met	Ala	Ile	Ile	
				35					40					45		
Val	Val	Ser	Leu	Asn	Ala	Lys	Asp	Pro	Asn	Val	Leu	Arg	Lys	Ile	Val	
				50					55					60		
Phe	Glu	Lys	Cys	Leu	Pro	Asn	Tyr	Glu	Lys	Asn	Gln	Asn	Pro	Ser	Pro	
				65					70					75		
Cys	Ile	Glu	Val	Lys	Pro	Asp	Ala	Gly	Tyr	Val	Val	Leu	Lys	Asp	Ile	
				85					90					95		
Asn	Gly	Pro	Leu	Gln	Tyr	Leu	Leu	Met	Pro	Thr	Thr	His	Ile	Ser	Gly	
				100					105					110		
Ile	Glu	Asn	Pro	Leu	Leu	Leu	Asp	Pro	Ser	Thr	Pro	Asn	Phe	Phe	Tyr	
				115					120					125		
Leu	Ser	Trp	Gln	Ala	Arg	Asp	Phe	Met	Ser	Xaa	Lys	Tyr	Gly	Lys	Pro	
				130					135					140		
Ile	Pro	Asp	Tyr	Ala	Ile	Ser	Leu	Thr	Ile	Asn	Ser	Lys	Lys	Gly	Arg	
				145					150					155		
Ser	Gln	Asn	His	Phe	His	Ile	His	Ile	Ser	Cys	Ile	Ser	Leu	Asp	Val	
				165					170					175		
Arg	Lys	Gln	Leu	Asp	Asn	Asn	Leu	Lys	Asn	Ile	Asn	Ser	Arg	Trp	Ser	
				180					185					190		
Pro	Leu	Ser	Gly	Gly	Leu	Asn	Gly	His	Lys	Tyr	Leu	Ala	Arg	Arg	Val	
				195					200					205		
Thr	Glu	Ser	Glu	Leu	Ala	Gln	Lys	Ser	Pro	Phe	Val	Met	Leu	Ala	Lys	
				210					215					220		
Glu	Val	Pro	Asn	Ala	His	Lys	Arg	Met	Gly	Asp	Tyr	Gly	Leu	Ala	Val	
				225					230					235		
Val	Gln	Gln	Ser	Asp	Asn	Ser	Phe	Val	Leu	Leu	Ala	Thr	Gln	Phe	Asn	
				245					250					255		
Pro	Leu	Thr	Leu	Asn	Arg	Ala	Ser	Ala	Glu	Glu	Ile	Gln	Asp	His	Glu	
				260					265					270		
Cys	Ala	Ile	Leu	Arg												
				275												

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...58
- (D) OTHER INFORMATION: /note= "surface antigen"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

Val	Leu	Thr	Ser	Gly	Asp	Met	Ile	Thr	Cys	Pro	Tyr	Cys	Gly	Arg	Ile
1				5				10						15	
Leu	Tyr	Ala	Glu	Ser	Thr	His	Glu	Ser	Asn	Ala	Gln	Pro	Pro	Lys	Glu
			20					25						30	
Ser	Gln	Pro	Lys	Glu	Ser	Gln	Glu	Glu	Ser	Gln	Glu	Glu	Ser	Gln	Glu
			35				40					45			
Glu	Ser	Gln	Glu	Ala	Val	Arg	Leu	Ile	Val						
			50				55								

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

Met	Ala	Leu	Asp	Lys	Arg	Ile	Trp	Met	His	Phe	Asp	Leu	Leu	Pro	Phe
1				5				10						15	
Val	Phe	Ile	Ile	Pro	Leu	Leu	Val	Val	Ser	Phe	Leu	Leu	Ile	Phe	Glu
			20					25						30	
Ser	Ser	Ala	Val	Leu	Ser	Leu	Lys	Gln	Gly	Val	Tyr	Tyr	Ala	Ile	Gly
			35				40					45			

Phe Leu Leu Phe Trp Val Val Phe Phe Ile Pro Phe Arg Lys Leu Asp
 50 55 60
 Arg Trp Leu Phe Ala Leu Tyr Trp Ala Cys Val Ile Leu Leu Ala Leu
 65 70 75 80
 Val Asp Phe Met Gly Ser Ser Lys Leu Gly Ala Gln Arg Trp Leu Val
 85 90 95
 Ile Pro Phe Thr Ser Ile Thr Leu Gln Pro Ser Glu Pro Val Lys Asn
 100 105 110
 Arg Xaa Ser Phe Ile Val Gly Ala Phe Xaa Xaa Asn Xaa Pro Asp Xaa
 115 120 125
 Leu Leu Arg Ala Met Ile Gly Ala Cys Phe
 130 135

(2) INFORMATION FOR SEQ ID NO:843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

Met Lys Leu Asn Asp Pro Phe Thr Ser Pro Asn Lys Ala Lys Lys Glu
 1 5 10 15
 Leu Ser Pro Lys Gly Phe Arg Gly Gly Leu Glu Ser Glu Ile Leu Leu
 20 25 30
 Gly Phe Val Leu Gln Lys Glu Arg Val Phe Leu His Thr His Glu His
 35 40 45
 Leu Glu Leu Ser His Glu Glu Glu Thr Arg Phe Phe Glu Leu Val Gly
 50 55 60
 Lys Arg Leu Asn Asp Cys Pro Ile Glu Tyr Leu Leu Gly Ser Cys Asp
 65 70 75 80
 Phe Tyr Gly Arg Ser Phe Phe Val Asn Glu His Val Leu Ile Pro Arg
 85 90 95
 Pro Glu Thr Glu Ile Leu Val Gln Lys Ala Leu Asn Ile Ile Ser Gln
 100 105 110
 Tyr His Leu Lys Glu Ile Gly Glu Ile Gly Ile Gly Ser Gly Cys Val

(2) INFORMATION FOR SEQ ID NO:845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

Val	Ile	Gln	Ser	His	Pro	Lys	Gln	Thr	Leu	Ile	Glu	Asp	Glu	Asn	Tyr
1				5					10					15	
Phe	Tyr	Ala	Asn	Lys	Gly	Leu	Tyr	Lys	Thr	Asn	Lys	Glu	Ala	Phe	Leu
			20					25					30		
Arg	Val	Tyr	Lys	Ile	Pro	Glu	Ser	Met	Pro	Ile	Glu	Lys	Arg	Glu	Ser
			35					40					45		
Leu	Ser	Lys	Val	Ser	Lys	Ile	Phe	Leu	Ala	Leu	Leu	Phe	Phe	Ile	Ser
			50				55				60				
Ser	Met	Leu	Phe	Gly	Ile	Phe	Trp	Arg	Leu	Pro	Lys	Arg	Leu	Asp	Thr
65					70					75				80	
Lys	Met	Ser	Leu	Glu	Ser	Ala	His	Lys	Asn	Glu	Leu	Glu	Asn	Ala	Phe
				85					90					95	
Gln	Arg	Tyr	Asp	Ala	Leu	Gly	Val	Arg	Phe	Glu	Asp	Ile	Ala	Gly	Val
			100					105					110		
Asn	Glu	Val	Lys	Glu	Glu	Leu	Leu	Glu	Val	Ile	Asp	Tyr	Leu	Lys	Lys
			115				120						125		

Pro

(2) INFORMATION FOR SEQ ID NO:846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

Met Phe Val Val Lys Met Val Leu Gly Phe Leu Ile Leu Leu Ser Pro
1 5 10 15
Leu Cys Ala Thr Gly Leu Asp Ile Ser Gln Thr Asp Ile Ile Glu Arg
20 25 30
Ser Leu Asn Phe Leu Leu Phe Val Gly Ile Leu Trp Tyr Phe Leu Ala
35 40 45
Lys Arg Leu Arg Ser Phe Leu His Ser Lys Ser Leu Glu Ile Ser Lys
50 55 60
Arg Leu Glu Glu Ile Gln Ala Gln Leu Lys Val Ser Lys Glu His Lys
65 70 75 80
Lys Lys Leu Leu Lys Glu Leu Glu Gln Ala Lys Glu Lys Ala Glu Leu
85 90 95
Ile Ile Ser Asp Ala Asn Lys Glu Ala Leu His Asp His Ala Lys Ile
100 105 110
Arg Ile Thr Asn Gln Asn Gly Cys Gly Lys Phe Asp Gln Lys Phe
115 120 125

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...276
- (D) OTHER INFORMATION: /note= "molybdate-binding periplasmic protein precursor"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

Met Arg Val Leu Glu Trp Lys Tyr Trp Leu Asn Thr Asp Lys Trp Asp
1 5 10 15
Thr Pro Thr Asn Lys Pro Pro Gln Thr Phe Lys Ile Gln Ile Phe Lys
20 25 30
Ile Gln Ile Gly Ile Ile Asn Asn Phe Asn His Leu Ile Lys Gly Ser
35 40 45

Ser Met Lys Asn Ala Phe Lys Ala Phe Ala Leu Leu Ile Val Phe Phe
 50 55 60
 Ser Asn Ala Leu Leu Ala Gln Asp Leu Lys Ile Ala Ala Ala Asn
 65 70 75 80
 Leu Thr Arg Ala Leu Lys Ala Leu Val Lys Glu Phe Gln Lys Glu His
 85 90 95
 Pro Lys Asp Ala Ile Asn Ile Ser Phe Asn Ser Ser Gly Lys Leu Tyr
 100 105 110
 Ala Gln Ile Ala Gln Asn Ala Pro Phe Asp Leu Phe Ile Ser Ala Asp
 115 120 125
 Ile Ala Arg Pro Lys Lys Leu Tyr Asp Glu Lys Ile Thr Pro Phe Lys
 130 135 140
 Glu Glu Val Tyr Ala Lys Gly Val Leu Val Leu Trp Ser Glu Asn Leu
 145 150 155 160
 Lys Met Asp Ser Leu Glu Ile Leu Lys Asp Pro Lys Ile Lys Arg Ile
 165 170 175
 Ala Met Ala Asn Pro Lys Leu Ala Pro Tyr Gly Lys Ala Ser Met Glu
 180 185 190
 Val Leu Asp Arg Leu Lys Leu Thr Pro Ser Leu Lys Ser Lys Ile Ile
 195 200 205
 Tyr Gly Ala Ser Ile Ser Gln Ala His Gln Phe Ile Ala Thr Lys Asn
 210 215 220
 Ala Gln Ile Gly Phe Gly Ala Leu Ser Leu Ile Asp Lys Lys Asp Lys
 225 230 235 240
 Asn Leu Ser Tyr Phe Ile Ile Asp Lys Thr Leu Tyr Asn Pro Ile Glu
 245 250 255
 Gln Ala Leu Ile Ile Thr Lys Asn Gly Ala Asn Asn Pro Leu Ala Lys
 260 265 270
 Val Phe Lys Asp
 275

(2) INFORMATION FOR SEQ. ID NO:848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

Val	Ala	Leu	Leu	Glu	Pro	Ser	Val	Met	Tyr	Leu	Thr	Glu	Lys	Tyr	Gln
1				5				10						15	
Tyr	Ser	Arg	Phe	Lys	Val	Thr	Trp	Gly	Leu	Val	Ala	Leu	Ile	Phe	Val
			20					25					30		
Val	Gly	Val	Val	Leu	Ile	Phe	Ser	Leu	His	Lys	Asp	Tyr	Lys	Asp	Tyr
			35					40					45		
Leu	Thr	Phe	Phe	Glu	Lys	Ser	Leu	Phe	Asp	Trp	Leu	Asp	Phe	Ala	Ser
			50				55				60				
Ser	Thr	Ile	Ile	Xaa	Pro	Leu	Gly	Gly	Met	Xaa	Thr	Phe	Ile	Phe	Met
65					70					75					80
Gly	Trp	Val	Leu	Lys	Lys	Glu	Lys	Leu	Arg	Leu	Leu	Ser	Ala	His	Phe
				85					90					95	
Leu	Gly	Pro	Lys	Leu	Phe	Ala	Thr	Trp	Tyr	Phe	Leu	Leu	Lys	Tyr	Ile
			100					105					110		
Thr	Pro	Leu	Ile	Val	Phe	Ser	Ile	Trp	Leu	Ser	Lys	Ile	Tyr		
			115					120					125		

(2) INFORMATION FOR SEQ ID NO:849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

Val	Gly	Leu	Met	Lys	Ile	Arg	Phe	Met	Gly	Arg	Ser	Val	Phe	Val	Gly
1				5				10						15	
Asp	Leu	Glu	Arg	Ile	Glu	Glu	Val	Ala	Arg	Phe	Glu	Glu	Phe	Trp	Leu
			20					25					30		
Leu	Gly	Gly	Gln	Lys	Ala	Ile	Lys	Glu	Pro	Arg	Arg	Leu	Val	Leu	Glu
			35					40					45		
Ile	Ala	Leu	Lys	His	Gln	Leu	Asn	Lys	Leu	Leu	Lys	Arg	Val	Gln	Lys
			50				55				60				
His	Phe	Lys	Glu	Asp	Glu	Leu	Gly	Ile	Phe	Lys	Gln	Met	His	Asp	Lys

65		70		75		80									
Lys	Ile	Gln	Ser	Val	Ala	Thr	Asn	Ser	Ile	Gly	Arg	Leu	Phe	Asp	Ile
				85					90					95	
Val	Ala	Phe	Ser	Leu	Gly	Val	Val	Gly	Thr	Ile	Ser	Phe	Glu	Ala	Glu
			100					105					110		
Ser	Gly	Gln	Val	Leu	Glu	Asn	Leu	Ala	Leu	Gln	Ser	Asp	Glu	Ile	Ala
			115				120					125			
Phe	Tyr	Pro	Phe	Glu	Ile	Lys	Asn	Ser	Val	Val	Arg	Leu	Lys	Glu	Phe
	130						135				140				
Tyr	Gln	Ala	Phe	Glu	Lys	Asp	Leu	Gly	Val	Leu	Glu	Pro	Lys	Arg	Ile
145					150					155					160
Ala	Lys	Lys	Phe	Phe	Asn	Ser	Leu	Val	Glu	Ile	Ile	Thr	Ala	Leu	Ile
				165					170					175	
Ala	Pro	Phe	Lys	Gly	His	Val	Val	Val	Cys	Ser	Gly	Gly	Val	Phe	Cys
			180					185					190		
Asn	Gln	Leu	Leu	Cys	Glu	Gln	Leu	Ala	Lys	Arg	Leu	Lys	Lys	Leu	Gln
		195					200					205			
Arg	Glu	Tyr	Phe	Phe	His	Lys	His	Phe	Pro	Pro	Asn	Asp	Arg	Ser	Ile
	210					215					220				
Pro	Val	Gly	Gln	Ala	Leu	Met	Ala	Tyr	Phe	Asn	Pro	Thr	Ile	Ile	Lys
225					230					235					240
Lys	Gly														

(2) INFORMATION FOR SEQ ID NO:850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

Val	Ser	Asp	Ser	Asn	Ala	Leu	Lys	Glu	Val	Phe	Leu	Asn	Ile	Ser	Ala
1				5				10					15		
Lys	Glu	Asp	His	Cys	Asp	Val	Leu	Ile	Asn	Ser	Ala	Gly	Tyr	Gly	Val
			20				25					30			
Phe	Gly	Ser	Val	Glu	Asp	Thr	Pro	Ile	Glu	Glu	Val	Lys	Lys	Gln	Phe

35	40	45
Ser Val Asn Phe Phe Ala Leu Cys Glu Val Val Gln Leu Cys Leu Pro		
50	55	60
Leu Leu Lys Asn Lys Pro Tyr Ser Lys Ile Phe Asn Leu Ser Ser Ile		
65	70	75
Ala Gly Arg Val Ser Met Leu Phe Leu Gly His Tyr Ser Ala Ser Lys		
85	90	95
His Ala Leu Glu Ala Tyr Ser Asp Ala Leu Arg Leu Glu Leu Lys Pro		
100	105	110
Phe Asn Val Gln Val Cys Leu Ile Glu Pro Gly Pro Val Lys Ser Asn		
115	120	125
Trp Glu Lys Thr Ala Phe Glu Asn Asp Glu Arg Lys Asp Ser Val Tyr		
130	135	140
Ala Leu Glu Val Asn Ala Ala		
145	150	

(2) INFORMATION FOR SEQ ID NO:851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

Val Ile Val Ala Trp Leu Phe Arg Phe Lys Ser Ile Ala Phe Ser Ile		
1	5	10
Leu Ile Thr Leu Leu Val Ile Leu Val Asp Ile Trp Val Tyr Ser Asp		
20	25	30
Val Arg Gln Phe Leu Leu Asp Thr Ser Ser Ser Phe Ile Trp Leu Leu		
35	40	45
Ile Ala Leu Leu Ile Lys Trp Gly Val Ile Val Ile Ser Ala Arg Lys		
50	55	60
Cys Tyr Gln Phe Ser Gln Lys Met Phe Ala Leu Ile Gln Arg Lys Arg		
65	70	75
Gln Ile Arg Glu Asn Leu Lys Asn Arg Ser Asn Arg Lys Asp Ala Lys		
85	90	95

Asn Phe Glu Lys Leu Ser Asn Ile Ala Glu Glu Ile Ile Ser Lys Lys
 100 105 110
 Gln Glu Glu Ser His His Lys Glu Asp Ser Asn Asp Glu Asn His Lys
 115 120 125
 Asp Lys Leu Ser Asn Ile Thr Glu Glu Met Ile Leu Lys Lys Gln Glu
 130 135 140
 Glu Leu Lys Ala Arg Lys Asp Lys Gly Asp
 145 150

(2) INFORMATION FOR SEQ ID NO:852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

Val Leu Met Ala Leu Xaa Asp Lys Arg Tyr Gly Leu Glu Ala Gly Ile
 1 5 10 15
 Lys Tyr Phe Thr Met Gly Ala Met Ala Ser Ala Phe Phe Ala Met Gly
 20 25 30
 Ala Met Ala Phe Tyr Leu Leu Thr Gly Ser Leu Asn Leu Glu Val Ile
 35 40 45
 Thr Leu Tyr Leu His Thr Glu Gly Ile Thr Asn Pro Met Leu Phe Ala
 50 55 60
 Met Gly Thr Ile Phe Leu Ile Gly Ala Ile Gly Phe Lys Val Ser Leu
 65 70 75 80
 Val Pro Phe His Thr Trp Met Pro Asp Val Tyr Glu Gly Asn Asn Pro
 85 90 95
 Val Phe Ala Ser Tyr Ile Ser Ile Val Pro Lys Ile Ala Gly Phe Val
 100 105 110
 Val Ala Thr Arg Leu Phe Gly Ala Phe Ile Asp Thr His Thr Ala Trp
 115 120 125
 Val Glu Asp Ile Phe Tyr Val Leu Ile Leu Met Thr Ile Thr Ile Pro
 130 135 140
 Asn Phe Ile Ala Leu Trp Gln Glu Asp Val Lys Arg Met Leu Ala Tyr
 145 150 155 160

Ser Ser Ile Ser His Ser Gly Phe Ala Leu Ala Cys Val Phe Ile His
 165 170 175
 Thr Glu Asp Ser Gln Gln Ala Met Phe Val Tyr Trp Phe Met Phe Ala
 180 185 190
 Phe Thr Tyr Ile Gly Ala Phe Gly Leu Leu Trp Leu Leu Lys Ser Arg
 195 200 205
 Glu Lys Thr Trp Asp Glu Arg Tyr Asp His Pro Tyr Ser Lys Phe Asn
 210 215 220
 Gly Leu Ile Lys Thr His Pro Leu Val Ala Ile Leu Gly Ala Ile Phe
 225 230 235 240
 Val Phe Gly Leu Ala Gly Ile Pro Pro Phe Ser Val Phe Trp Gly Lys
 245 250 255
 Phe Leu Ala Val Glu Ser Ala Leu Glu Ser Asn His Ile Leu Leu Ala
 260 265 270
 Val Val Met Leu Val Asn Ser Ala Val Ala Ala Phe Tyr Tyr Phe Arg
 275 280 285
 Trp Leu Val Ala Met Phe Phe Asn Lys Pro Leu Gln Thr Gln Ser Tyr
 290 295 300
 Ala Lys Thr Ile Phe Thr Pro Lys Thr Pro Pro Cys Pro Phe Met Arg
 305 310 315 320
 Ser Leu Leu Pro Trp Arg
 325

(2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

Met Asn Tyr Pro Asn Leu Pro Asn Ser Ala Leu Xaa Ile Ser Glu Gln
 1 5 10 15
 Pro Glu Val Lys Glu Ile Thr Asn Glu Leu Leu Lys Gln Leu Gln Asn
 20 25 30
 Ala Leu Arg Ser Asn Ala His Phe Ser Glu Gln Val Glu Leu Ser Leu

35	40	45
Lys Cys Ile Val Arg Ile Leu Glu Val Leu Leu Ser Leu Asp Phe Phe		
50	55	60
Lys Asn Ala Asn Glu Ile Asp Ser Ser Leu Arg Asn Ser Ile Glu Trp		
65	70	75 80
Leu Thr Asn Ala Gly Glu Ser Leu Lys Leu Lys Met Lys Glu Tyr Glu		
	85	90 95
Arg Phe Phe Ser Glu Phe Asn Thr Ser Met His Ala Asn Glu Gln Glu		
	100	105 110
Val Thr Asn Thr Leu Asn Ala Asn Ala Glu Asn Ile Lys Ser Xaa Ile		
	115	120 125
Lys Xaa Leu Glu Asn Gln Leu Ile Glu Thr Thr Thr Arg Leu Leu Thr		
130	135	140
Ser Tyr Gln Ile Phe Leu Asn Gln Ala Arg Asp Asn Ala Asn Asn Gln		
145	150	155 160
Ile Thr Lys Asn Lys Thr Xaa Ser Leu Glu Ala Ile Thr Gln Ala Lys		
	165	170 175
Asn Asn Ser		

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

Met Ile Asn Ser Lys Lys Ser Leu Lys Lys Gly Leu Arg Gly Phe Phe		
1	5	10 15
Lys Ile Leu Lys Asp Arg Asn Gly Ala His Phe Ser Cys Gly Ala Thr		
	20	25 30
Ser Gly Phe Gly Leu Glu Ile Ala Lys Ala Phe Leu Gln Lys Asn His		
	35	40 45
Val Val Phe Gly Thr Gly Arg Arg Gln Glu Asn Leu Gln Lys Leu Gln		
50	55	60
Leu Ala Tyr Pro Lys Arg Phe Ile Pro Leu Cys Phe Asp Leu Gln Asn		

65		70		75		80									
Lys	Pro	Glu	Thr	Lys	Arg	Ala	Ile	Glu	Thr	Ile	Phe	Ser	Met	Thr	Asp
				85					90					95	
Arg	Ile	Asp	Ala	Leu	Ile	Asn	Asn	Ala	Gly	Leu	Ala	Leu	Gly	Leu	Asn
			100					105					110		
Lys	Ala	Tyr	Glu	Cys	Glu	Leu	Asp	Asp	Trp	Glu	Val	Met	Ile	Asp	Thr
		115					120					125			
Asn	Ile	Lys	Gly	Leu	Leu	His	Leu	Thr	Arg	Leu	Ile	Leu	Pro	Ser	Met
	130					135					140				
Ile	Glu	His	Asp	Gln	Gly	Thr	Ile	Ile	Asn	Leu	Gly	Ser	Ile	Ala	Gly
145					150					155					160
Thr	Tyr	Ala	Tyr	Pro	Gly	Gly	Xaa	Val	Tyr	Gly	Ala	Ser	Lys	Ala	Xaa
				165					170					175	
Val	Lys	Gln	Xaa	Ser	Xaa	Asn	Leu	Arg	Ala	Asp	Val	Ala	Gly	Thr	Asn
			180					185					190		
Thr	Arg	Gly	Arg	Arg	Trp	Asn	Pro	Gly	Cys	Val	Ala	Lys	Pro	Lys	Val
		195					200					205			
Ser	Arg	Val	Arg	Gly	Lys	Gly	Asp	Lys	Pro	Lys	Pro	Lys	Ser	Gly	Tyr
	210					215					220				
Glu	Lys	His	Pro	Leu	Pro	Gln	Thr	Thr	Arg	Gln	Gly	Leu	Thr	Ser	Gly
225					230					235					240

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1...160
- (D) OTHER INFORMATION: /note= "flagellar biosynthetic protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

Val	Phe	Ala	Thr	Asp	Ser	Ser	Ser	Phe	Ser	Met	Gly	Leu	Thr	Met	Ala
1					5				10					15	
Ser	Ala	Tyr	Glu	Pro	Ile	Ser	Gly	Ser	Gln	Lys	Pro	Ile	Val	Gly	Gln

20	25	30
Ala Leu Leu Leu Leu Ala Ile Leu Ile Leu Leu Asp Leu Ser Phe His		
35	40	45
His Gln Ile Ile Leu Phe Val Asp His Ser Leu Lys Ala Val Pro Leu		
50	55	60
Gly Arg Phe Val Phe Glu Pro Glu Leu Ala Lys Asn Ile Val Lys Ala		
65	70	75
Phe Ser His Leu Phe Val Ile Gly Phe Ser Met Ala Phe Pro Ile Leu		
85	90	95
Cys Leu Val Leu Leu Ser Asp Ile Ile Phe Gly Met Ile Met Lys Thr		
100	105	110
His Pro Gln Phe Asn Leu Leu Ala Ile Gly Phe Pro Val Lys Ile Ala		
115	120	125
Ile Gly Phe Val Gly Ile Ile Leu Ile Ala Ser Ala Ile Met Gly Arg		
130	135	140
Phe Lys Glu Glu Ile Ser Leu Ala Phe Ser Val Ile Ser Lys Ile Phe		
145	150	155
		160

(2) INFORMATION FOR SEQ ID NO:856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

Met Tyr Gly Val Lys Glu Ile Lys Asp Lys Ile Asp Lys Gln Leu His
1 5 10 15
Asn Asn Asp His Leu Phe Glu Gly Leu Phe Gly Glu Lys Glu Asp Leu
20 25 30
Lys Lys Leu Val Ser Met Phe Gly Gln Leu Arg Phe Gln Lys Arg Trp
35 40 45
Ser Gln Thr Pro Arg Val Pro Gln Thr Ser Val Leu Gly His Thr Leu
50 55 60
Cys Val Ala Ile Met Gly Tyr Leu Leu Ser Phe Asp Leu Lys Ala Cys
65 70 75 80

Lys Ser Met Arg Ile Asn His Phe Leu Gly Gly Leu Phe Pro
85 90

(2) INFORMATION FOR SEQ ID NO:857:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

Met	Thr	Leu	Asp	Asp	Leu	Leu	Gly	Gly	Ser	Leu	Asp	Pro	His	Cys	Phe	1	5	10	15
Cys	Lys	Pro	Leu	Ile	Lys	Thr	Lys	Lys	Asp	Gln	Glu	Arg	Leu	Leu	Ser	20	25	30	
Leu	Ala	Leu	Lys	Ala	His	Pro	Lys	Ile	Ser	Phe	Gly	Lys	Asp	Ser	Ala	35	40	45	
Pro	His	Phe	Ile	Ser	Lys	Lys	His	Ser	Ala	Asn	Ile	Pro	Ala	Gly	Ile	50	55	60	
Phe	Ser	Ala	Pro	Ile	Leu	Leu	Pro	Ala	Leu	Cys	Glu	Leu	Phe	Glu	Lys	65	70	75	80
His	Asn	Ala	Leu	Glu	Asn	Leu	Gln	Ala	Phe	Ile	Ser	Asp	Asn	Ala	Lys	85	90	95	
Lys	Ile	Tyr	Ala	Leu	Asp	Asn	Leu	Pro	Ser	Lys	Lys	Ala	His	Leu	Ser	100	105	110	
Lys	Lys	Pro	Phe	Ile	Val	Pro	Thr	His	Thr	Leu	Cys	Leu	Asn	Glu	Lys	115	120	125	
Ile	Ala	Ile	Leu	Arg	Gly	Gly	Glu	Thr	Leu	Ser	Trp	Asn	Leu	Gln	Glu	130	135	140	
Ile	Ala															145			

(2) INFORMATION FOR SEQ ID NO:858:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

Val	Ser	Gly	Val	Val	Leu	Ser	Lys	Phe	Asp	Ser	Asp	Ser	Lys	Gly	Gly	
1				5					10					15		
Ile	Ala	Leu	Gly	Ile	Thr	Tyr	Gln	Leu	Gly	Leu	Pro	Leu	Arg	Phe	Ile	
			20					25					30			
Gly	Ser	Gly	Glu	Lys	Ile	Pro	Asp	Leu	Asp	Val	Phe	Met	Pro	Glu	Arg	
			35				40					45				
Ile	Val	Gly	Arg	Leu	Met	Gly	Ala	Gly	Asp	Ile	Ile	Ser	Leu	Ala	Glu	
	50					55					60					
Lys	Thr	Ala	Ser	Val	Leu	Asn	Pro	Asn	Glu	Ala	Lys	Asp	Leu	Ser	Lys	
65					70				75						80	
Lys	Leu	Lys	Lys	Gly	Gln	Phe	Thr	Phe	Asn	Asp	Phe	Leu	Asn	Gln	Ile	
				85					90					95		
Glu	Lys	Val	Lys	Lys	Leu	Gly	Ser	Met	Ser	Ser	Leu	Ile	Ser	Met	Ile	
			100					105					110			
Pro	Gly	Leu	Gly	Asn	Met	Ala	Ser	Ala	Leu	Lys	Asp	Thr	Asp	Leu	Glu	
			115				120					125				
Ser	Ser	Leu	Glu	Val	Lys	Lys	Ile	Lys	Ala	Met	Val	Asn	Ser	Met	Thr	
	130					135					140					
Lys	Lys	Glu	Arg	Glu	Asn	Pro	Glu	Ile	Leu	Asn	Gly	Ser	Arg	Arg	Lys	
145					150				155						160	
Arg	Ile	Ala	Leu	Gly	Xaa	Gly	Leu	Glu	Xaa	Xaa	Glu	Ile	Asn	Arg	Ile	
				165					170					175		
Ile	Lys	Arg	Phe	Asp	Gln	Ala	Ser	Lys	Met	Ala	Lys	Arg	Leu	Thr	Asn	
			180					185					190			
Lys	Lys	Gly	Ile	Ser	Asp	Leu	Met	Asn	Leu	Xaa	Xaa					
			195				200									

(2) INFORMATION FOR SEQ ID NO:859:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

Met	Gly	Val	Leu	Gly	Met	Phe	Ala	Phe	Phe	Ser	Trp	Val	Phe	Leu	Phe	
1				5					10					15		
Lys	His	Asn	Leu	Ser	His	Lys	Ile	Arg	Leu	Tyr	His	Glu	Lys	Lys	Asp	
			20					25					30			
Phe	Asp	Lys	Leu	Leu	Lys	Gln	Ile	Leu	Ser	Gln	Asp	Thr	Gln	Lys	Thr	
		35					40					45				
Phe	Leu	Lys	Thr	Lys	Phe	Lys	Ser	Asp	Leu	Ala	Lys	Asn	Leu	Ser	Gln	
	50					55					60					
Ile	Leu	Ala	Arg	Tyr	Asp	Leu	Lys	Ala	Asp	Leu	Asn	Thr	Pro	Asn	Ser	
65					70					75					80	
Gly	Cys	Glu	Lys	Val	Asp	Asn	Leu	Phe	Lys	His	Tyr	His	Asn	Ile	Glu	
				85					90					95		
Asn	Asn	Thr	Leu	Glu	Pro	Lys	Asp	His	Ala	Lys	His	Ser	Leu	Ala	Tyr	
			100					105					110			
Glu	His	Ala	Tyr	Phe	Ser	Lys	Arg	Leu	Lys	Ala	Phe	Ile	His	Asn	Asp	
		115					120					125				
Leu	Lys	Asn	Ala	Phe	Glu	Val	Leu	Thr	Asn	Ala	Gln	Ile	Pro	Leu	Glu	
	130					135					140					
Leu	Arg	Arg	Tyr	Ala	Tyr	Arg	Asn	Arg	Pro	Lys	Arg	Gln	Gln	Lys	Arg	
145					150					155					160	
Gly	Phe	Lys	Gly	Cys	Glu	Cys	Asp	Ala	Arg	Gly	Phe	Gly				
				165					170							

(2) INFORMATION FOR SEQ ID NO:860:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

Val Ser Val Pro Ala Thr Ser Ala Asn Leu Gly Pro Gly Phe Asp Cys

1	5	10	15
Leu Gly Leu Ser Leu Asn Leu Arg Asn Arg Phe Phe Ile Glu Pro Ser	20	25	30
Asn Ile His Ala Val Lys Leu Val Gly Glu Gly Glu Gly Ile Pro Lys	35	40	45
Phe Leu Thr Asn Asn Ile Phe Thr Lys Val Phe Tyr Glu Ile Leu Lys	50	55	60
Lys His Gly Asn Asp Gly Ser Phe Lys Phe Leu Leu His Asn Lys Val	65	70	75
Pro Ile Thr Arg Gly Met Gly Ser Ser Ser Ala Met Ile Val Gly Ala	85	90	95
Val Ala Ser Ala Phe Ala Phe Leu Gly Phe Ala Phe Asp Arg Glu Asn	100	105	110
Ile Leu Asn Thr Ala Leu Ile Tyr Glu Asn His Pro Asp Asn Ile Thr	115	120	125
Pro Ala Val Phe Gly Gly Tyr Asn Ala Ala Phe Val Glu Lys Lys Lys	130	135	140
Val Ile Ser Leu Lys Thr Lys Ile Pro Ser Phe Leu Lys Ala Val Met	145	150	155
Val Ile Pro Asn Arg Val Ile Ser Thr Lys Gln Ser Arg His Leu Cys	165	170	175
Pro Ser Val Thr Ala Cys Lys Lys Ala Cys Leu Thr Phe Arg Met Arg	180	185	190
Val			

(2) INFORMATION FOR SEQ ID NO:861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

Val Ala Lys Asn Leu Val Ala Ser Gly Val Cys Asp Lys Ala Thr Val	1	5	10	15
Gln Leu Ala Tyr Ala Ile Gly Val Ile Glu Pro Val Ser Ile Tyr Val				

20	25	30
Asn Thr His Asn Thr Ser Lys His Ser Ser Ala Glu Leu Glu Lys Cys		
35	40	45
Val Lys Ser Val Phe Lys Leu Thr Pro Lys Gly Ile Ile Glu Ser Leu		
50	55	60
Asp Leu Leu Arg Pro Ile Tyr Ser Leu Thr Ser Ala Tyr Gly His Phe		
65	70	75
Gly Arg Glu Leu Glu Glu Phe Thr Trp Glu Lys Thr Asn Lys Val Glu		
	85	90
		95
Glu Ile Lys Ala Phe Phe Lys Arg		
100		

(2) INFORMATION FOR SEQ ID NO:862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

Val Arg Leu Phe Arg Phe Val Gly Trp Tyr Tyr Phe Lys Tyr Phe Leu		
1	5	10
Ile Val Leu Leu Ala Leu Glu Leu Phe Phe Val Gly Ile Asp Ser Leu		
	20	25
		30
Lys Tyr Ala Asp Lys Met Pro Asp Ser Ala Asn Met Ile Ile Leu Phe		
	35	40
		45
Phe Thr Tyr Asp Ile Leu Phe Ala Leu Asn Tyr Thr Leu Pro Ile Ser		
	50	55
		60
Leu Leu Leu Ala Met Val Leu Phe Tyr Ile Thr Phe Ile Lys Ser Asn		
65	70	75
		80
Gln Tyr Thr Ala Leu Leu Ser Ile Gly Phe Ser Lys Cys Gln Ile Leu		
	85	90
		95
Ser Pro Ile Phe Leu Ile Ser Leu Phe Phe Thr Ala Val Tyr Val Gly		
	100	105
		110
Leu Asn Ala Thr Pro Phe Val Tyr Met Glu Glu Lys Thr Gln Asn Leu		
	115	120
		125

Ile	Tyr	Lys	Asp	Asn	Ser	Leu	Ser	Val	Ser	Glu	His	Leu	Leu	Val	Lys	130	135	140
Tyr	Asn	Asp	Asp	Tyr	Val	Tyr	Phe	Asp	Lys	Ile	Asn	Pro	Leu	Leu	Gln	145	150	155
Lys	Ala	Gln	Asn	Ile	Lys	Val	Phe	Arg	Leu	Lys	Asp	Lys	Thr	Leu	Glu	165	170	175
Ser	Tyr	Ala	Glu	Ala	Lys	Glu	Ala	Phe	Phe	Glu	Asp	Lys	Tyr	Trp	Ile	180	185	190
Leu	His	Asp	Thr	Thr	Ile	Tyr	Glu	Met	Pro	Leu	Ser	Phe	Glu	Leu	Gly	195	200	205
Ala	Asn	Ala	Leu	Asn	Thr	Thr	His	Leu	Glu	Thr	Phe	Lys	Thr	Leu	Lys	210	215	220
Asn	Phe	Arg	Pro	Lys	Val	Leu	Asp	Thr	Ile	Tyr	Gln	Asn	Lys	Pro	Ala	225	230	235
Val	Ser	Ile	Thr	Asp	Ala	Leu	Leu	Ser	Leu	His	Ala	Leu	Val	Arg	Gln	245	250	255
Asn	Ala	Asp	Thr	Lys	Lys	Val	Arg	Ser	Phe	Leu	Tyr	Val	Phe	Ala	Ile	260	265	270
Leu	Pro	Phe	Phe	Val	Pro	Phe	Leu	Ser	Val	Leu	Ile	Ala	Tyr	Phe	Ser	275	280	285
Pro	Ser	Leu	Ala	Arg	Tyr	Glu	Asn	Leu	Ala	Leu	Leu	Gly	Leu	Lys	Phe	290	295	300
Ile	Ile	Ile	Thr	Leu	Val	Val	Trp	Gly	Leu	Phe	Phe	Ala	Leu	Gly	Lys	305	310	315
Phe	Ser	Ile	Ser	Gly	Ile	Leu	Ile	Pro	Glu	Ile	Gly	Val	Leu	Ser	Pro	325	330	335
Phe	Phe	Val	Phe	Leu	Ala	Leu	Ser	Leu	Trp	Tyr	Phe	Lys	Lys	Leu	Asn	340	345	350
Lys	Arg	Leu														355		

(2) INFORMATION FOR SEQ ID NO:863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

```
Val Glu Lys Ala His Pro Asp Val Phe Asn Leu Leu Leu Gln Val Leu
1           5           10           15
Asp Glu Gly His Leu Thr Asp Ser Lys Gly Val Arg Val Asp Phe Lys
          20           25           30
Asn Thr Ile Leu Ile Leu Thr Ser Asn Val Ala Ser Gly Ala Leu Leu
          35           40           45
Glu Glu Asp Leu Ser Glu Ala Asp Lys Gln Lys Ala Ile Lys Glu Ser
          50           55           60
Leu Arg Gln Phe Phe Lys Pro Glu Phe Leu Asn Arg Leu Asp Glu Ile
65           70           75           80
Ile Ser Phe Asn Ala Leu Asp Ser His Ala Ile Ile
          85           90
```

(2) INFORMATION FOR SEQ ID NO:864:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864

```
Leu Val Phe Leu Asp Arg Arg Leu Ile Val Met Val Thr Asp Ser Lys
1           5           10           15
Gly Ser Arg Tyr Ile Asn Val His Ile Leu Phe Arg Gln Ile Ser Leu
          20           25           30
Tyr Ala Leu Leu Ser Val Val Gly Ser Leu Leu Phe Leu Gly Val Ser
          35           40           45
Leu Leu Val Leu Asn Lys Glu Ile Lys Asn Ile Glu Lys Gln His Ala
          50           55           60
Leu Xaa Thr Lys Glu Phe Glu Lys Lys Arg Glu Thr Asn Glu Xaa Leu
65           70           75           80
Ser Xaa
```

(2) INFORMATION FOR SEQ ID NO:865:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(B) TYPE: amino acid

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

Leu Ser Leu Met Xaa Val Leu Asn Ala Lys Glu Cys Val Xaa Pro Ile
1 5 10 15

Thr Arg Ser Val Lys Tyr His Gln Gln Ser Ala Glu Ile Arg Ala Leu
20 25 30

Gln Leu Gln Ser Tyr Lys Met Ala Lys Met Ala Leu Asp Asn Asn Leu
35 40 45

Lys Leu Val Lys Asp Lys Lys Pro Ala Val Ile Leu Asp Leu Asp Glu
50 55 60

Thr Val Leu Asn Thr Phe Asp Tyr Ala Gly Tyr Leu Val Lys Asn Cys
65 70 75 80

Ile Lys Tyr Thr Pro Glu Thr Trp Asp Lys Phe Glu Lys Glu Gly Ser
85 90 95

Leu Thr Leu Ile Pro Gly Ala Leu Asp Phe Leu Glu Tyr Ala Asn Ser
100 105 110

Lys Gly Val Lys Ile Phe Tyr Ile Ser Asn Arg Thr Gln Lys Asn Lys
115 120 125

Ala Phe Thr Leu Lys Thr Leu Lys Ser Phe Lys Leu Pro Gln Val Ser
130 135 140

Glu Glu Ser Val Leu Leu Lys Glu Lys Gly Lys Pro Lys Ala Val Arg
145 150 155 160

Arg Glu Leu Val Ala Lys Asp Tyr Ala Ile Val Leu Gln Val Gly Asp
165 170 175

Thr Leu His Asp Phe Asp Ala Ile Phe Ala Lys Asp Ala Lys Asn Ser
180 185 190

Gln Glu Gln Gln Ala Lys Val Leu Gln Asn Ala Gln Lys Phe Gly Thr
195 200 205

Glu Trp Ile Ile Leu Pro Asn Ser Leu Tyr Gly Thr Trp Glu Asp Gly
210 215 220

Pro Ile Lys Ala Trp Gln Asn Lys Lys

(2) INFORMATION FOR SEQ ID NO:866:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

Met	Ile	Tyr	Gly	Val	Leu	Asp	Gly	Leu	Phe	Leu	Ala	Ile	Leu	Gln	Ala	1	5	10	15
Gln	Asn	Tyr	Arg	Phe	His	Ser	Leu	Tyr	Leu	Phe	Glu	Glu	Asn	Leu	Asp	20	25	30	
Leu	Phe	Lys	Ile	Ser	Cys	Tyr	Phe	Ala	Arg	Tyr	Glu	Asp	Leu	Ile	Lys	35	40	45	
Lys	Gly	Ala	Lys	Leu	Phe	Ile	Gln	Gly	Phe	Phe	Asn	Pro	Asn	Glu	Leu	50	55	60	
Lys	Met	Asp	Phe	Leu	Lys	Arg	Pro	Ile	Thr	His	Ser	Phe	Leu	Lys	Leu	65	70	75	80
Glu	Ile	Met	Pro	Tyr	Lys	Ser	Ala	Phe	Asn	Leu	Arg	Met	Arg	Glu	Asn	85	90	95	
Ile	Gln	Ser	Tyr	Tyr	Lys	Gln	Ala	Leu	Arg	Gly	Trp	Gly	Ser	Phe	Glu	100	105	110	
Asp	Glu	Leu	Leu	Gly	Leu	Lys	Asn	Thr	Leu	Lys	Asn	Leu	Pro	Leu	Tyr	115	120	125	
Gln	Thr	Leu	Lys	Thr	Lys	Pro	Lys	Lys	Ile	Asn	Ala	Pro	Ile	Cys	Val	130	135	140	
Val	Gly	Asn	Gly	Pro	Ser	Leu	Asp	Leu	Leu	Leu	Asp	Phe	Leu	Lys	Glu	145	150	155	160
Asn	Glu	Glu	Lys	Phe	Ile	Ile	Phe	Ser	Cys	Gly	Thr	Ala	Leu	Lys	Pro	165	170	175	
Leu	Lys	Ala	His	Gly	Val	Lys	Val	Asp	Phe	Gln	Ile	Glu	Val	Glu	Arg	180	185	190	
Ile	Asp	Tyr	Leu	Lys	Glu	Val	Leu	Glu	Arg	Ala	Pro	Leu	Glu	Asp	Thr	195	200	205	

Pro Leu Met Gly Ala Asn Met Leu Asn Pro Asn Ala Phe Asp Leu Ala
 210 215 220

Lys Glu Ala Leu Met Phe Met Arg Gly Gly Ser Ala Cys Ala Val
 225 230 235

(2) INFORMATION FOR SEQ ID NO:867:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

Met Leu Ala Ala Gly Leu Thr Leu Pro Glu Phe Gly Cys Tyr Leu Ser
 1 5 10 15

His Tyr Leu Leu Trp Lys Glu Cys Val Lys Leu Asp Gln Pro Val Val
 20 25 30

Ile Leu Glu Asp Asp Val Thr Leu Glu Ser His Phe Met Gln Ala Leu
 35 40 45

Glu Asp Cys Leu Lys Ser Pro Phe Asp Phe Val Arg Leu Tyr Gly Cys
 50 55 60

Tyr Trp Tyr Tyr Gln Arg Asp Lys Ile Pro Cys Phe Ala Gln Arg Ile
 65 70 75 80

Cys Ile Ser Ser Leu
 85

(2) INFORMATION FOR SEQ ID NO:868:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

Met	Leu	Ala	Phe	Leu	Lys	Thr	Pro	Arg	Asn	Ser	Ala	Phe	Ala	Leu	Gly	1	5	10	15
Ile	Phe	Val	Gly	Ala	Leu	Leu	Phe	Tyr	Trp	Cys	Ala	Leu	Arg	Leu	Ser	20	25	30	
His	Ser	Asp	Phe	Thr	Tyr	Leu	Leu	Pro	Leu	Ile	Ile	Val	Leu	Val	Ala	35	40	45	
Leu	Val	Tyr	Gly	Val	Leu	Phe	Tyr	Leu	Leu	Leu	Tyr	Phe	Glu	Asn	Pro	50	55	60	
Tyr	Phe	Arg	Leu	Leu	Ser	Phe	Leu	Gly	Ser	Ser	Phe	Ile	His	Pro	Phe	65	70	75	80
Gly	Phe	Asp	Trp	Leu	Val	Pro	Asp	Ser	Phe	Phe	Ser	Tyr	Ser	Val	Phe	85	90	95	
Arg	Val	Asp	Lys	Leu	Ser	Leu	Gly	Leu	Ile	Phe	Leu	Ala	Cys	Ile	Phe	100	105	110	
Leu	Ser	Ala	Gln	Asn	Leu	Lys	Lys	Tyr	Arg	Met	Ile	Gly	Val	Leu	Leu	115	120	125	
Leu	Leu	Gly	Ala	Leu	Asp	Phe	His	Phe	Phe	Lys	Ile	Ser	Asp	Leu	Lys	130	135	140	
Glu	Val	Gly	Asn	Ile	Glu	Leu	Val	Ser	Thr	Arg	Thr	Pro	Gln	Asp	Leu	145	150	155	160
Lys	Phe	Asp	Ser	Asn	Tyr	Leu	Asn	Asn	Ile	Glu	Asn	Asn	Ile	Leu	Lys	165	170	175	
Glu	Ile	Lys	Leu	Ala	Gln	Ser	Lys	Gln	Lys	Thr	Leu	Ile	Val	Phe	Pro	180	185	190	
Glu	Thr	Ala	Tyr	Pro	Ile	Ala	Leu	Glu	Asn	Ser	Pro	Phe	Lys	Thr	Gln	195	200	205	
Leu	Glu	Asp	Leu	Ser	Asp	Lys	Ile	Ala	Ile	Leu	Ile	Gly	Thr	Leu	Arg	210	215	220	
Ala	Gln	Gly	Tyr	Ser	Leu	Tyr	Asn	Ser	Ser	Phe	Leu	Phe	Ser	Lys	Lys	225	230	235	240
Ser	Val	Gln	Ile	Ala	Asp	Lys	Val	Ile	Leu	Ala	Pro	Phe	Gly	Glu	Ile	245	250	255	
Met	Pro	Leu	Pro	Glu	Phe	Leu	Gln	Lys	Pro	Leu	Glu	Lys	Leu	Phe	Phe	260	265	270	
Ala	Arg	Ala	Leu	Ile	Tyr	Thr	Ala	Thr	Leu	Pro	Ile	Ser	Ala	Ile	Leu	275	280	285	
His																			

(2) INFORMATION FOR SEQ ID NO:869:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 436 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

Met	Asn	Asp	Pro	Lys	His	Val	Val	Tyr	Val	Trp	Leu	Asp	Ala	Leu	Leu	1	5	10	15
Asn	Tyr	Ala	Ser	Ala	Leu	Gly	Tyr	Leu	Asn	Gly	Leu	Asp	Asn	Lys	Met	20	25	30	
Ala	His	Phe	Glu	Arg	Ala	Arg	His	Ile	Val	Gly	Lys	Asp	Ile	Leu	Arg	35	40	45	
Phe	His	Ala	Ile	Tyr	Trp	Pro	Ala	Phe	Leu	Met	Ser	Leu	Asn	Leu	Pro	50	55	60	
Leu	Phe	Lys	Gln	Leu	Cys	Val	His	Gly	Trp	Trp	Thr	Ile	Glu	Gly	Val	65	70	75	80
Lys	Met	Ser	Lys	Ser	Leu	Gly	Asn	Val	Leu	Asp	Ala	Gln	Lys	Leu	Ala	85	90	95	
Met	Glu	Tyr	Gly	Ile	Glu	Glu	Leu	Arg	Tyr	Phe	Leu	Leu	Arg	Glu	Val	100	105	110	
Pro	Phe	Gly	Gln	Asp	Gly	Asp	Phe	Ser	Lys	Lys	Ala	Leu	Val	Glu	Arg	115	120	125	
Ile	Asn	Ala	Asn	Leu	Asn	Asn	Asp	Leu	Gly	Asn	Leu	Leu	Asn	Arg	Leu	130	135	140	
Leu	Gly	Met	Ala	Lys	Lys	Tyr	Phe	Asn	Tyr	Ser	Leu	Lys	Ser	Thr	Lys	145	150	155	160
Ile	Thr	Ala	Tyr	Tyr	Pro	Lys	Glu	Leu	Glu	Lys	Ala	His	Gln	Ile	Leu	165	170	175	
Asp	Asn	Ala	Asn	Ser	Phe	Val	Pro	Lys	Met	Gln	Leu	His	Lys	Ala	Leu	180	185	190	
Glu	Glu	Leu	Phe	Asn	Ile	Tyr	Asp	Phe	Leu	Asn	Lys	Leu	Ile	Ala	Lys	195	200	205	
Glu	Glu	Pro	Trp	Val	Leu	His	Lys	Asn	Asn	Glu	Ser	Glu	Lys	Leu	Glu	210	215	220	
Ala	Leu	Leu	Ser	Leu	Ile	Ala	Asn	Thr	Leu	Leu	Gln	Ser	Ser	Phe	Leu				

225		230		235		240
Leu Tyr Ala Phe Met Pro Lys Ser Ala Met Lys Leu Ala Ser Ala Phe						
	245			250		255
Arg Val Glu Ile Thr Pro Asn Asn Tyr Glu Arg Phe Phe Lys Ala Lys						
	260			265		270
Lys Leu Gln Asp Met Val Leu Gln Asp Thr Glu Pro Leu Phe Ser Lys						
	275			280		285
Ile Glu Lys Ile Glu Lys Ile Glu Lys Ile Glu Lys Ile Glu Lys Ile						
	290			295		300
Glu Lys Gly Glu Glu Ala Leu Ala Glu Lys Ala Glu Lys Lys Glu Lys						
305		310		315		320
Glu Lys Ala Pro Pro Thr Gln Glu Asn Tyr Ile Ser Ile Glu Asp Phe						
	325			330		335
Lys Lys Val Glu Ile Lys Val Gly Leu Ile Lys Glu Ala Gln Arg Ile						
	340			345		350
Glu Lys Ser Asn Lys Leu Leu Arg Leu Lys Val Asp Leu Gly Glu Asn						
	355			360		365
Arg Leu Arg Gln Ile Ile Ser Gly Ile Ala Leu Asp Tyr Glu Pro Glu						
	370			375		380
Ser Leu Val Gly Gln Met Val Cys Val Val Ala Asn Leu Lys Pro Ala						
385		390		395		400
Lys Leu Met Gly Glu Met Ser Glu Gly Met Ile Leu Ala Val Arg Asp						
	405			410		415
Asn Asp Asn Leu Ala Leu Ile Ser Pro Thr Arg Glu Lys Ile Ala Gly						
	420			425		430
Ser Leu Ile Ser						
	435					

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

Met Lys Arg Pro Ile Ser Lys Leu Lys Gln Asn Phe Leu Gln Phe Lys
 1 5 10 15
 His Ser Phe Asn Lys His Leu Asp Lys Tyr Ser Leu Tyr Tyr Arg Leu
 20 25 30
 Phe Asn Ile Ser Ser Ile Val Ile Gly Phe Leu Ile Ala Leu Phe Ser
 35 40 45
 Tyr Gly Ala Gly Val Ile Leu Val Tyr Pro Ile Leu Phe Leu Phe Ala
 50 55 60
 Leu Ile Ile Lys Pro Ser Phe Phe Tyr Tyr Thr Thr Tyr Leu Leu Leu
 65 70 75 80
 Leu Val Ser Leu Ser Ile Ile Ser Lys Tyr Tyr Leu Leu Ser His Ala
 85 90 95
 Asn Phe Thr Met Lys Leu Ile Met Leu Met Thr Gln Trp Gln Asn Trp
 100 105 110
 Phe Leu

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

Met Gly Phe Glu Lys Ser Ile Leu Asp Asn Leu Asn Gly Ala Gln Lys
 1 5 10 15
 Ile Val Ala Cys His Ile Gln Gly Pro Leu Leu Ile Leu Ala Gly Ala
 20 25 30
 Gly Ser Gly Lys Thr Lys Thr Leu Thr Ser Arg Leu Ala Tyr Leu Ile
 35 40 45
 Gly Ala Cys Gly Val Pro Ser Glu Asn Thr Leu Thr Leu Thr Phe Thr
 50 55 60
 Asn Lys Ala Ser Lys Glu Met Gln Glu Arg Ala Leu Lys Leu Leu Lys
 65 70 75 80
 Asn Gln Ala Leu Ile Pro Pro Leu Leu Cys Thr Phe His Arg Phe Gly
 85 90 95

Leu Leu Phe Leu Arg Gln His Met Asn Leu Leu Lys Arg Ala Cys Asp
 100 105 110
 Phe Ser Val Leu Asp Ser Asp Glu Val Lys Thr Leu Cys Lys Gln Leu
 115 120 125
 Lys Ile Ser Asn Phe Arg Ala Ser Ile Ser Gln Ile Lys Asn Gly Met
 130 135 140
 Met Asp Leu Ser Val Gln Asp Ser Glu Cys Tyr Lys Ala Tyr Glu Leu
 145 150 155 160
 Tyr Gln Asn Ala Leu Lys Lys Asp Asn Leu Val Glu Phe
 165 170

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

Leu Ile Ala Leu Arg Val Thr Ala Trp Lys Val Xaa Ala Met Lys Arg
 1 5 10 15
 Leu His Leu Ser Val Lys Asp Ala Glu Asn Phe Asp Ala Ile Leu Arg
 20 25 30
 Glu Arg Pro Phe Phe Lys Asp Leu Ile Glu Phe Met Val Ser Gly Pro
 35 40 45
 Val Val Val Met Val Leu Glu Gly Lys Asp Ala Val Ala Lys Asn Arg
 50 55 60
 Glu Leu Met Gly Ala Thr Asp Pro Lys Leu Ala Gln Lys Gly Thr Ile
 65 70 75 80
 Arg Ala Asp Phe Ala Glu Ser Ile Asp Ala Asn Ala Val His Gly Ser
 85 90 95
 Asp Ser Leu Glu Asn Ala His Asn Glu Ile Ala Phe Phe Phe Ala Ala
 100 105 110
 Arg Glu Phe
 115

(2) INFORMATION FOR SEQ ID NO:873:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1...127
 - (D) OTHER INFORMATION: /note= "SODIUM-DEPENDENT PROLINE TRANSPORTER"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

```

Val Phe Thr Tyr Ser Leu Gly Gln Val Phe Phe Ser Leu Ser Ile Gly
1           5           10           15

Leu Gly Ile Asn Ile Thr Tyr Ala Ala Val Thr Asp Lys Thr Gln Asn
          20           25           30

Leu Leu Lys Ser Thr Ile Trp Val Val Leu Ser Gly Ile Leu Ile Ser
          35           40           45

Leu Val Xaa Gly Leu Met Ile Phe Thr Phe Val Phe Glu Tyr Gly Ala
          50           55           60

Asn Val Ser Gln Gly Thr Gly Leu Ile Phe Thr Ser Leu Pro Val Val
65           70           75           80

Phe Gly Gln Met Gly Ala Ile Gly Val Pro Cys Phe Asn Ser Phe Leu
          85           90           95

Ala Arg Ala Arg Phe Cys Trp His His Phe Tyr Gly Gly Phe Ile Arg
          100          105          110

Ala Lys Arg Asp Val Ser Tyr Arg Lys Val Ser Ile Leu Ser Phe
          115          120          125

```

(2) INFORMATION FOR SEQ ID NO:874:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

Met Lys Pro Leu His Phe Ser His Leu Asp Arg Glu Gln Ser Gly Asp
1 5 10 15
Val Gly Phe Ile Ile Lys Asn Leu Ile Phe Leu Gly Val Phe Ser Leu
20 25 30
Leu Gly Trp Leu Asn Thr Glu Tyr Phe Leu Trp Pro Ser Met Leu Glu
35 40 45
Leu Lys Lys Ile Leu Leu Glu Glu Asn Arg Lys Lys Ser Val Leu Glu
50 55 60
Tyr Ala Gln Arg His Phe Glu Thr Ala Leu Ala Asn Tyr Arg Asn Gln
65 70 75 80
Lys Glu Thr Ser Glu Ser Leu Leu Lys Ile Phe Asn Asp Glu Glu Ser
85 90 95
Arg Arg Ile Leu Glu Lys Ile Leu Lys Lys Cys Phe Asp Ala Tyr Lys
100 105 110
Ile Lys Pro Leu Leu Ser Gln Asn Pro Ser Gln Lys Thr Gln Phe Phe
115 120 125
Ile Met Ala Arg Ala Ser Glu Leu Glu Lys Thr Tyr Leu Phe Phe Thr
130 135 140
Leu Ile Asn Lys Tyr Leu
145 150

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

Met Asn Ala Leu Lys Arg Ala Cys Leu Arg Leu Met Gly Glu Thr Asn
1 5 10 15
Thr Asp Asp Leu Xaa Pro Xaa Ser Asp Ala Phe Thr Arg Ser Asp Ile
20 25 30
Pro Leu His Ala Lys Ala Met Leu Lys Asn Arg Ile Glu Asn Tyr Glu
35 40 45

Gln Arg Ile Glu Ala Ile Lys Thr Lys Gly Val Pro Val Ala Tyr Val
 50 55 60
 Gly Asp Val Val Gly Thr Gly Ser Ser Arg Lys Ser Ala Thr Asn Ser
 65 70 75 80
 Ile Met Trp His Phe Gly Lys Asp Ile Pro Phe Val Pro Asn Lys Arg
 85 90 95
 Ser Gly Gly Ile Val Ile Gly Gly Val Ile Ala Pro Ile Phe Phe Ala
 100 105 110
 Thr Cys Glu Asp Ser Gly Ala Leu Pro Ile Val Ala Asp Val Lys Asp
 115 120 125
 Leu Lys Glu Gly Asp Ile Ile Lys Ile Tyr Pro Tyr Lys Gly Glu Ile
 130 135 140
 Thr Leu Asn Asp Lys Val Val Ser Thr Phe Lys Leu Glu Pro Glu Thr
 145 150 155 160
 Leu Leu Asp Glu Val Arg Ala Ser Gly Arg Ile Pro Leu Ile Ile Gly
 165 170 175
 Arg Gly Leu Thr Asn Lys Ala Arg Lys Phe Leu Gly Arg Arg Ile Gly
 180 185 190
 Ser Val Gln Lys Thr Phe Arg Pro Ser Ser Ala Leu Arg Leu His Phe
 195 200 205
 Ala

(2) INFORMATION FOR SEQ ID NO:876:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

Met Leu Ser Ala His Gln Pro Phe Lys Asn Tyr Pro Asp Leu Ile Lys
 1 5 10 15
 Lys Glu Leu Gln Glu His Asn Ala Tyr Ala Ser Val Ala Ser Gly Val
 20 25 30
 Pro Ala Met Cys Asp Gly Ile Thr Gln Gly Tyr Glu Gly Met Glu Leu
 35 40 45

Ser Leu Phe Ser Arg Asp Val Ile Ala Leu Ser Thr Xaa Val Gly Leu
 50 55 60
 Ser His Asn Val Phe Asp Gly Ala Phe Phe Leu Gly Val Cys Asp Lys
 65 70 75 80
 Ile Val Pro Gly Leu Leu Ile Gly Ala Leu Ser Phe Gly Asn Leu Ala
 85 90 95
 Ser Val Phe Val Pro Ser Gly Pro Met Val Ser Gly Ile Glu Asn Tyr
 100 105 110
 Lys Lys Ala Lys Ala Arg Gln Asp Phe Ala Met Gly Lys Ile Asn Arg
 115 120 125
 Glu Glu Leu Leu Lys Val Glu Met Gln Ser Tyr His Asp Val Gly Thr
 130 135 140
 Cys Thr Phe Tyr Gly Thr Ala Asn Ser Asn Gln Met Met Met Glu Phe
 145 150 155 160
 Met Gly Leu His Val Ala Asn Ser Ser Phe Ile Asn Pro Asn Asn Pro
 165 170 175
 Leu Arg Lys Val Leu Val Glu Glu Ser Ala Lys Arg Leu Ala Ser Gly
 180 185 190
 Lys Val Leu Pro Leu Ala Lys Leu Ile Asp Glu Lys Ser Ile Leu Asn
 195 200 205
 Ala Leu Ile Gly Leu Met Ala Thr Gly Gly Ser Thr Asn His Thr Leu
 210 215 220
 His Leu Ile Ala Ile Ala Asp Leu Val Gly
 225 230

(2) INFORMATION FOR SEQ ID NO:877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

Leu Met Trp Leu Lys Thr Leu Thr Leu Gln Thr Leu Asn Thr Asp Lys
 1 5 10 15
 Ala Leu Gln Glu Phe Ser Lys Thr Met Glu Ala Phe Lys Thr Lys Leu

20					25					30					
Ile	Gln	Ser	Ala	Asn	Asp	Val	His	Ser	Glu	Thr	Ser	Arg	Ala	Ala	Ile
		35					40					45			
Ala	Asn	Asp	Leu	Glu	Arg	Leu	Lys	Glu	His	Met	Ile	Asn	Val	Ala	Asn
	50					55					60				
Thr	Ser	Ile	Gly	Gly	Glu	Phe	Leu	Phe	Gly	Gly	Ser	Lys	Val	Asp	Arg
65					70					75					80
Pro	Pro	Ile	Asp	Ser	Asn	Gly	Lys	Tyr	His	Gly	Asn	Gly	Glu	Asp	Leu
				85					90					95	
Asn	Ala	Leu	Ile	Ser	Ser	Asp	Asn	Leu	Val	Pro	Tyr	Asn	Ile	Ser	Gly
		100						105					110		
Gln	Asp	Leu	Phe	Leu	Gly	Thr	Asp	Lys	Asp	Lys	His	Lys	Leu	Ile	Thr
	115						120					125			
Thr	Asn	Ile	Lys	Leu	Leu	Asn	Gln	Asn	Lys	Leu	Xaa	Pro	Asp	Val	Met
	130					135					140				
Asp	Ala	Leu	Glu	His	Ser	Ser	Leu	Pro	Glu	Glu	Val	Phe	Ile	Lys	Pro
145					150					155					160
Ser	Asp	Thr	Leu	Arg	Glu	Leu	Ile	Gly	Asp	Asn	Asp	Lys	Asn	Pro	Thr
				165					170					175	
Asn	Asp	Pro	Lys	Glu	Phe	Phe	Tyr	Leu	Gln	Gly	Ile	Arg	Pro	Asp	Gly
		180						185					190		
Ser	Ser	Phe	Lys	Glu	Lys	Phe	Ala	Leu	Asp	Lys	Ala	Tyr	Gln	Asn	Gln
		195					200						205		
Glu	Ser	Ala	Thr	Lys	Val	Ser	Asp	Leu	Leu	Asp	Lys	Ile	Gly	His	Ala
	210					215					220				
Tyr	Gly	Asn	Thr	Ser	Gln	Asn	Lys	Val	Val	Asp	Val	Ser	Leu	Asn	Asn
225					230					235					240
Trp	Gly	Gln	Ile	Glu	Ile	Lys	Asn	Leu	Thr	Pro	Gly	Ser	Glu	Asn	Leu
			245						250					255	
Asp	Phe	His	Leu	Ile	Ser	Ser	Asp	Gly	Asp	Phe	Asp	Asp	Leu	Asp	Ala
			260					265					270		
Leu	Arg	Ser	Ser	Gly	Lys	Arg	Val	Thr	Glu	Tyr	Val	Lys	Ser	Ala	Phe
		275					280					285			
Val	Thr	Asp	Arg	Ser	Leu	Ser	Gln	Val	Lys	Ala	Val	Pro	Asn	Met	Tyr
	290					295						300			
Asn	Pro	Lys	Val	Leu	Glu	Ile	Pro	Ser	Val	Phe	Val	Thr	Lys	Asp	Asn
305					310					315					320
Val	Leu	Ala	Asn	Lys	Asn	Thr	Lys	Leu	Ser	Glu	Ile	Phe	Gly	Asp	Lys
				325					330					335	

Val Glu Thr Leu Lys Ile Asn Ala Ser Arg Leu Gly Asp Glu Ser Ala
340 345 350

Ile Lys Ile Pro Asn Leu Pro Ile Asn Leu Asp Ile Pro Ile Leu Leu
355 360 365

Asp Val Lys Asn Ser Thr Ile Lys Asp Leu Lys Asp Ala Ile Lys Glu
370 375 380

Arg Phe Asn Asn Glu Gly Gly Cys Gly Asn
385 390

(2) INFORMATION FOR SEQ ID NO:878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

Leu Lys Ala Leu Asn Asp Cys Met Val Phe Phe His Lys Lys Ile Ile
1 5 10 15

Leu Asn Phe Ile Tyr Ser Leu Met Val Ala Phe Leu Phe His Leu Ser
20 25 30

Tyr Gly Val Leu Leu Lys Ala Asp Gly Met Ala Lys Lys Gln Thr Leu
35 40 45

Leu Val Gly Glu Arg Leu Val Trp Asp Lys Leu Thr Leu Leu Gly Phe
50 55 60

Leu Glu Lys Asn His Ile Pro Gln Lys Leu Tyr Tyr Asn Leu Ser Ser
65 70 75 80

Gln Asp Lys Glu Leu Ser Ala Glu Ile Gln Ser Asn Val Thr Tyr Tyr
85 90 95

Xaa Phe Lys Arg Cys Lys
100

(2) INFORMATION FOR SEQ ID NO:879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

Met	Lys	Phe	Leu	Lys	Phe	Phe	Ala	Ser	Ser	Val	Thr	Leu	Asp	Glu	Lys
1				5					10					15	
Phe	Leu	Met	Phe	Leu	Leu	Cys	Asn	Ala	Leu	Ser	Asn	Ala	Tyr	Lys	Asn
			20					25					30		
Ser	Asp	Leu	Phe	Ser	Phe	Ser	Lys	Gly	Phe	Leu	Gly	Ala	Phe	Leu	Ile
		35					40					45			
Gly	Phe	Val	Val	Tyr	Tyr	Gly	Cys	Ala	Leu	Ile	Pro	Lys	Lys	Arg	Leu
	50					55					60				
Lys	Tyr	Ser	Leu	Glu	Trp	Leu	Phe	Ile	Gly	Ser	Gly	Ile	Ile	Phe	Ser
65					70					75					80
Val	Ala	Glu	Ile	Phe	Thr	Leu	Phe	Met	Phe	Lys	Met	Pro	Phe	Ser	Lys
				85					90					95	
Gly	Leu	Ile	Asp	Thr	Leu	Leu	Ala	Thr	Asn	Ser	Ser	Glu	Thr	Met	Ala
			100					105					110		
Phe	Ile	Lys	Ser	Tyr	Lys	Asn	Tyr	Leu	Leu	Tyr	Tyr	Ala	Leu	Ile	Leu
		115					120					125			
Ile	Ala	Leu	Leu	Ile	Ala	Ile	Lys	Ile	Ile	Arg	Phe	Arg	Ala	Leu	Val
	130						135				140				
Pro	Gly	Val	Ile	Ala	Ser	Val	Leu	Gly	Leu	Ser	Ile	Leu	Thr	Ile	Gly
145					150					155					160
Ser	Val	Arg	Asn	Ile	Lys	His	Leu	Thr	Lys	Asn	Asp	Ala	Ile	Leu	Lys
			165						170					175	
Arg	Ser	Leu	Phe	Ser	Leu	Ser	Leu	Ala	Arg	Gly	Phe	Tyr	Ser	Ala	Tyr
			180					185					190		
Leu	Ser	Leu	Phe	Asp	Arg	Gln	Gln	Ala	Ile	Lys	Phe	Tyr	Ser	Phe	Leu
		195					200					205			
Asn	Asn	Leu	Tyr	Leu	Pro	Ser	Asp	Tyr	Leu	Ser	Ser	Thr	Gly	Asp	Ile
	210					215					220				
Ser	Asn	Val	Val	Leu	Val	Ile	Ala	Lys	Ala	Arg	Ala	Glu	Ile	Ser	Cys
225					230					235					240
Asn	Ser	Met	Ala	Ile	Ala	Phe	Leu	Ile	Ile	Pro	Tyr	Thr	Ser	Glu	Leu
			245					250						255	

Ala Asn Glu Arg Glu Arg Glu Arg Glu
 260 265

(2) INFORMATION FOR SEQ ID NO:880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

Met	Lys	Phe	Phe	Leu	Leu	Lys	Lys	Phe	Ser	Xaa	Phe	Leu	Asn	Thr	Gln	1	5	10	15
Thr	His	Phe	Asn	Leu	Lys	Arg	Leu	Asn	Ala	Ser	Ser	Phe	Leu	Leu	Glu	20	25	30	
Thr	Phe	Ser	Lys	Glu	Lys	His	Ala	Phe	Val	Val	Asp	Leu	Ser	Ala	Pro	35	40	45	
Tyr	Ile	Gly	Leu	Ser	Lys	Lys	Pro	Pro	Glu	Ser	Val	Leu	Lys	Asn	Thr	50	55	60	
Leu	Ala	Leu	Asp	Phe	Cys	Leu	Asn	Lys	Phe	Thr	Lys	Asn	Ala	Lys	Ile	65	70	75	80
Leu	Gln	Ala	Asn	Val	Ile	Asp	Asn	Asp	Arg	Ile	Leu	Glu	Ile	Lys	Gly	85	90	95	
Ala	Lys	Asp	Leu	Ala	Tyr	Lys	Ser	Glu	Thr	Phe	Ile	Leu	Arg	Leu	Glu	100	105	110	
Met	Ile	Pro	Lys	Lys	Ala	Asn	Leu	Met	Ile	Leu	Asp	Gln	Glu	Lys	Cys	115	120	125	
Val	Ile	Glu	Ala	Phe	Arg	Phe	Asn	Asp	Arg	Val	Ala	Lys	Asn	Asp	Ile	130	135	140	
Leu	Gly	Ala	Leu	Pro	Pro	Asn	Ile	Tyr	Glu	His	Gln	Glu	Glu	Asp	Leu	145	150	155	160
Asp	Phe	Lys	Gly	Leu	Leu	Asp	Ile	Leu	Glu	Lys	Asp	Phe	Leu	Ser	Tyr	165	170	175	
Gln	His	Lys	Glu	Leu	Glu	His	Lys	Lys	Asn	Gln	Ile	Ile	Lys	Arg	Leu	180	185	190	
Asn	Ala	Gln	Lys	Glu	Arg	Leu	Lys	Glu	Lys	Leu	Glu	Lys	Leu	Glu	Asp	195	200	205	

Pro	Lys	Thr	Leu	Gln	Leu	Glu	Ala	Lys	Glu	Leu	Gln	Thr	Gln	Ala	Ser	210	215	220	
Leu	Leu	Leu	Thr	Tyr	Gln	His	Leu	Ile	Asn	Arg	Arg	Glu	Asn	Arg	Val	225	230	235	240
Ile	Leu	Lys	Asp	Phe	Glu	Asp	Lys	Glu	Cys	Met	Ile	Glu	Ile	Asp	Lys	245	250	255	
Ser	Met	Pro	Leu	Asn	Ala	Phe	Ile	Asn	Lys	Lys	Phe	Thr	Leu	Ser	Lys	260	265	270	
Lys	Lys	Lys	Gln	Lys	Ser	Gln	Phe	Leu	Tyr	Leu	Glu	Glu	Glu	Asn	Leu	275	280	285	
Lys	Glu	Lys	Ile	Ala	Phe	Lys	Glu	Asn	Gln	Ile	Asn	Tyr	Val	Arg	Asp	290	295	300	
Ala	Ala	Glu	Glu	Ser	Val	Leu	Glu	Met	Phe	Met	Pro	Val	Lys	Asn	Ser	305	310	315	320
Lys	Ile	Lys	Arg	Pro	Met	Asn	Gly	Tyr	Glu	Val	Leu	Tyr	Tyr	Lys	Asp	325	330	335	
Xaa	Lys	Xaa	Gly	Leu	Gly	Lys	Thr	Lys	Lys	Arg	Ile	Ser	Ser	Phe	Tyr	340	345	350	
Lys	Thr	Gln	Xaa	Arg	Met	Ile	Xaa	Gly	Cys	Xaa						355	360		